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(54) Title: METHODS OF DIAGNOSIS OF CANCER COMPOSITIONS AND METHODS OF SCREENING FOR MODULA-TORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers. Related methods and compositions that can be used for diagnosis and treatment of those cancers are disclosed. Also described herein are methods that can be used to identify modulators of selected cancers.

METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

CROSS-REFERENCES TO RELATED APPLICATIONS

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This application claims priority to USSN 60/323,469, filed Setember 17, 2001; USSN 60/355,145, filed February 8, 2002; USSN 60/369,899, filed April 4, 2002; USSN 60/323,887, filed September 20, 2001; USSN 60/355,257, filed February 8, 2002; USSN 60/325,114, filed September 25, 2001; USSN 60/340,944, filed October 29, 2001; USSN 60/350,666, filed November 13, 2001; and USSN 60/372,246, filed April 12, 2002; each of which is incorporated herein by reference for all purposes.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in cancer; and to the use of such expression profiles and compositions in the diagnosis, prognosis, and therapy of cancer. The invention further relates to methods for identifying and using agents and/or targets that modulate cancer.

BACKGROUND OF THE INVENTION

Cancer is a major cause of morbidity in the United States. For example, in 1996, the American Cancer Society estimated that 1,359,150 people were diagnosed with a malignant neoplasm and 554,740 died from one of these diseases. Cancer is responsible for 23.9 percent of all American deaths and is exceeded only by heart disease as a cause of mortality (33 percent). Unfortunately, cancer mortality is increasing and sometime early in this century, cancer is expected to become the leading cause of mortality in the United States as it already is in Japan.

Cancers share the charactaristic of disordered control over normal cell division, growth, and differentiation. Their initial clinical manifestations are extremely heterogeneous, with over 70 types of cancer arising in virtually every organ and tissue of the body. Moreover, some of those similarly classified cancer types may represent multiple different molecular diseases. Unfortunately, some cancers may be virtually asymptomatic until late in the disease course, when treatment is more difficult, and prognosis grim.

Treatment for cancer typically includes surgery, chemotherapy, and/or radiation therapy. Although nearly 50 percent of cancer patients can be effectively treated using these methods, the current therapies all induce serious side effects which diminish quality of life. The identification of novel therapeutic targets and diagnostic markers will be important for improving the diagnosis and treatment of cancer patients.

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Recent advances in molecular medicine have increased the interest in tumor-specific antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues, preferably accessible from the vasculature and at the cell surface, and ideally not expressed in normal adult tissues. Expression in tissues that are dispensable for life, however, may be tolerated, e.g., reproductive organs. Examples of antigens that are currently available for the detection and treatment of certain cancers include Her2/neu and the B-cell antigen CD20. Humanized monclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. See Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. See Maloney, et al. (1997) Blood 90:2188-2195; Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

The elucidation of a role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is valuable for improving the current treatment of cancer patients. Accordingly, provided herein are molecular targets for therapeutic intervention in various defined cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate cancer.

SUMMARY OF THE INVENTION

The present invention provides methods for determining the presence or absence of a pathological cell in a patient, the method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-68 in a biological sample from the patient, thereby determining the presence or absence of the pathological cell. In certain embodiments of the method, the pathology is described in Table 1, including a cancer; the biological sample comprises isolated nucleic acids; the nucleic acids are mRNA; the biological sample is tissue from an organ which is affected by the pathology of Table 1, including a cancer; a further step is used of amplifying nucleic acids before the step of detecting

the nucleic acid; the detecting is of a protein encoded by the nucleic acid; the nucleic acid comprises a sequence as described in Tables 2A-68; the detecting step is carried out by using a labeled nucleic acid probe, utilizing a biochip comprising at sequence at least 80% identical to a sequence as described in Tables 2A-68, or detecting a polypeptide encoded by the nucleic acid; or the patient is undergoing a therapeutic regimen to treat the pathology of Table 1, or is suspected of having the pathology or cancer.

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Compostions are also provided, e.g., an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-68, including, e.g., those which are labeled; an expression vector comprising such nucleic acid; a host cell comprising such expression vector; an isolated polypeptide which is encoded by such a nucleic acid molecule comprising a sequence as described in Tables 2A-68; or an antibody that specifically binds the polypeptide. In particular embodiments, the antibody is: conjugated to an effector component, is conjugated to a detectable label (including, e.g., a fluorescent label, a radioisotope, or a cytotoxic chemical), an antibody fragment, or is a humanized antibody.

Additional methods are provided, including methods for specifically targeting a compound to a pathological cell in a patient, the method comprising administering to the patient an antibody, as described, thereby providing the targetting. Others include, e.g., methods for determining the presence or absence of a pathological cell in a patient, the methods comprising contacting a biological sample with an antibody, as described. In more particular methods, the antibody is: conjugated to an effector component, or to a fluorescent label; or the biological sample is a blood, serum, urine, or stool sample.

Further methods include those for identifying a compound that modulates a pathology-associated polypeptide, the method comprising steps of: contacting the compound with a pathology-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-68; and determining the functional effect of the compound upon the polypeptide. Another drug screening assay method comprises steps of: administering a test compound to a mammal having a pathology of Table 1 or a cell isolated therefrom; and comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-68 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of the pathology.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for various disorders, e.g., angiogenesis, fibrosis, and various defined forms of cancer, including metastatic cancer, as well as methods for screening for compositions which modulate such conditions. Also provided are methods for treating such disorders or cancers. See, e.g., American Society of Clinical Oncology (ed. 2001) ASCO Curriculum: Symptom Management Kendall/Hunt, ISBN: 0787277851; Bonadonna, et al. (2001) Textbook of Breast Cancer (2d ed.) Dunitz Martin, ISBN: 1853178241; Devita and Hellman (eds. 2001) Cancer Principles and Practice of Oncology (2 vols.), Lippincott Williams, ISBN: 0781723876; Howell, et al. (2001) Breast Cancer Isis Medical Media, ISBN: 1901865584; Kaye and Laws (2001) Brain Tumours: An Encyclopedic Approach (2d ed.) Churchill Livingstone, ISBN: 0443064261; Mihm, et al. (2001) The Melanocytic Proliferation: A Comprehensive Textbook of Pigmented Lesions Wiley-Liss, ISBN: 0471252719; Montgomery and Aaron (2001) Clinical Pathology of Soft-Tissue Tumors Marcel Dekker, ISBN: 0824702905; Petrovich, et al. (eds. 2001) Combined Modality of Central Nervous System Tumors (Medical Radiology) Springer Verlag, ISBN: 3540660534; Rosen (2001) Rosen's Breast Pathology Lippincott Williams and Wilkins, ISBN: 0781723795; Shah, et al. (2001) Oral Cancer Isis Medical Media, ISBN: 189906687X; Weiss and Goldblum (2001) Enzinger and Weiss's Soft Tissue Tumors (4th ed.) Mosby, ISBN: 0323012000; Abeloff, et al. 20 (eds. 2000) Clinical Oncology (2d ed.) Churchill Livingstone, ISBN: 044307545X; American Society of Clinical Oncology (ed. 2000) Cancer Genetics and Cancer Predisposition Testing Kendall/Hunt, ISBN: 0787276154; Fletcher (2000) Diagnostic Histopathology of Tumors (2 vols. 2d ed.) Churchill Livingstone, ISBN: 0443079927; Vogelzang (ed. 2000) Comprehensive Textbook of Genitourinary Oncology (2d ed.) Lippincott Williams and Wilkins, ISBN: 25 0683306456; Holland, et al. (eds. 2000) Holland-Frei Cancer Medicine (Book with CD-ROM 5th ed.) Decker, ISBN: 1550091131; Turrisi, et al. (2000) Lung Cancer Isis Medical Media, ISBN: 1901865428; Bartolozzi and Lencioni (eds. 1999) Liver Malignancies: Diagnostic and Interventional Radiology (Medical Radiology) Springer Verlag, ISBN: 3540647562; Gasparini (ed. 1999) Prognostic Variables in Node-Negative and Node-Positive Breast Cancer Kluwer, 30 ISBN: 0792384474; Hansen (ed. 1999) The LASLC Textbook of Lung Cancer: International Association for the Study of Lung Cancer Dunitz Martin, ISBN: 1853177083; Raghavan, et al. (eds. 1999) Textbook of Uncommon Cancer (2nd ed.) Wiley, ISBN: 0471929212; Thawley, et

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al. (eds. 1999) Comprehensive Management of Head and Neck Tumors (2 vols.) Saunders, ISBN: 0721655823; Whittaker and Holmes (eds. 1999) Leukemia and Related Disorders (3d ed.) Blackwell Science, ISBN: 0865426074; Aapro (ed. 1998) OncoMedia: Medical Oncology (CD-ROM) Elsevier Science, ISBN: 0080427480; Abeloff (1998) Clinical Oncology (Library 5 Version 2 CD-ROM Individual Version 2.0 Windows and Macintosh) Harcourt Brace, ISBN: 0443075557; Benson (ed. 1998) Gastrointestinal Oncology (Cancer Treatment and Research, CTAR 98) Kluwer, ISBN: 0792382056; Brambilla and Brambilla (eds. 1998) Lung Tumors: Fundamental Biology and Clinical Management (Vol 124) Marcel Dekker, ISBN: 0824701607; Canellos, et al. (eds. 1998) The Lymphomas Saunders, ISBN: 0721650309; Greenspan and 10 Remagen (1998) Differential Diagnosis of Tumors and Tumor-Like Lesions of Bones and Joints Lippincott Williams and Wilkins Publishers, ISBN: 0397517106; Hiddemann (ed. 1998) Acute Leukemias VII: Experimental Approaches and Novel Therapies (Haematologie Und Bluttransfusion, Vol 39), Springer Verlag, ISBN: 3540635041; Husband and Reznek (1998) Imaging in Oncology (2 vols.) Mosby, ISBN: 1899066489; Leibel and Phillips (eds. 1998) 15 Textbook of Radiation Oncology Saunders, ISBN: 0721653367; Maloney and Miller (eds. 1998) Cutaneous Oncology: Pathophysiology, Diagnosis, and Management Blackwell Science, ISBN: 0865425175; Mittal, et al. (eds. 1998) Advances in Radiation Therapy Kluwe, ISBN: 0792399811; Oldham (ed. 1998) Principles of Cancer Biotherapy (3d ed.) Kluwer, ISBN: 0792335074; Ozols (ed. 1998) Gynecologic Oncology Kluwer, ISBN: 0792380703; Parkin, et 20 al. (eds. 1998) Cancer Incidence in Five Continents (Iarc Scientific Publications, No 143) Oxford University Press, ISBN: 9283221435; Perez and Brady (eds. 1998) Principles and Practice of Radiation Oncology Lippincott Williams and Wilkins, ISBN: 0397584164; Black, et al. (eds. 1997) Cancer of the Nervous System Blackwell Science, ISBN: 0865423849; Bonadonna, et al. (1997) <u>Textbook of Breast Cancer:</u> A Clinical Guide to Therapy Blackwell Science, ISBN: 1853173487; Pollock (ed. 1997) Surgical Oncology Kluwer, ISBN: 25 0792399005; Sheaves, et al. (eds. 1997) Clinical Endocrine Oncology Blackwell Science, ISBN: 086542862X; Vahrson (1997) Radiation Oncology of Gynecological Cancers Springer Verlag, ISBN: 0387567682; Walterhouse and Cohn (eds. 1997) Diagnostic and Therapeutic Advances in Pediatric Oncology Kluwer, ISBN: 0792399781; Aisner (ed. 1996) Comprehensive Textbook of Thoracic Oncology Lippincott, Williams and Wilkins, ISBN: 0683000624; Bertino, et al. (eds. 1996) Encyclopedia of Cancer (3 vols.) Academic, ISBN: 012093230X; Cavalli, et al. (1996) Textbook of Medical Oncology Dunitz Martin, ISBN: 1853172901;

Peckham, et al. (eds. 1995) Oxford Textbook of Oncology (2-Vols.) Oxford University Press, ISBN: 0192616854; and Freireich and Kantarjian (eds. 1996) Molecular Genetics and Therapy of Leukemia (Cancer Treatment and Research, V. 84) Kluwer, ISBN: 0792339126.

In particular, identification of markers selectively expressed on defined cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of the diseases, e.g., as provided in Table 1, which subsets may actually require very different treatments. Moreover, the markers may also be important in related diseases to the specific disorders and cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

Tables 2B-66C provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in cancer samples, particularly sequences involved in angiogenisis, prostate cancer (including androgen independent and taxol resistant prostate cancer), breast cancer, colorectal cancer, cervical cancer, bladder cancer, lung cancer, ovarian cancer, uterine cancer, glioblastoma, Ewing sarcoma, and lung fibrosis. Tables 2A-67 also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

Definitions

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The term "cancer protein" or "cancer polynucleotide" or "cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably about 92%, 94%, 96%, 97%,

98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-68; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-68, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-68 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, preferably 90%, 91%, 93%, 95%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-68. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "cancer polypeptide" and a "cancer polynucleotide," include both naturally occurring or recombinant forms.

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A "full length" cancer protein or nucleic acid refers to a cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains elements normally contained in one or more naturally occurring, wild type cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival samples, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an

animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

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The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 70% identity, preferably 75%, 80%, 85%, 90%, 91%, 93%, 95%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known.

Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology

algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Wiley).

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Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negativescoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62

scoring matrix (see Henikoff and Henikoff (1992) <u>Proc. Natl. Acad. Sci. USA</u> 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences. See, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787. One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

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An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as E. coli, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein

encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified. In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

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The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain somebasic chemical structure as a naturally occurring amino acid. Amino acid mimetic refers to a chemical compound that has a structure that is different from the general chemical structure of an amino acid, but that functions similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variant" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the

genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

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As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton (1984) Proteins: Structure and Molecular Properties Freeman).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (eds. 2001) Molecular Biology of the Cell (4th ed.) Garland; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules

Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide.

"Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a

polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

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"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkahge, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphophoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, e.g., phosphoramidate (Beaucage, et al. (1993) <u>Tetrahedron</u> 49:1925-1963 and references therein; Letsinger (1970) <u>J. Org. Chem.</u> 35:3800-3803; Sprinzl, et al. (1977) <u>Eur. J. Biochem.</u> 81:579-589; Letsinger, et al. (1986) <u>Nucl. Acids Res.</u> 14:3487-499; Sawai, et al. (1984) <u>Chem. Lett.</u> 805, Letsinger, et al. (1988) <u>J. Am. Chem. Soc.</u> 110:4470-4471; and Pauwels, et al. (1986) <u>Chemica Scripta</u> 26:141-149), phosphorothioate (Mag, et al. (1991) <u>Nucleic Acids Res.</u> 19:1437-441; and U.S. Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) <u>J. Am.</u>

Chem. Soc. 111:2321-2322), O-methylphophoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach, Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-1897; Meier, et al. (1992) Chem. Int. Ed. Engl. 31:1008-1010; Nielsen (1993) Nature 365:566-568; 5 Carlsson, et al. (1996) Nature 380:207, all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy, et al. (1995) Proc. Natl. Acad. Sci. USA 92:6097-101; non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141, and 4,469,863; Kiedrowski, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; Letsinger, et al. (1994) 10 Nucleoside and Nucleotide 13:1597-xxx; Chapters 2 and 3 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs, et al. (1994) J. Biomolecular NMR 34:17; Horn, et al. (1996) Tetrahedron Lett. 37:743-xxx) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 in 15 Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins, et al. (1995) Chem. Soc. Rev. pp. 169-176). Several nucleic acid analogs are described in Rawls (page 35, June 2, 1997) C&E News.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in at least two advantages. The PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

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The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. The depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also

provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

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A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies, antigens, or epitope tags; and c) colored or fluorescent dyes. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ³H, ¹⁴C, ³²P, ³⁵S, or ¹²⁵I, electron-dense reagents, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable such as alkaline phosphatase, beta-galactosidase, or horseradish peroxidase. Methods are known for conjugating the antibody to the label. See, e.g., Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem, and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, enzymes or substrates, tags such as epitope tags, toxins; activatable moieties, chemotherapeutic agents; lipases; antibiotics; or radioisotopes, e.g., emitting "hard" beta, radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, e.g., covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals,

electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, methods using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

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As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein, or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed, or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such

nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

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Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. The protein may be isolated or purified away from some or most of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. An isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a skin cancer protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under

environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

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An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology) (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01-1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., about 10-50 nucleotides) and at least about 60° C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times

background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32°-48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50-65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications, Academic Press, NY.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is typically at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous references, e.g., Ausubel, et al. (eds. 1991 and supplements) <u>Current Protocols in Molecular Biology</u> Wiley.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the cancer protein or nucleic acid, e.g., a physiological, functional, physical, or chemical effect, such as the ability to decrease cancer. It includes ligand binding activity; cell viability; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing

metastasis; and other characteristics of cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the cancer protein, measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring growth, cellular proliferation, cell viability, cellular transformation, growth factor or serum dependence, tumor specific marker levels, invasiveness into Matrigel, tumor growth and metastasis in vivo, mRNA and protein expression, and other characteristics of cancer cells. The functional effects can be evaluated by many means, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

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"Inhibitors", "activators," and "modulators" of cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules, and the like. Such assays for inhibitors and activators include, e.g., expressing the cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of cancer can also be identified

by incubating cancer cells with the test compound and determining increases or decreases in the expression of 1 or more cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more cancer proteins, such as cancer proteins encoded by the sequences set out in Tables 1-68.

Samples or assays comprising cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (e.g., two to five fold higher relative to the control), more preferably 1000-3000% higher.

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The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (2d ed.) Wiley-Liss.

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy. See, Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes.

Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

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Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce F(ab)'2, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The F(ab)'2 may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the F(ab)'2 dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many techniques known. See, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985) pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other

organisms such as other mammals, may be used to express humanized antibodies.

Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of cancer-associated sequences

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In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or cancer tissue or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different cancer states, information regarding which genes are important (including both up-and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of a cancer.

The identification of sequences that are differentially expressed in cancer versus non-cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Maliganant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine the stage of cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression

profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the cancer expression profile. This may be done by making biochips comprising sets of the important cancer genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

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Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in cancer relative to normal tissues and/or non-malignant disease, or in different types of related diseases, herein termed "cancer sequences." As outlined below, cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the cancer sequences are from humans; however, cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (e.g., dogs, cats, etc.). Cancer sequences from other organisms may be obtained using the techniques outlined below.

Cancer sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the skin cancer sequences are recombinant nucleic acids. These nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the cancer sequences.

A cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

For identifying cancer-associated sequences, the cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and

non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing cancer samples with metastatic cancer samples from other cancers, such as lung, stomach, gastrointestinal cancers, etc. Samples of different stages of cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, and not limited to lung, heart, brain, liver, stomach, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the cancer screen that are expressed in a significant amount in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensible, e.g., female or male specific). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs were there expression.

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In a preferred embodiment, cancer sequences are those that are up-regulated in cancer; that is, the expression of these genes is higher in the cancer tissue as compared to non-cancer or non-malignant tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Uniformity among relevant samples is also preferred.

Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is available, see, e.g., Benson, et al. (1998) Nuc. Acids Res. 26:1-7; and http://www.ncbi.nlm.nih.gov/. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH. See

Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, cancer sequences are those that are down-regulated in the cancer; that is, the expression of these genes is lower in cancer tissue as compared to non-cancerous tissue. "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

Informatics

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The ability to identify genes that are over or under expressed in cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with cancer or related diseases. See Tables 1 and 3. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. Similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing cancer, e.g., the identification of cancer-associated sequences described herein, provide an abundance of information which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

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An array of methods for indexing and retrieving biomolecular information is available. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multidimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures. See also Baxevanis, et al. (2001) Bioinformatics: A Practical Guuide to the Analysis of Genes and Proteins Wiley; Mount (2001) Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Durbin, et al. (eds. 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge University Press; Baxevanis and Oeullette (eds. 1998) Bioinformatics: A Practical Guide to the

Analysis of Genes and Proteins (2d. ed.) Wiley-Liss; Rashidi and Buehler (1999)

Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et al. (eds. 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Humana Press; Higgins and Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach Oxford University Press; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

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In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

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The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer

program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values. See, e.g., Ewens and Grant (2001) Statistical Methods in Bioinformatics: An Introduction Springer-Verlag. Mathematical approaches can also be used to conclude whether similarities or differences in the gene expression exhibited by different samples are significant. See, e.g., Golub, et al. (1999) Science 286:531-537; Duda, et al. (2001) Pattern Classification Wiley; and Hastie, et al. (2001) The Elements of Statistical Learning:

Data Mining, Inference, and Prediction Springer-Verlag. One approach to determine whether a sample is more similar to or has maximum similarity with a given condition between the sample and one or more pools representing different conditions for comparison; the pool with the smallest vector angle is then chosen as the most similar to the biological sample among the pools compared.

30 Characteristics of cancer-associated proteins

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Cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the cancer protein is an

Intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Alberts, et al. (eds. 1994) Molecular Biology of the Cell (3d ed.) Garland). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity, and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

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An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. These motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322.

In another embodiment, the cancer sequences are transmembrane proteins.

Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity

and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site http://psort.nibb.ac.jp/). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, and interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors, and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves

be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

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In another embodiment, the cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of cancer nucleic acids

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As described above, cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

As detailed elsewhere, percent identity can be determined using an algorithm such as BLAST. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively. Alignment may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleotides than those of the nucleic acids described, the percentage of homology may be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, e.g., homology of sequences shorter than those of the sequences identified will be determined using the number of nucleosides in the shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, e.g., nucleic acids which hybridize under high stringency to a described nucleic acid, or its complement, or is also found on naturally occurring mRNAs is considered a cancer sequence. In another embodiment, less stringent hybridization conditions are used; e.g., moderate or low stringency conditions may be used; see Ausubel, supra, and Tijssen, supra.

The cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-68, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, using the sequences provided herein, extended sequences, in either direction, of the cancer genes can be obtained, using techniques well known for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, http://www.ncbi.nlm.nih.gov/UniGene/).

Once a cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant cancer nucleic acid can

be further used as a probe to identify and isolate other cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant cancer nucleic acids and proteins.

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The cancer nucleic acids of the present invention are used in several ways. In one embodiment, nucleic acid probes to the cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, RNAi, and/or antisense applications. Alternatively, cancer nucleic acids that include coding regions of cancer proteins can be put into expression vectors for the expression of cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and 15 the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8-100 bases long, with from about 10-80 bases being preferred, and from about 30-50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

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Nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, e.g., streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds, and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often, the substrate may contain discrete individual sites appropriate for individual partitioning and identification. The number of possible substrates is very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonJ, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. See WO 0055627.

Generally the substrate is planar, although other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube for flow-

through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups, and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

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In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside. In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChipTM technology.

Often, amplification-based assays are performed to measure the expression level of cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of cancer-associated RNA. Methods of quantitative amplification are well known.

Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) <u>PCR Protocols</u>, A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560-569, Landegren, et al. (1988) Science 241:1077-1080, and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat. Acad. Sci. USA 87:1874-1878), dot PCR, linker adapter PCR, etc.

Expression of cancer proteins from nucleic acids

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In a preferred embodiment, cancer nucleic acids, e.g., encoding cancer proteins, are used to make a variety of expression vectors to express cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press) to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in

the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the cancer protein. Numerous types of appropriate expression vectors and suitable regulatory sequences are known for a variety of host cells.

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In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known, and are useful in the present invention.

An expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoeffler, supra; and Kitamura, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:9146-9150.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known and will vary with the host cell used.

The cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a cancer protein, under the appropriate conditions to induce or cause expression of the cancer protein. Conditions appropriate for cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are Saccharomyces cerevisiae and other yeasts, E. coli, Bacillus subtilis, Sf9 cells, C129 cells, 293 cells, Neurospora, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line), and various other human cells and cell lines.

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In a preferred embodiment, the cancer proteins are expressed in mammalian cells. Mammalian expression systems may be used, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, supra). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenlyation signals include those derived from SV40.

Methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, are available, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of nonbacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the cancer protein in bacteria. The protein is either secreted into the growth media (grampositive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known, and include vectors for Bacillus subtilis, E. coli, Streptococcus cremoris, and Streptococcus lividans, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using techniques such as calcium chloride treatment, electroporation, and others.

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In one embodiment, cancer proteins are produced in insect cells using, e.g., expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors.

In a preferred embodiment, a cancer protein is produced in yeast cells. Yeast expression systems are well known, and include expression vectors for Saccharomyces cerevisiae, Candida albicans and C. maltosa, Hansenula polymorpha, Kluyveromyces fragilis and K. lactis, Pichia guillerimondii and P. pastoris, Schizosaccharomyces pombe, and Yarrowia lipolytica.

Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the cancer protein is a cancer peptide, the nucleic acid encoding the peptide may

be linked to other nucleic acid for expression purposes. Fusion with detection epitope tags can be made, e.g., with FLAG, His6, myc, HA, etc.

In a preferred embodiment, the cancer protein is purified or isolated after expression. Cancer proteins may be isolated or purified in a variety of ways depending on what other components are present in the sample and the requirements for purified product, e.g., natural conformation or denatured. Standard purification methods include ammonium sulfate precipitations, electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the cancer protein may be purified using a standard anticancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. See, e.g., Walsh (2002) Proteins: Biochemistry and Biotechnology Wiley, Hardin, et al. (eds. 2001) Cloning, Gene Expression and Protein Purification Oxford Univ. Press; Wilson, et al. (eds. 2000) Encyclopedia of Separation Science Academic Press; and Scopes (1993) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

Variants of cancer proteins

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Also included within one embodiment of cancer proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85%, and most preferably greater than 90%. In some embodiments the homology will be as high as about 93-95% or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques, as are outlined above for nucleic acid homologies.

Cancer proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of cancer proteins are portions or fragments of the wild type sequences herein. In addition, as

outlined above, the cancer nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence.

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In one embodiment, the cancer proteins are derivative or variant cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative cancer peptide will often contain at least one amino acid substitution, deletion, or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at many residue positions within the cancer peptide.

Also included within one embodiment of cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional, or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as a naturally occurring analogue, although variants can also be selected which have modified characteristics.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1-20 amino acids, although considerably larger insertions may be tolerated. Deletions generally range from about 1-20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions, or combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the

alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships described.

The variants typically exhibit essentially the same qualitative biological activity and will elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of cancer proteins as needed. Alternatively, the variant may be designed such that a biological activity of the cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

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Substantial changes in function or immunological identity are sometimes made by selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. Substitutions which generally are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g., serine or threone is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, valine, or alanine; (b) a cysteine or proline is substituted for (or by) another residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

Variants typically exhibit a similar qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the skin cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the cancer protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking cancer polypeptides to a water-

insoluble support matrix or surface for use in a method for purifying anti-cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl, or tyrosyl residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1992) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

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Another type of covalent modification of the cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence cancer polypeptide. Glycosylation patterns can be altered in many ways. Different cell types to express cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence cancer polypeptide (for O-linked glycosylation sites). The cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. See, e.g., WO 87/05330; pp. 259-306 in Aplin and Wriston (1981) CRC Crit. Rev. Biochem.

Removal of carbohydrate moieties present on the cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for

amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) <u>Arch. Biochem. Biophys.</u> 259:52-57 and Edge, et al. (1981) <u>Anal. Biochem.</u> 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases. See, e.g., Thotakura, et al. (1987) <u>Meth. Enzymol.</u> 138:350-359.

Another type of covalent modification of cancer comprises linking the cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

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Cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a cancer polypeptide fused to another heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxylterminus of the cancer polypeptide. The presence of such epitope-tagged forms of a cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are available. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Natl. Acad. Sci. USA 87:6393-6397).

Also included are other cancer proteins of the cancer family, and cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related cancer proteins from humans or other organisms. Particularly useful probe and/or PCR primer sequences include the unique areas of the cancer nucleic acid sequence. Preferred PCR primers are from about 15-35 nucleotides in length, with from about 20-30 being preferred, and may contain inosine as needed. The conditions for PCR reaction have been well described (e.g., Innis, PCR Protocols, supra).

In addition, cancer proteins can be made that are longer than those encoded by the nucleic acids of the Tables, e.g., by the elucidation of extended sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

Cancer proteins may also be identified as being encoded by cancer nucleic acids. Thus, cancer proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

Antibodies to cancer proteins

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In a preferred embodiment, when the cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from a protein sequence set out in the tables.

Methods of preparing polyclonal antibodies exist (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1-68 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum

albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). Various immunization protocols may be used.

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The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 59-103 in Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine, or human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for another antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to cancer protein are capable of reducing or eliminating a biological function of a cancer protein, in a naked form or conjugated to an effector moiety, as is described below. That is, the addition of anti-cancer protein antibodies (either polyclonal or preferably monoclonal) to cancer tissue (or cells containing cancer) may reduce or eliminate the cancer. Generally, at least a 25% decrease in activity, growth, size, or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

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In a preferred embodiment the antibodies to the cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be essentially performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human antibodies can also be produced using phage display libraries (Hoogenboom and Winter (1992) <u>J. Mol. Biol.</u> 227:381-388; Marks, et al. (1991) <u>J. Mol. Biol.</u> 222:581-597) or human monoclonal antibodies (e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) <u>Monoclonal Antibodies and Cancer Therapy</u> Liss; and Boerner, et al. (1991) <u>J. Immunol.</u> 147:86-95). Similarly, human antibodies can be made by introducing human immunoglobulin loci into

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transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-851; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of cancer with an antibody raised against cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted cancer protein, e.g., in autocrine signaling.

In another preferred embodiment, the cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane cancer protein. The antibody may be a competitive, non-

competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the cancer protein. The antibody may also be an antagonist of the cancer protein. Further, the antibody may prevent activation of the transmembrane cancer protein, or may induce or suppress a particular cellular pathway. In one aspect, when the antibody prevents the binding of other molecules to the cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF-α, TNF-β, IL-1, INF-γ, and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, cancer may be treated by administering to a patient antibodies directed against the transmembrane cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a cancer protein. In another aspect the therapeutic moiety may modulate the activity of molecules associated with or in close proximity to a cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase or protein kinase activity associated with cancer, or be an attractant of other cells, such as NK cells.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane cancer proteins not only serves to increase the local

concentration of therapeutic moiety in the cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

In another preferred embodiment, the cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto may contain a signal for that target localization, e.g., a nuclear localization signal.

The cancer antibodies of the invention specifically bind to cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related sequences is often also important.

Detection of cancer sequence for diagnostic and therapeutic applications

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In one aspect, the RNA expression levels of genes are determined for different cellular states in the cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing cancer) and in cancer tissue (and in some cases, for varying severities of cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus

permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; e.g., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChipTM expression arrays. See, Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis, and RNase protection. As outlined above, preferably the change in expression (e.g., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

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Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to cancer genes, e.g., those identified as being important in a cancer or disease phenotype, can be evaluated in a cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the cancer protein are detected. Although DNA or RNA encoding the cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA, or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after

immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method, detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxygenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a cancer protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

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In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane, or intracellular proteins) are used in diagnostic assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of cancer, e.g., for prognostic or diagnostic purposes. Detection of these proteins in putative cancer tissue allows for detection, prognosis, or diagnosis of cancer or similar disease, and for selection of therapeutic strategy. In one embodiment, antibodies are used to detect cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the cancer protein is detected, e.g., by immunoblotting with antibodies raised against the cancer protein.

In another preferred method, antibodies to the cancer protein find use in in situ imaging techniques, e.g., in histology. See, e.g., Asai, et al. (eds. 1993) Methods in Cell Biology:

Antibodies in Cell Biology (vol. 37) Academic Press. In this method, cells are contacted with from one to many antibodies to the cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a

detectable label. In another method the primary antibody to the cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of cancer proteins. Many other histological imaging techniques are also provided by the invention.

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In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of cancer proteins. Antibodies can be used to detect a cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous cancer protein.

In a preferred embodiment, in situ hybridization of labeled cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, a diagnosis, a prognosis, or a prediction may be based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple genes may be useful in various combinations. As above, cancer probes may be attached to biochips for the detection and quantification of cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

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In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-88; Heid (1996) Genome Res. 6:986-994.

In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the cancer phenotype or an identified physiological function of a cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be

monitored, e.g., through the use of antibodies to the cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell.

Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Modulators of cancer

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Expression monitoring can be performed to identify compounds that modify the expression of one or more cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate cancer, modulate cancer proteins, bind to a cancer protein, or interfere with the binding of a cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the cancer phenotype or the expression of a cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induced a cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or

less than 1500, or less than 1000, or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs, or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of a cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

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In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis. See, e.g., Janzen (2002) High Throughput Screening: Methods and Protocols Humana; Devlin (ed. 1997) High Throughput Screening: The Discovery of Bioactive Substances Dekker; and Mei and Czarnik (eds. 2002) Integrated Drug Discovery Techniques Dekker.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be

synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37:1233-1251).

Preparation and screening of combinatorial chemical libraries is well known. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat. Acad. Sci. USA 90:6909-6913, vinylogous polypeptides (Hagihara, et al. 10 (1992) J. Amer. Chem. Soc. 114:6568-570), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-662), oligocarbamates (Cho, et al. (1993) Science 261:1303-1305), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658-xxx). See, generally, 15 Gordon, et al. (1994) J. Med. Chem. 37:1385-1401, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33 Baum 20 (Jan 18, 1993) C&EN; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

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A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices are suitable for use with the present invention. The nature and

implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

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The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of cancer gene transcription, inhibition, or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate entire procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins. describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test

compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5-30 amino acids, with from about 5-20 amino acids being preferred, and from about 7-15 being particularly preferred. The peptides may be digests of naturally occurring proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines, or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of cancer can also be nucleic acids, as defined above.

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As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of prokaryotic or eukaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in

vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

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In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

These assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246, and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate, and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used

to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states of individual genes, forming a gene expression profile.

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Screens are performed to identify modulators of the cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition, screens can be done for genes that are induced in response to a candidate agent or treatment process. After identifying a modulator based upon its ability to suppress a cancer expression pattern leading to a normal expression pattern (or its converse), or to modulate a single cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated cancer tissue reveals genes that are not expressed in normal tissue or cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for cancer genes or proteins. In particular, these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of cancer cells that have an associated cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell

surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

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Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on cancer activity. By defining such a signature for the cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins" or a "cancer modulatory protein". The cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the cancer modulatory protein is a fragment. In a preferred embodiment, the cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of the Tables. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequences are sequence variants as further described herein.

Preferably, the cancer modulatory protein is a fragment of about 14-24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine.

In one embodiment the cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the cancer protein is conjugated to BSA.

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Measurements of cancer polypeptide activity, or of cancer or the cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, a cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5-48 hours. In one embodiment, the cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA, and the like with an antibody that selectively binds to the cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNAse protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or

the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins." The cancer protein may be a fragment, or alternatively, the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

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In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a cancer protein and a candidate compound, and determining the binding of the compound to the cancer protein. Preferred embodiments utilize the human cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes, and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflonTM, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not

sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein, or other innocuous protein or other moiety.

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In a preferred embodiment, the cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.), and the like.

The determination of the binding of the test modulating compound to the cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ¹²⁵I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (e.g., a cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between about 4-40° C. Incubation

periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1-1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

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In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the cancer protein and thus is capable of binding to, and potentially modulating, the activity of the cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent.

Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the cancer proteins. In one embodiment, the methods comprise combining a cancer protein and a competitor in a first sample. A second sample comprises a test compound, a cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native cancer protein, but cannot bind to modified cancer proteins. The structure of the cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein.

Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

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A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc., which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting cancer cell division is provided. The method comprises administration of a cancer inhibitor. In another embodiment, a method of inhibiting cancer is provided. The method may comprise administration of a cancer inhibitor. In a further embodiment, methods of treating cells or individuals with cancer are provided, e.g., comprising administration of a cancer inhibitor.

In one embodiment, a cancer inhibitor is an antibody as discussed above. In another embodiment, the cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are available, as described below.

Soft agar growth or colony formation in suspension

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Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described, e.g., in Freshney (1998) <u>Culture of Animal Cells: A Manual of Basic Technique</u> (3d ed.) Wiley-Liss; Freshney (2000) <u>Culture of Animal Cells: A Manual of Basic Technique</u> (4th ed.) Wiley-Liss; and Garkavtsev, et al. (1996) <u>Nature Genet.</u> 14:415-20.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (2000), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. See, Freshney (1998), supra.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) <u>J. Natl. Cancer Insti.</u> 37:167-175; Eagle, et al.(1970) <u>J. Exp. Med.</u> 131:836-879); Freshney, supra. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

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Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly, tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal. counterparts. See, e.g., Folkman (1992) Sem. Cancer Biol. 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1998), supra. Also, see, Unkeless, et al. (1974) <u>J. Biol. Chem.</u> 249:4295-4305; Strickland and Beers (1976) <u>J. Biol. Chem.</u> 251:5694-5702; Whur, et al. (1980) <u>Br. J. Cancer</u> 42:305-312; Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) <u>Biological Responses in Cancer</u> Plenum; Freshney (1985) <u>Anticancer Res.</u> 5:111-130.

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate cancer-associated sequences.

Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved,

or by prelabeling the cells with ¹²⁵I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), supra.

Tumor growth in vivo

Effects of cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the cancer gene is disrupted or in which a cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous cancer gene with a mutated version of the cancer gene, or by mutating the endogenous cancer gene, e.g., by exposure to carcinogens.

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A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is reimplanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288-1292). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) <u>J. Natl. Cancer Inst.</u> 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) <u>Br. J. Cancer</u> 38:263-272; Selby, et al. (1980) <u>Br. J. Cancer</u> 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10⁶ cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of cancer Antisense and RNAi Polynucleotides

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In certain embodiments, the activity of a cancer-associated protein is down-regulated, or entirely inhibited, by the use of an inhibitory or antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species. Analogs are comprehended by this invention so long as they function effectively to hybridize with the cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for cancer molecules. A preferred antisense molecule is for a cancer sequences in the Tables, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14-30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) <u>Sciencexpress</u> (21March2002); Sharp (1999) <u>Genes Dev.</u> 13:139-141; and Cathew (2001) <u>Curr. Op. Cell Biol.</u> 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be

effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) <u>Nature</u> 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

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In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) <u>Adv. in Pharmacology</u> 25: 289-317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990)

Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No.

5,254,678. Methods of preparation are described in, e.g., WO 94/26877; Ojwang, et al. (1993)

Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human

Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126.

Polynucleotide modulators of cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-cancer antibody that reduces or eliminates the biological activity of an endogenous cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic

acid encoding a cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the cancer sequence is down-regulated in cancer, such state may be reversed by increasing the amount of cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous cancer gene or administering a gene encoding the cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/0386.

Alternatively, e.g., when the cancer sequence is up-regulated in cancer, the activity of the endogenous cancer gene is decreased, e.g., by the administration of a cancer antisense or other inhibitor, e.g., RNAi.

In one embodiment, the cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to cancer proteins. Similarly, the cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The cancer antibodies may be coupled to standard affinity chromatography columns and used to purify cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the cancer protein.

20 Methods of identifying variant cancer-associated sequences

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Without being bound by theory, expression of various cancer sequences is correlated with cancer. Accordingly, disorders based on mutant or variant cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant cancer genes, e.g., determining all or part of the sequence of at least one endogenous cancer gene in a cell. In a preferred embodiment, the invention provides methods of identifying the cancer genotype of an individual, e.g., determining all or part of the sequence of at least one cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced cancer gene to a known cancer gene, e.g., a wild-type gene.

The sequence of all or part of the cancer gene can then be compared to the sequence of a known cancer gene to determine if any differences exist. This can be done using known

homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the cancer gene of the patient and the known cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the cancer genes are used as probes to determine the number of copies of the cancer gene in the genome.

In another preferred embodiment, the cancer genes are used as probes to determine the chromosomal localization of the cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the cancer gene locus.

10 Administration of pharmaceutical and vaccine compositions

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In one embodiment, a therapeutically effective dose of a cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable using known techniques. See, e.g., Ansel, et al. (1999) Pharmaceutical Dosage Forms and Drug Delivery Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharmaceut. Assn.; and Pickar (1998) Dosage Calculations Thomson. Adjustments for cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary. U.S. Patent Application No. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in cancer.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the cancer proteins and modulators may be directly applied as a solution or spray.

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The pharmaceutical compositions of the present invention comprise a cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid, and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts, and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are available.

The compositions for administration will commonly comprise a cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents, and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate, and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., (1980) Remington's Pharmaceutical Science (18th ed.) Mack, and Hardman and Limbird (eds. 2001) Goodman and Gilman: The Pharmacologial Basis of Therapeutics (10th ed.) McGraw-Hill.

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent.

The compositions containing modulators of cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender,

administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present cancer protein-modulating compounds can be administered alone or in combination with additional cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

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In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the Tables, such as RNAi, antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors, and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA, or other foreign genetic material into a host cell (see, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the cancer coding regions) can be administered in a gene therapy application. These cancer genes can include inhibitory applications, e.g., as inhibitory RNA, gene therapy (e.g., for incorporation into the genome), or antisense compositions.

Cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses. Such vaccine compositions can

include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341-349), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294,; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in 5 immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 10 379, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-540; Kieny, et al. (1986) Bio/Technology 4:790-795; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al. 15 (1995) Nature Med. 1:649-653), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al., p 423, in Kaufmann (ed. 1996) Concepts in Vaccine Development de 20 Gruyter; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis, or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, 30 Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron, or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes;

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biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff et. al. (1990) Science 247:1465-1468, as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gum") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

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For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors are availablel for therapeutic administration or immunization, e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like. See, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing a cancer gene or portion of a cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a cancer patient. The cancer gene used for DNA vaccines can encode full-length cancer proteins, but more preferably encodes portions of the cancer proteins including peptides derived from the cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a cancer gene. For example, cancer-associated genes or sequence encoding subfragments of a cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure

provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment, cancer genes find use in generating animal models of cancer. When the cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein inhibitory or antisense RNA directed to the cancer gene will also diminish or repress expression of the gene. Animal models of cancer find use in screening for modulators of a cancer-associated sequence or modulators of cancer. Similarly, transgenic animal technology, including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the cancer protein. When desired, tissue-specific expression or knockout of the cancer protein may be necessary.

It is also possible that the cancer protein is overexpressed in cancer. As such, transgenic animals can be generated that overexpress the cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods will find use as animal models of cancer and are additionally useful in screening for modulators to treat cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

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For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications, such kits may include at least one of the following: assay reagents, buffers, cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative cancer polypeptides or polynucleotides, small molecule inhibitors of cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials

typically comprise written or printed materials, they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to, electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing cancer-associated activity. Optionally, the kit contains biologically active cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will typically be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

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Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Table 1 lists medical conditions, abnormalities, or organs affected by disease, referred to in Tables 2A-68, for which markers have been identified, and other related medical conditions (including various stages and/or metastases) in which those markers will also be useful, e.g., in therapeutic, diagnostic, prognostic, subsetting, vaccine, and other uses.

od vessels/anglogenesis: hemangiomas, lymphangiomas, wound healing, tissue remodeling, psoriasis, ischemic, heart disease, inflammatory diseases (e.g., arthritis, asthma, chronic branchitis), atheroscierosis, endometriosis, presumed ocular histoplasmosis syndrome, hypoxia, solid tumors, lymphomas, autoimmune diseases (e.g., RA, SLE, juvenile chronic arthritis, pigmented vibonodular synovitis, etc.), retinal neovascularization syndromes (e.g., diabetic retinopathy, macutar degeneration, presumed ocular histoplasmosis syndrome, etc.), scleritis/conjunctivitis, hypertrophic scars (teatoid), birth control, uterine throtic

bladder: cardinoma in situ, papillary cardinomas, transitional cell cardinoma bone marrow: Ewing sarcoma, sarcomas arising from skeletal and extreskeletal connective tissues, including the peripheral nervous system

10 brain: giloblastoma, oligodendroglioma, anablastic astrocytoma, meningioma, medulablastoma, neuroblastoma, ependymoma, schwaruroma, craniopharyngioma, pineoblastoma, pineocytoma

breast ductal carcinoma in situ, lobular carcinoma in situ

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cervic cancer of the cervic, vagina, or vulva color/vagina, or vulva 15

esophagus: premalignant or predisposing conditions (e.g., esophagilis), squamous cell cancers (e.g., cancers of the head and neck, tung, or cervix), gastrodigestive carcinomas (e.g., cancers of the stomach, colon, or rectum) 20

(e.g., cancers of the stomach, coten, or rectum)
birosis: lung fibrosis (diopathic pulmonary fibrosis, hypersensitivity pneumonitis,interstitial pneumonitis, nonspecific Idiopathic pneumonitis), chronic obstructive pulmonary disease
(e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, cirmosis (liver fibrosis), renal fibrosis, scienderma, wound heating
head end neck: tumors of the nesad cavity, paranesal sinuses, nasopharyru, oral cavity, oral pharyru, ip, laryru, hypopharyru, salivary glands, paragangtiomas, esophagus
kidney: clear cell (nonpapillary) carcinoma, papillary carcinoma, chromophobe renal carcinoma, hypemephroma, adenocarcinoma, sporadic renal carcinomas, hereditary renal
carcinomas (von Hippel-Lindau disease), carcinoma of the renal pelvis, ureteral carcinoma, fibroma, papillary adenoma, anglomyotipoma, oncocytoma
leukocytes; caute lymphotiastic leukemia/lymphoma, matignant transformation of immature, precursor 8 (pre-8) or precursor 1 (pre-11) lymphocytes, or lymphoblastis, erthritis,
Inflammation, wound heating 25

Inflammation, wound healing

liver. hepatilis (e.g., types A, B, C), benign epithelial tumors and tumor bile conditions, primary malignant epithelial tumors, primary malignant mesenchymal tumors, tumors of the grafibladder or bile duct

30 lung: lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinold, ung: ung cancer, smar cen ung carcinoma (oar cen carcinoma), non-smar cen carcinomas (e.g., squamous cen carcinoma, acenocarcinoma, iarge cen ung carcinoma, carcinom, granulomatous), fibrosts (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitied pneumonitis, non-specific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), estima, bronchitectasis, escophageal cancer ovary: ovarian carcinoma (e.g., epithelial (serous tumors, mucinous tumors, endometricid tumors), gérm cell (e.g., teratomas, chronicarcinomas, polyembryomas, embryomat carcinoma, endodermal sinus tumor, dysgerminoma, gonadoblastoma), stromal carcinomas (e.g., granulosal stromal cell tumors)), fallopian tube carcinoma, peritoneal carcinoma,

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pancreas: adenocarcinoma, ductal adenocarcinoma, mucinous cyst adenocarcinoma, acinar cell carcinoma, unclassified large cell carcinoma, small cell carcinoma pancreatoblastoma, duct-ectatic mucin-hypersecreting turnor, mucinous cyst adenoma, pantillary cystic neoplasm, serous cyst adenoma, diabetes mellits, chronic pancreatitis prostate: epithelial neoplasms (e.g., adenocarcinoma, small cell turnors, transitional cell carcinoma, carcinoma in situ, and basel cell carcinoma), carcinosarcoma, non-epithelial neoplasms (e.g., mesenchymal and lymphoma), germ cell turnors, prostatic intreprihelial neoplasia (PIN), hormone independent prostate cancer, benign prostate hyperplasia,

skin/metanoma: metanoma, tentigo (common benign localized hyperplasia of metanocytes), nevocellular nevi (congenital or acquired neoplasm of metanocytes), actinic keratosis

(overgrowth of outer layers of skin), basel cell carcinoma, Merkel cell carcinoma, benign fibrous histocytons (dermal neoplasms of fibroblasts and histocytons) dermal officerant control of the skin), xanthomas (tumor-like collections of foamy histocytes within the dermis), dermal vascular tumors, sebornheic kerstoses (benign tumor), ecanthosis nigricans (benign or malignant hyperplasta and hyperplastalion of skin), and squamous cell carcinomas of the skin, lung, carrix, esophagus, utarus, head, neck, or bladder

stomach: edenocarcinoma, squamous cell carcinoma, adenoacanthoma, carcinoid, leiomyosarcoma, gastrifis (chronic atrophic, H. pylori associated), hyperplastic polyps, lipoma, leiomyoma, esophageal adenocarcinomas

testicles: germ cell tumors (including seminomas, embryonal carcinomas, teretomas, choriccarcinomas, yolk sac tumors), sex chord stromal tumors (including Leydig cell tumors, Sertoli cell tumors, and Granulosa cell tumors), germ cell and gonadal stromal elements (e.g., gonadoblestomas), adnaval and paratesticular tumors (e.g., mesothellomas, soft tissue sarcomas, and adnaval of the rete testes), miscellaneous neoplasms (including carcinoid, lymphoma, and cysts)

uterus: epithelial lumors (e.g., endometrioid, papillary endometrioid, papillary serous, clear cell, mucinous), mesenchymal tumors (e.g., endometrial stromal sarcoma, leiomyosarcoma, nonspecific sarcomas), mixed lumors (e.g., malignant mixed mullerian tumors, adenosarcoma)

55 Tebles 28-66C list accession numbers for Pkeys lacking UnigenetD's for Tables 2A-66C, respectively. For each probeset is listed gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Tables 2C-66C list genomic positioning for Pikeys tacking Unigene ID's and accession numbers in Tables 2A-66C, respectively. For each predicted exon is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed. 60

TABLE 2A: ABOUT 1031 GENES UP-REGULATED IN ACUTE LYMPHOCYTIC LEUKEMIA (ALL)

Table 2A lists about 1031 genes up-regulated in acute lymphocytic leukemia (ALL) compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Eos Hu01 GeneChip array such that the ratio of "average" leukemia to "average" normal adult tissues was greater than or equal to 1.7. The "average" teukemia level was set to the 85° percentile amongst various ALL samples. The "average" normal adult tissue level was set to the 85° percentile amongst various non-malignant tissues. In order to 65 remove gene-specific background levels of non-specific hybridization, the 7.5h percentile value amongst various non-matignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkev:

Unique Eos probeset Identifier number Exemplar Accession number, Genbank accession number Unigeneil):

Unigene number Unigene gene title Unigene Title:

	Traile of Refice that the Hotel and							
75	Pkey 100458 113089	ExAcc \$74019 T40707	UniGeneID Hs.247979 Hs.270862	UniGene Tille pre-B lymphocyte gene 1 ESTs	R1 46.8 20.4			
	106956 101447	R06428 M21305	Hs.226351	ESTs gb:Human alpha satellite and satellite 3	15.8 13.8			
80	113009 126947 100893	T23699 Z40778 BE245294	Hs.7246 Hs.191837 Hs.180789	ESTs ESTs S164 protein	12.5 11.4 11.1			
	101050 132114	AU077324 NM_006152	Hs.1832 Hs.40202	neuropepilda Y lymphoid-restricted membrane protein	11.0 10.7			

	404004	4 4 504 604	11-0005		
	101304 105687	AA001021 AA767526	Hs.6665 Hs.22030	thyroid hormone receptor interactor 8	10.4
	112727	T91029	Hs.15069	paired box gene 5 (B-cell lineage specif ESTs	9.1 9.0
_	109788	T79971	Hs.12432	Homo sepiens clone 24407 mRNA sequence	8.7
5	113374	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.8
	130466	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	7.7
	109384 112602	AA219172	Hs.86849	ESTs	7.6
	125278	AW004045 Al218439	Hs.203365 Hs.129998	ESTs enhancer of polycomb 1	6.6
10	112167	N99591	Hs.25587	ESTs, Weakly similar to T00329 hypotheti	6.5 6.4
	116355	AA789133	Hs.88650	ESTs	5.8
	123440	AI733692	Hs.112488	ESTs	5.5
	100918	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	5.4
15	101879 109260	AA176374 AW978515	Hs.243886	nuclear autoantigenic sperm protein (his	5.4
13	129213	A1146494	Hs.131915 Hs.109525	KIAA0863 protein	5.4
	120809	AA346495	110.103023	ESTs, Weakly similar to IRX2_HUMAN IROQU gb:EST52657 Fetal heart II Homo septens	5.4 5.4
	105498	H68279	Hs.24937	transformer-2 alpha (htra-2 alpha)	5.1
20	114840	AA447591	Hs.87359	ESTs, Highly similar to RB18_HUMAN RAS-R	5.0
20	103304	BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	4.9
	113983	W87415	Hs.55298	HLA-B associated transcript-1	4.8
	115844 120712	Al373062 AF193339	Hs.332938 Hs.102506	hypothetical protein MGC5370 eukaryotic translation initiation factor	4.8
	107794	AA019255	16.102500	gb:ze56e10.s1 Soares retina N2b4HR Homo	4.8 4.7
25	135101	U82275	Hs.94498	leukocyte immunoglobulin-like receptor,	4.6
	129898	AI672731	Hs.13258	ESTs	4.6
	113494	T91451	Hs.86538	ESTs	4.6
	115004 113074	AA329340 AK001335	Hs.4867	mannosyl (alpha-1,3-)-glycoprotein beta-	4.5
30	112326	R55822	Hs.31137 Hs.4268	protein tyrosine phosphatase, receptor t ESTs	4.5 4.4
	105169	BE245294	Hs.180789	S164 protein	4.4
	117048	H89732	Hs.230113	EST	4.3
	123133	AA487264	Hs.154974	Homo saplens mRNA; cDNA DKFZp667N064 (fr	4.3
35	111394	AA412227	Hs.16131	hypothetical protein FLJ12876	4.3
55	106112 114414	AL117518 AW152166	Hs.3686 Hs.182113	KIAA0978 protein ESTs	4.2
	125219	AI804331	Hs.99423	ATP-dependent RNA helicase	4.2 4.2
	114995	AA769266	Hs.193657	ESTs	4.2
40	123338	AA504249	Hs.187585	ESTs	4.1
40	126666	AA648888	Hs.151999	EST8	4.1
	112908 116640	8E281000 X89984	Hs.3530	TLS-associated serine-arginine protein 2	4.1
	109292	AW975746	Hs.211563 Hs.188662	B-ceil CLL/lymphoma 7A KIAA1702 protein	4.0
	131724	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	4.0 4.0
45	119772	AJ250839	Hs.58241	gene for serine/(hreonine protein kinase	4.0
	134453	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	4.0
	123562 103226	AA177088 X75042	Hs.190065	ESTS	4.0
	127610	AA960867	Hs.44313 Hs.150271	v-rei avian reticuloendotheliosis viral ESTs, Highly similar to unnamed protein	3.9
50	119873	AI660149	Hs.44865	lymphoid enhancer-binding factor 1	3.9 3.9
	115553	AJ275986	Hs.71414	transcription factor (SMIF gens)	3.9
	131844	AJ419294	Hs.324342	ESTs	3.8
	123360 111180	AA532718	Hs.178604	ESTs	3.8
55	129426	AI798851 AF077953	Hs.283108 Hs.111323	hemoglobin, gamma G Protein inhibitor of activated STAT X	3.8
	105434	AA252111	Hs.15200	EST8	3.8 3.8
	119073	BE245360	Hs.279477	ESTs	3.8
	127003	AW816515		ATPase, Class V, type 100	3.7
60	118325 115998	T51138 AA448488	Hs.90489	ESTs	3.7
00	119830	AW054922	Hs.338829 Hs.53478	ribosomai protein L44 Homo sepiens cDNA FLJ 12366 fis, clone MA	3.7
	104584	AA704538	Hs.193777	ESTs	3.7 3.6
	105212	AA205334	Hs.324278	Homo sapiens mRNA; cDNA DKFZp566M063 (f	3.6
65	109223	AW000714		ESTs	3.6
05	112605	R79374	Hs.29852	ESTs	3.5
	105733 120562	AA767669 BE244580	Hs.10242 Hs.302267	ESTs hypothetical protein FLJ10330	3.5
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	3.5 3.5
70	127834	AW301022		EST	3.5
70	115147		Hs.38399	hypothetical protein MGC2454	3.5
	115185		Hs.105461	hypothetical protein FLJ20357	3.5
	113921 115835	AW976530 AA521410		hypothetical protein FLJ22402 ESTs	3.5
	123503			ESTs, Wealdy similar to 178885 serine/th	3.5 3.5
75	128527	AA504583		transcription factor 3 (E2A immunoglobul	3.5 3.4
	128743		Hs.2730	haterogeneous nuclear ribonucleoprotein	3.4
	117031		11- 4000-0	gb:yw21a02.s1 Morton Fetal Cochlea Homo	3.4
	123149 102581		Hs.105676 Hs.77256	ESTS	3.4
80	103158			enhancer of zeste (Drosophila) homolog 2 hematopoletically expressed homeobox	3.4
	107599	AW664072		ESTs	3.4 3.4
	125556	AB033064	Hs.334806	KIAA1238 protein	3.4
	103331	AI825463	Hs.147996	protein kinase, X-linked	3.4

	114387	AIEEE141	(l- 40		
	119040	AI655141 R02394	Hs.107720 Hs.269436	ESTs, Weakly similar to A54295 Interfer ESTs, Moderately similar to PC4259 ferri	3.4
	100305	NM_004941	Hs.171872	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeo	3.4 3.4
5	129818 133445	771092 AC005262	Hs.172572	nypothetical protein FLJ20093	3.3
•	132111	AW500857	Hs.73797 Hs.40137	guantne nucleotide binding protein (G pr anaphase-promoting complex 1; melotic ch	3.3
	105292	AF128542	Hs.166846	polymerase (DNA directed), epsilon	3.3 3.3
	118397 118922	BE139479 AW206193	Hs.161492 Hs.91065	ESTs	3.3 3.2
10	132344	AW977189	Hs.45719	hypothetical protein DKFZp761B2423 KIAAD823 protein	3.2
	129889	AA810932	Hs.131899	ESTs. Weakly similar to T00370 hypotheti	3.2 3.2
	123670 116291	A1189844 AW410377	Hs.112708 Hs.41502	ESTS, Moderately strailar to ZN91_HUMAN Z	3.2
1.5	105289	AB020638	Hs.103000	hypothetical protein FLJ21276 KIAA0831 protein	32 32 32
15	105583	AA278907	Hs.3530	TLS-associated serine-arginine protein	3.2
	104796 111657	BE620712 R07364	Hs.33026 Hs.268667	hypothelical protein PP2447	3.2
	134174	AF283770	Hs.79530	ESTs, Weakly similar to ALU1_HUMAN ALU CD79A antigen (immunoglobulin-associated	3.2
20	126077 133733	M78772	Hs.210836	EST8	3.2 3.1
20	124847	AK000476 W07701	Hs.75798 Hs.304177	hypothetical protein	3.1
	127879	AA768098	Hs.189079	Homo sapiens clone FLB8503 PRO2286 mRNA, ESTs	3.1
	113108 110343	AW516695	Hs.8438	ESTs	3.1 3.1
25	102935	AW138703 BE561850	Hs.17268 Hs.80506	ESTs	3.1
	111676	AB040882	Hs.109778	small nuclear ribonucleoprotein polypept KIAA1449 protein	3.1
	127311 108830	AA492582	Hs.322404	hypothetical protein MGC4175	3.1 3.1
20	111330	AA131743 BE247767	Hs.193352 Hs.18166	ESTs KIAA0870 protein	3.1
30	104246	AF016032	Hs.201377	lysosomal apyrase-like 1	3.1
	126668 124724	AA011616 H20816	Hs.269877	EST8	3.1 3.1
	114794	AJ751157	Hs.112423 Hs.101395	Homo saplans mRNA; cDNA DKFZp586:1420 (f hypothetical protein MGC11352	3.1
35	134599	X99226	Hs.284153	Fanconi anemia, complementation group A	3.1 3.0
33	130314 100265	NM_014674 D38521	Hs.154332	KIAA0212 gene product	3.0
	115005	A1760825	Hs.112396 Hs.111339	KIAA0077 protein ESTs	3.0
	123433	AW450922	Hs.112478	ESTs	3.0 3.0
40	127798 117403	AA737068 H84455	Hs.294078 Hs.40639	EST ₅	3.0
	107111	A1298448	Hs.22870	ESTs chromodomain helicase DNA binding protel	3.0
	105698 108358	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	3.0 3.0
	132066	MB1933 A1929392	Hs.1634 Hs.181195	cell division cycle 25A	3.0
45	130303	BE245294	Hs.180789	OnaJ (Hsp40) homolog, subfamily B, membe S164 protein	2.9
	104596 112197	AF067804	Hs.15423	hypothetical protein HOCMC04P	2.9 2.9
	132809	NM_003655 AF036144	Hs.5637 Hs.5734	ESTs	2.9
50	100877	X80821	Hs.27973	meningtoma expressed antigen 5 (hyaturon KIAA0874 protein	2.9 2.9
50	108147 133674	Al972094 AW851121	Hs.286221	Homo sepiens cDNA FLJ13741 fis, clone PL	29
	129001	AA443323	Hs.75497 Hs.107812	Homo sepiens cONA: FLJ22139 fis, clone H BPOZ protein	2.9
	131920	BE002320	Hs.287864	Homo sapiens cONA FLJ14030 fis, clone HE	2.9 2.9
55	134709 113577	NM_006290 Al300699	Hs.211600 Hs.278937	tumor necrosis factor, alpha-induced pro	2.8
	115839	BE300266	Hs.28935	PRO0470 protein transductn-like enhancer of split 1, hom	2.8
	129969 128659	N57818		gb:yv59d07.s1 Soares fetal liver spleen	2.8 2.8
	105011	AW630087 BE091926	Hs.103315 Hs.16244	trinucleotide repeat containing 1	2.8
60	129294	AF172940	Hs.184542	mitotic spindie colled-coil related prot CGI-127 protein	2.8
	104518 · 107796	H20816	Hs.112423	Homo saplens mRNA; cONA DKFZp58611420 (f	2.8 2.7
	106331	AA058848 AB037742	Hs.60797 Hs.24338	ESTs KIAA1321 prolein	2.7
65	127692	AI021912	Hs.187983	EST8	2.7
05	131916 124971	AA025978 T23800	Hs.34569	ESTs .	27 27
	129428	AA256906	Hs.151001 Hs.111364	hypothetical protein FLJ14728	2.7
	118348	AW408588	Hs.91052	ESTs, Wealdy similar to ubiquitous TPR m ESTs, Moderately similar to ALU5_HUMAN A	27
70	113219 131720	T59257 Z68128	Hs.269528	ESTS, Moderately similar to ALUS_HUMAN A	27 27
. •	109593	AW196801	Hs.3109 Hs.6685	Rho GTPase activating protein 4 thyroid hormone receptor interactor 8	27
	135359	AF043722	Hs.99491	RAS guanyl releasing protein 2 (calcium	2.7
	131689 117457	ABQ12124 N29682	Hs.30696 Hs.44071	transcription factor-like 5 (basic helix	27 27
75	121073	H48199	Hs.112184	ESTs, Wealdy simitar to ALUS_HUMAN ALU DKFZP588J0619 protein	2.7
	125069	H81306	Hs.194485	ESTs	2.7 2.7
	118456 124271	Al381911 AW293223	Hs.334859	KIAA1814 protein	27
90	112369	AW966243	Hs.8928 Hs.4243	hypothetical protein FLJ20291 hypothetical protein FLJ12650	27
80	115866	AW062629	Hs.52081	KIAA0887 protein	27 2.7
	132543 124494	BE568452 N54831	Hs.5101 Hs.271381	protein regulator of cylokinesis 1	2.7
	104799	AA029703		ESTs, Weakly straiter to I38022 hypothet gb:ze95h08.s1 Soares_fetal_heart_NbHH19W	2.7
				Cupit 1944	2.7

	120510	AI796395	Un 444227	ESTA	••
	129781		Hs.111377 Hs.124707	ESTs ESTs	2.6 2.6
	122698	AA456112	Hs.99410	ESTs	2.6
_	106995	AB023139	Hs.37892	KIAA0922 protein	2.6
5	105502	BE464016	Hs.238956	ESTs	2.6
	128671 107059	A1885045	Hs.211586	phosphoinosliide-3-kinase, regulatory s	26
	126502	BE614410 T10077	Hs.23044 Hs.13453	RAD51 (S. cerevisiae) homolog (E coli Re hypothetical protein FLJ14753	2.6 2.6
	129703	BE388665	Hs. 179999	Homo saplens, clone IMAGE:3457003, mRNA	26
10	111219	N68836	Hs.19247	ESTs, Moderately similar to ALUC_HUMAN	2.6
	133529	W45623	Hs.74571	ADP-ribosylation factor 1	26
	125626	AI038854	Hs.180789	S164 protein	2.6
	111189 113148	N67603 BE151985	Hs.272130 Hs.5722	ESTs, Weatly similar to S65824 reverse hypothetical protein FLJ23316	2.6
15	125562	AI494372	Hs.98968	hypothetical protein FLJ23058	26 26
	102263	U29171	Hs.75852	casein kinase 1, della	26
	118835	AA535246	Hs.50852	ESTs	2.6
	103141	X66113	Hs.75584	polymyositis/scleroderma autoantigen 2 (2.6
20	109598 127262	R40515 AA828125	Hs.21248	ESTS	26
20	129620	D79338	Hs.239720	gb:od71a09.s1 NCL_CGAP_Ov2 Homo saplens CCR4-NOT transcription complex, subunit	26 26
	125905	A1678638	Hs.6456	chaperonin containing TCP1, subunit 2 (b	26
	123255	AA830335	Hs.105273	ESTs	2.6
25	133160	N54968	Hs.66309	hypothetical protein MGC11061	26
25	109638 119896	AW977747 AA731836	Hs.119120 Hs.137319	E3 ubiquitin ligase SMURF1	26
	134770	M89957	Hs.89575	ESTs CD798 antigen (immunoglobutin-essociated	26 26
	119403	AL117554	Hs.119908	nucleolar protein NOPS/NOP58	2.6
20	129563	AF119664	Hs.27299	transcriptional regulator protein	2.6
30	111719	AI655806	Hs.179262	ESTs	26
	103982 125032	AA218558	Hs.7905	sorting nextn 9	2.6
	131426	T74B84 AL122045	Hs.26703	gb:yc58d02.s1 Stratagene liver (937224) CCR4-NOT transcription complex, subunit	2.5
	131938	AF176085	Hs.34956	neural polypyrimidine tract binding prot	2.5 2.5
35	102450	U48251	Hs.75871	protein kinase C binding protein 1	2.5
	133761	AF041430	Hs.75922	brain protein I3	2.5
	126339 118967	AA152106	Hs.4859	cyclin L anla-6a	2.5
	123110	A1668670 AA486256	Hs.216756 Hs.193510	ESTs EST	2.5 . 2.5
40	114092	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.5
	113247	T63856	Hs.193430	ESTs, Wealdy similar to 2109260A B cell	2.5
	122024	AA431296	Hs.139433	ESTs .	2.5
	106657 126127	AW854339 N95428	Hs.33476	hypothetical protein FLJ11937	2.5
45	111836	R58394	Hs.25119	gb:zb80d09.s1 Soares_senescent_fibroblas ESTs, Weakly similar to YEX0_YEAST HYPOT	2.5 2.5
	121470	AA558958	Hs.324751	ESTs	2.5
	120132	W57554	Hs.125019	ESTs	2.5
	107731	AA016086	Hs.272106	ESTs, Weakly strallar to 138022 hypotheti	2.5
50	118122 106589	Al186671 AK000933	Hs.48008	ESTS	2.5
	129948		Hs.28661 Hs.263988	Homo sapiens cDNA FLJ 10071 fis, clone HE ESTs	2.5 2.5
	115652		Hs.38178	hypothetical protein FLJ23468	2.5
	103076	NM_001034		ribonucleolide reductase M2 polypeptide	2.5
55	131019	W28614	Hs.306155	chorlonic somatomammotropin hormone 1 (p	2.5
55	100512 105393	D13317 AF167570	Hs.78915 Hs.256583	GA-binding protein transcription factor,	2.5
	100571	L14561	Hs.78548	interleukin enhancer binding factor 3, 9 ATPase, Ca++ transporting, plasma membra	2.5 2.5
	106890	AA489245	Hs.88500	mitogen-activated protein kinase 8 Inte	2.5
60	104276		Hs.284288	hqp0256 protein	2.5
60	113283 118078		Hs.12947	EST	2.5
	120796		Hs.47790 Hs.96820	EST ESTs	2.5
	106265		Hs.236463	Homo sapiens mRNA; cDNA DKFZp586i0521 (f	2.5 2.5
15	102507		Hs.193044	potassium inwardly-rectifying channel, a	2.5
65	106508		Hs.30348	ESTs	2.5
	104568 103698		Hs.172182	poly(A)-binding protein, cytoplasmic 1	2.5
	113947		Hs.6685	thyroid hormone receptor interactor 8 gb:zh53d03.s1 Soares_fetal_liver_spleen_	2.5 2.5
	132112		Hs.40154	jumonji (mouse) homolog	25
70	129052		Hs.158210	hypothetical protein MGC2555	24
	117265		Hs.43005	RAB9-like protein	2.4
	107834 113119		Hs.40838	ESTS	24
	133726		Hs.252716	gb:yb18b11.s1 Strategene fetal spleen (9 oxysterol-binding protein-related protei	2.4 2.4
75	120548		Hs.187634	ESTs	24
	121545	AA412442	Hs.98132	ESTs	24
	131138		Hs.23413	KIAA1273 protein	2.4
	126589 115475		Hs.187698 Hs.40193	Homo saplens cytomegalovirus partial fus trypothelical protein KIAA1259	. 24
80	103760		Hs.183842	ubiquitin B	2.4 2.4
_	127889	Al147408	Hs.144941	ESTs .	24
	124457	AK000680	Hs.266175	phosphoprotein associated with GEMs	2.4
	113721	AF143885	Hs.18190	EST	2.4

	129079	AK000157	Hs.108502	hypothetical protein FLJ20150	2.4
	123530	AA608705	Hs.187772	ESTs	2.4
	123592	AA805331	Hs.112837	ESTs	24
5	113474 116728	R50752 F13687	Hs.23856 Hs.227976	hypothetical protein MGC5297 EST	24 24
•	101759	M80244	Hs.184601	solute carrier family 7 (cationic amino	24
	131686	NM_012296		GRB2-essociated binding protein 2	2.4
	127841 102737	AW136558 R51790	Hs.125246 Hs.239483	ESTs Human clone 23933 mRNA sequence	2.4 2.4
10	129673	D38552	Hs.1191	KIAA0073 protein	24
	133095	BE048490	Hs.180677	zinc finger protein 162	2.4
	124540 113609	N63232	No 10076	gbryz39a12.s1 Morton Fetal Cochlea Homo	2.4
	128828	T93263 Z40313	Hs.16875 Hs.106330	ESTs, Weakly similar to S23650 retrovir Homo sapters clone IMAGE:23371, mRNA seq	2.4 2.4
15	129059	AW069534	Hs.279583	CGI-81 protein	2.4
	134092	AA218558	Hs.7905	sorting nextin 9	2.4
	132317 135278	BE262438 AA399542	Hs.44592 Hs.229671	beta-1,4 mannosyltransferase EST, Moderately similar to PEPTIDYL-PROL	2.4 2.4
	128468	T23625	Hs.150580	putative translation initiation factor	24
20	127407	AW089514	Hs.279681	heterogeneous nuclear ribonucleoprotein	24
	132342	AW162758	Hs.45232	ESTs, Weekly similar to ALU5_HUMAN ALU S	2.4
	113518 100330	AW367788 AW410976	Hs.323954 Hs.77152	postmeiolic segregation increased 2-lik minichromosome meintenance deficient (S.	2.4 2.4
~-	116046	BE395293	Hs.94491	hypothetical protein FLJ20297	24
25	123910	AA621262	Hs.179923	ESTs, Weakly similar to S65657 alpha-1C-	2.4
	101651 100114	AL037111	Hs.75841	galactose-1-phosphate uridylyltransferas	24
	125038	X02308 AA812234	Hs.82962 Hs.270134	thymidylate synthetase hypothetical protein FLJ20280	2.4 2.4
20	135191	X16866	Hs.301086	cytochrome P450, subfamily IID (debrisog	2.4
30	123258	AA490929	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGUL	2.4
	132380 114046	AW373665 BE018658	Hs.46853 Hs.141003	ESTs Homo saplens cDNA: FLJ21691 fis, clone C	2.4 2.3
	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	2.3
25	134839	D63479	Hs.115907	diacylglycerol kinase, delta (130kD)	2.3
35	105734 101086	Al952797 AA382524	Hs.10888	hypothetical protein FLI21709	2.3
	118349	N63788	Hs.250959 Hs.94149	histatin 1 ESTs, Weakly similar to ALU1_HUMAN ALU S	' 2.3 2.3
	101194	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.3
40	130588	AL030996	Hs.16411	hypothetical protein LOC57187	2.3
40	101875 118751	BE241753 N74210	Hs.74592 Hs.50454	special AT-rich sequence binding protein ESTs	2.3 2.3
	125174	W51835	Hs.231082	EST	23
	105966	AA142984	Hs.5344	adaptor-related protein complex 1, gamma	2.3
45	104624	AA353125	Hs.184721	ESTs .	2.3
73	131263 105014	AU077002 AA121123	Hs.24950 Hs.269267	regulator of G-protein signalling 5 ESTs, Wealdy similar to AF161361 1 HSPC	2.3 2.3
	123423	AA598484	110.200207	gb:as38f04.s1 Gessler Wilms tumor Homo s	23
	128531	H03721	Hs.2953	ribosomal protein S15a	23
50	108876 130215	AI733860 BE301883	Hs.191453 Hs.152707	ESTs glioblastoma amplified sequence	2.3
-	132232	AI522273	Hs.42640	ESTs	2.3 2.3
	132664	Al740461	Hs.54542	ESTs	2.3
	105991 100253	AA215701	Hs.186541	ESTs, Weakly similar to 138022 hypotheti	2.3
55	105574	D38024 AA045281	Hs.157425 Hs.268175	double homeobox, 2 phosphoprotein associated with GEMs	23 23
	100780	BE561958	Hs.302063	immunoglobulin heavy constant mu	2.3
	134984	AI803516	Hs.272891	hippocalcin-like protein 4	2.3
	132786 104952			hypothetical protein MGC2668	2.3 2.3
60	119127	AA708035	Hs.12248	desmoplakin (DPI, DPII) ESTs	23
	104857	A1920902	Hs.19058	ESTs, Moderately similar to S65657 alpha	2.3
	107592 113378		Hs.60049	ESTs	2.3
	129228		Hs.14757 Hs.239307	ESTs tyrosyl-IRNA synthetase	2.3 2.3
65	106898	AA490069	Hs.306676	Homo sepiens cDNA FLJ14302 fis, clone PL	2.3
-	130734			KIAA1052 protein	2.3
	125728 113697	AW954565 197183	Hs.57987 Hs.17992	B-cell CLL/lymphoma 118 (zinc finger pro Homo sepiens mRNA; cDNA DKFZp434J1726 (f	23 23
	107104		Hs.15243	nucleolar protein 1 (120kD)	2.3
70	134267	A1174596	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	2.3
	105777 115308		Hs.23096	ESTs	23
	133363	AI866286	Hs.88746 Hs.71962	ESTs 1 ESTs, Wealdy similar to B36298 proline-r	2.3 2.3
75	129535	AA397972		chimerin (chimaerin) 1	23
75	121520		Hs.164785	ESTs	2.3 2.3
	123808 105700			gb:ae58g11.s1 Stralagene lung cardnoma	2.3
	120820			hypothelical protein FLB6421 EST	2.3 2.3
00	128721	AW40391	Hs.266175	phosphoprotein associated with GEMs	2.3
80	107711		Hs.220687	ESTS	2.3 2.3
	102564 131868		Hs.79067 3 Hs.33532	MAD (mothers against decapentaplegic, Dr zino finger protein 151 (pHZ-67)	23 23
	122333			ESTs, Moderately similar to T34561 hypot	2.3
				88	
				00	
				•	

	118865	AA736405	Hs.54530	ESTs	2.3
	128952	AL043463	Hs.6755	RaP2 interacting protein 8	2.3
	133772	BE379867	Hs.76038	isopentenyl-diphosphate della isomerase	2.3
_	111795	A1435437	Hs.24567	ESTs, Wealthy similar to KBF3_HUMAN NUCL	23
5	103437	AV655598	Hs.184211	peptidase (mitochondrial processing) bet	23
	123060	AA482027	Hs.142569	ESTs, Weakly similar to I38022 hypotheti	2.3
	125466	R08234	Hs.180461	ESTS	2.3
	100892 121613	BE245294 AA416879	Hs.180789 Hs.193195	S164 protein	2.3
10	133665	AL036883	Hs.75450	ESTs, Weskly similar to 2109260A 8 cett	2.3
10	129248	W04606	Hs.171637	delta steep inducing peptide, immunoreac hypothetical protein MGC2528	2.2
	126153	H85692	Hs.40730	ESTs	2.2 2.2
	125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA	2.2
	104960	AA558877	Hs.8928	hypothetical protein FLJ20291	2.2
15	113941	AA531016	Hs.22399	hypothetical protein FLJ14824	2.2
	112540	R69751		gb:yl40a10.s1 Soares placenta Nb2HP Homo	2.2
	105322	TB7179	Hs.16346	ESTs, Wealdy similar to S57447 HPBRII-7	2.2
	112003	AW978731	Hs.301824	hypothetical protein PRO1331	2.2
20	134733 114620	N87353 AA642974	Hs.89421	CBF1 Interacting corepressor	2.2
20	123451	Al793211	Hs.165372	gb:nr60h01.s1 NCI_CGAP_Lym3 Homo saplens	22
	130850	AB040922	Hs.20237	ESTs, Moderately similar to ALU1_HUMAN A OKFZP566C134 protein	2.2
	105561	AA262881	Hs.323836	ESTs, Weakly similar to alternatively s	2.2 2.2
~-	125957	H41694		gb:yo06b06r1 Soares adult brain N2b5HB5	2.2
25	130362	BE513050	Hs.279681	heterogeneous nuclear ribonucleoprotein	2.2
	122682	AA984531	Hs.159293	ESTs	2.2
	124250	AA350256	Hs.323875	EST, Weakly similar to 2109260A B cell	2.2
	131392	AA235153	Hs.26320	TRABID protein	2.2
30	128845	AW503978	Hs.10849	basement membrane-induced gene	2.2
50	130453 126973	U80735 W46653	Hs.173854	PAX transcription activation domain inte	2.2
	103156	BE259039	Hs.251928 Hs.129953	nuclear pore complex interacting protein	2.2
	103163	AU077018	Hs.3235	Ewing sarcoma breakpoint region 1 keratin 4	22
	109252	BE440157	Hs.85944	ESTs	2.2 2.2
35	131163	AA099524	Hs.23754	ESTs .	2.2
	115292	AA279958	Hs.88872	ESTs	2.2
	122591	AJ188219	Hs.99311	ESTs, Weakly similar to HSJ2_HUMAN DNAJ	2.2
	124977	F04819	Hs.190452	KIAA0365 gene product	2.2
40	103319	XB3492	Hs.82359	tumor necrosis factor receptor superfami	22
70	100370 128992	D79989	Hs.184884	KIAA0167 gene product	2.2
	129928	H04150 Al338993	Hs.107708 Hs.134535	ESTS	2.2
	108451	AA079195	113,104303	ESTs gb:zm92h12.s1 Stratagene overlan cancer	2.2
	133910	AW835281	Hs.77500	ublquitin specific protease 4 (proto-onc	2.2 2.2
45	106288	AB037742	Hs.24336	KIAA1321 protein	22
	134125	NM_014781	Hs.50421	KIAA0203 gene product	2.2
	101379	X02994	Hs.1217	adenosine deaminase	2.2
	112276	R53442	Hs.26038	ESTs, Wealdy similar to 138022 hypothet	22
50	106251 125394	R12607	Hs.35101	profine-rich Gla (G-carboxyglutamic acid	2.2
50	103392	BE178502 X94563	Hs.173772	ESTs, Weakly similar to 178885 serine/th	2.2
	112853	T02843		gb:H.saplens dbl/ecbp gene exon 1 & 2. gb:F811H5 Fetal brain, Stratagene Horno s	2.2
	133195	A1434760	Hs.279949	KIAA1007 protein	2.2 2.2
	135050	AK001887	Hs.259842	protein kinase, AMP-activated, gamma 2 n	2.2
55	131381	M92642	Hs.26208	collagen, type XVI, alpha 1	2.2
	134104	L35253	Hs.79107	mitogen-activated protein kinase 14	2.2
	105225	AA211777		gb:zn57d02.s1 Stratagene muscla 937209 H	2.2
	131320 114419	AA505691	Hs.145696	splicing factor (CC1.3)	22
60	103634	AI248013 BE541733	Hs.106532 Hs.180877	ESTs. Weakly similar to 138588 reverse t	2.2
-	134624	AF035119	Hs.8700	H3 histone, family 3B (H3.3B) deteted in liver cancer 1	2.2
	126524	Z45455	Hs.182447	heterogeneous nuclear ribonucleoprotein	2.2 2.2
	115556	AL031778	Hs.797	nuclear transcription factor Y, alpha	2.2
	111898	R38944	Hs.183475	Homo sapiens clone 25061 mRNA sequence	2.2
65	100415	D86970	Hs.75822	TGF81-induced anti-apoptotic factor 1	2.2
	103898	AA248884		gb:k3517.seq.F Human fetal heart, Lambda	2.2
	129501	AI631811	Hs.180403	STRIN protein	2.2
	127251	AA938428	Hs.128638	ESTs	22
70	100613 116332	X52078 AA491208	Hs.101047	transcription factor 3 (E2A immunoglobut	2.2
, 0	128897	AW979134	Hs.62620 Hs.10700	chromosome 6 open reading frame 1 hypothetical protein	2.2
	111777	AK001100	Hs.41690	desmocollin 3	2.2
	128604	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	2.2 2.2
76	125585	AW298113	Hs.92909	SON DNA binding protein	2.2
75	129584	AV656017	Hs.184325	CGI-76 protein	22
	114461	AA531187	Hs.126705	ESTs .	22
	121387	AA405854		gb:zu66g08.s1 Soeres_testis_NHT Homo sap	2.2
	109339	AA314554	Hs.27774	ESTs, Highly similar to AF161349 1 HSPC0	2.2
80	129179 106711	AW969025	Hs.109154	ESTs	2.2
-	106424	BE390125 H61005	Hs.143187 Hs.37902	hypothetical protein	22
	123949		Hs.208957	ESTs EST	22
	127256		Hs.267967	ESTs, Moderately similar to ALUS_HUMAN	2.2
					2.2

	404060	AFATTOOT	***		
	104868 132984	AF173867	Hs.28906	glucocorticoid modulatory element bindin	2.2
	126383	BE539199 AB032977	Hs.62112 Hs.6298	zinc finger protein 207	2.2
	130557	H51825	Hs.268911	KIAA1151 protein	2.2
5	119232	AI855226	Hs.117659	ESTs, Weakly similar to S65824 reverse ESTs, Weakly similar to T46481 hypotheti	2.2
_	105715	BE621800	Hs.29444	putative small membrane protein NID87	2.2
	124691	R05835	Hs.110153	ESTs	2.2 2.2
	113849	N94768	Hs.16400	ESTs. Weakly similar to KIAA1435 protein	22
10	117040	AW970600	Hs.303261	ESTs	2.2
10	128767	M85169	Hs_1050	pleckstrin homology, Sec7 and colled/col	2.2
	120602	AA808018	Hs.109302	ESTs	2.2
	107182	AJ311782	Hs.20013	GCIP-Interacting protein p29	2.2
	107357	U63973	Hs.103501	modopsin kinase	2.2
15	125499 126872	H10543		gb:ym04c08.r1 Soares infant brain 1NIB H	21
12	113233	AW450979 T61955	Hs.279867	gb:U-H-BI3-gb-a-12-0-UI.s1 NCL_CGAP_Su	2.1
	128367	AWB11791	Hs.150742	CGI-59 protein ESTs	2.1
	127432	AW067708	Hs.170311	heterogeneous nuclear ribonucleoprotein	21
	114021	AW235215	Hs.16145	EST8	2.1
20	104455	AL110261	Hs.157211	DKFZP586B0621 protein	2.1 2.1
	134966	AW402389	Hs.920	modulator recognition factor I	21
	129765	M86933	Hs.1238	amelogentn (Y chromosome)	21
	133461	NM_000762	Hs.334345	cytochrome P450, subfamily IIA (phenobar	21
25	109639	AA082650	Hs.6217	Homo saplens cDNA FLJ12521 fis, clone NT	2.1
25	129794	AF161399	Hs.23259	hypothetical protein FLJ13433	21
	134869	AL157518	Hs.90421	PRO2463 protein	2.1
	110256	H63947	Hs.237955	RAB7, member RAS encogene family	2.1
	128817 120906	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	2.1
30	134354	NM_000734 M90391	Hs.82127	CD3Z antigen, zeta polypeptide (TIT3 com	2.1
-	106048	AW883367	Hs.301732	Interleukin 16 (lymphocyte chemoattracta hypothetical protein MGC5306	2.1
	128352	AW137413	Hs.169942	ESTs	21
	115348	AA281562	Hs.292100	ESTs .	21 21
~ ~	123474	AA599209		gb:ag34b11.s1 Jia bone marrow stroma Hom	2.1
35	107121	AB015427	Hs.250493	zinc finger protein 219	2.1
	118509	N22617	Hs.43228	Homo saplens cDNA FLJ11835 fis, clone HE	21
	135051	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	2.1
	109442	AW296134	Hs.86999	ESTs, Weakly similar to S65657 alpha-1C-	21
40	126661	AA009835	Hs.269521	ESTs	2.1
TU	129270 125568	AA357185	Hs.109918	ras homolog gene family, member H	2.1
	132867	AW615398 AF226667	Hs.105613	ESTs CTP continues II	21
	124656	AW297702	Hs.58553 Hs.102915	CTP synthese II ESTs	2.1
	128954	AA346839	Hs.209100	DKFZP434C171 protein	2.1
45	132985	AL045579	Hs.62113	KIAA0717 protein	2.1 2.1
	119247	BE269047	Hs.65234	hypothetical protein FLJ20596	2.1
	106688	N66397	Hs.334825	Homo sapiens cDNA FLJ14752 fis, clone NT	21
	131009	AF169802	Hs.22142	cytochrome b5 reductase b5R.2	2.1
50	112170	BE246743	Hs.288529	hypothetical protein FLJ22635	21
20	130755	BE293520	Hs.18910	prostate cancer overexpressed gene 1	21
	117357 101613	N24829	11- 400000	gb:yx98h12.s1 Soares melanocyte 2NbHM Ho	2.1
	127644	M24283	Hs.168383	Intercellular adhesion molecule 1 (CD54)	2.1
	101183	N88858 AA442324	Hs.155101 Hs.795	ATP synthase, H+ transporting, mitochond	21
55	100420	D86983	Hs.118893	H2A histone family, member O Melanoma essociated gene	2.1
	129879	AK001698	Hs.13109	Ran binding protein 11	21 21
	122311	NM_014913		KIAA0863 protein	21
	130566	R85474	Hs.16073	ESTs	21
60	113517	AI874223	Hs.293560	ESTs	2.1
60	115810	AA426026	Hs.187615	ESTs	2.1
	108743	Al580150	Hs.71074	ESTs	21
	129255	Al961727	Hs.109804	H1 histone family, member X	2.1
	120766 126893	AA764879 AJ252060	Hs.12570	tubulin-specific chaperone d	2.1
65	115254	AJ252060 AA279024	Hs.26320	TRABID protein	2.1
05	105865	BE279383	Hs.269316 Hs.26557	ESTs, Weakly strollar to \$65657 alpha-1C	2.1
	120999	AI972375	Hs.29826	hypothetical brain protein my038	21
	125636	H12382	Hs.25119	ESTs, Weakly similar to YEXO_YEAST HYPOT	2.1
	117997	N52090	Hs.47420	EST	2.1
70	104333	D82418	Hs.29626	hypothetical brain protein my038	2.1 2.1
	134315	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	21
	135332	AW3938B3	Hs.98968	hypothetical protein FLJ23058	21
	107279	S57296	Hs.323910	v-erb-b2 avian erythroblastic teukernia	21
75	133097	W03512	Hs.6479	hypothetical protein MGC13272	2.1
75	112563	AW961220	Hs.29282	milogen-activated protein kinase kinase	21
	121782	AW452957	Hs.334698	Homo sapiens, clone MGC:15203, mRNA, com	2.1
	111567	F12628	Hs.334786	hypothetical protein MGC15040	21
	133912 134076	H42679 AF086215	Hs.77522	major histocompatibility complex, class	2.1
80	116665	F04405		gb:Homo sepiens full length insert cDNA	2.1
-5	133562	M60721	Hs.74870	gb:HSC2SB082 normalized infant brain cDN	2.1
	129092	D56365	Hs.63525	H2.0 (Drosophila)-lika homeo box 1 poly(rC)-binding protein 2	2.1
	106869	AW975382	Hs.292679	ESTs	2.1
					2.1
				00	

	130820 126277	AL353934 AB037847	Hs.288798 Hs.15441	hypothetical protein FLJ21012 Crm (Cramped Drosophila)-like	21 21
	106392	BE350058	Hs.36787	chromodomain helicase DNA binding protei	2.1
5	131902	AA180145	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	21
,	120734 113070	AA299948 AB032977	Hs.6298	gb:EST12544 Uterus turnor I Horno sapiens KIAA1151 protein	2.1 2.1
	116031	AA452239	Hs.103329	KIAA0970 protein	21
	123869	AA620924	Hs.112923	EST	2.1
10	108145 109061	AA424791 AA160898	Hs.5734	meningioma expressed entigen 5 (hyzłuron gb:zo79c07.s1 Stratagene pancreas (93720	21 21
~ •	126348	T16243	Hs.6473	Homo sapiens cDNA FLJ13992 fis, clone Y7	21
	133231	AK000517	Hs.6844	hypothetical protein FLJ20510	2.1
	123132 117452	AI061582 N34687	Hs.324179 Hs.44054	Homo saplens cDNA FLJ12371 fis, clone MA	21 21
15	128538	R44214	Hs.101189	ninein (GSK3B interacting protein) ESTs	21
	111945	R40683	Hs.124944	ESTs	21
	119155 124382	R61715 ALD46406	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN	21
	129198	N57532	Hs.103483 Hs.109315	KIAA1798 protein KIAA1415 protein	21 21
20	122059	AA431737	Hs.98749	EST, Moderately similar to T42871 hypoth	21
	115843 112558	AA404276	Hs.123253	hypothetical protein FLJ22009	2.0
	115355	AK001621 AA262292	Hs.15921 Hs.88445	hypothetical protein FLJ 10759 ESTs	2.0 2.0
26	130724	AK001507	Hs.306084	Homo saplens clone FLB6914 PRO1821 mRNA.	20
25	125360 104926	AW898892	Hs.189741	ESTS	2.0
	119468	BE298808 Al911535	Hs.33363 Hs.6657	DKFZP434N093 protein hypothetical protein bK1048E9.5	2.0 2.0
	132891	BE267143	Hs.59271	U2(RNU2) small nuclear RNA auxillary fac	2.0
30	100237 105335	D30715	Hs.306333	Human PAP (pancreatitis-associated prot	2.0
50	105555	AW291165 AA357001	Hs.25447 Hs.34045	ESTs hypothetical protein FLJ20764	2.0 2.0
	126053	H84450		gb:yu62d01.r1 Weizmann Olfactory Epithel	20
	115084	BE383668	Hs.42484	hypothetical protein FUI 10618	2.0
35	128408 132311	Al183407 Al765559	Hs.143704 Hs.20072	EST myosin regulatory light chain interactin	2.0 2.0
	113626	T94318	Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	2.0
	116379	AA448588	Hs.71252	hypothetical protein DKFZp761C169	20
	105474 108922	AL134843 AA115268	Hs.219614 Hs.269263	f-box and leucine-rich repeat protein 11 ESTs	2.0 2.0
40	123720	AA609734	Hs.112755	EST	2.0
	128902	AA036637	Hs.107052	ESTs SOT-	2.0
	113226 106798	AI821008 BE252749	Hs.10697 Hs.20558	ESTs hypothelical protein FLJ20345	2.0 2.0
4.5	106665	BE090009	Hs.323164	hypothetical protein MGC2217	2.0
45	105952	AJ767152	Hs.181400	ESTs, Wealdy similar to 178885 serine/th	20
	127248 112972	AA364195 AI684745	Hs.165983	gb:ES175015 Pineal gland II Homo saplens hypothetical C2H2 zinc finger protein FL	2.0 2.0
	128148		Hs.126637	ESTs	2.0
50	116176		Hs.288708	hypothetical protein FLJ21562	2.0
50	126457 112610	AA007489 AW500108	Hs.50382 Hs.23643	ESTs serine/threonine protein kinase MASK	2.0 2.0
	109249	AA194730	Hs.268189	hypothetical protein FLJ20436	2.0
	121292 128606		15- 400400	gb:zv65f11.s1 Soares_total_fetus_Nb2HF8_	2.0
55	127705		Hs.102402	Mad4 homolog gb:AJ003322 Selected chromosome 21 cDNA	2.0 2.0
	134874	AF219139	Hs.87726	KIAA0154 protein; ADP-ribosylation facto	2.0
	107529 116411		Hs.296585	nucleolar protein (KKE/D repeat)	2.0
	111576		Hs.321618 Hs.15489	hypothetical protein FLJ12525 ESTs	2.0 2.0
60	127002	AL353940	Hs.24979	hypothetical protein DKFZp761P1010	2.0
	112662 126250		Hs.268814	ESTS	2.0
	101045		Hs.321247	Homo septens mRNA; cDNA DKFZp586A181 (fr gb:Human proliferating cell nuclear anti	2.0 2.0
65	117188	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
65	122110		Hs.301240	metanocortin 1 receptor (alpha metanocyt	2.0
	119849 124395		Hs.272095	ESTs ESTs, Weakly similar to 138022 hypotheti	2.0
	131600	NM_00437	7 Hs.29331	camitine palmitoyltransferase I, muscle	2.0
70	112774		Hs.35455	ESTs	2.0
70	109751 102377		Hs.6679 Hs.29656	hHDC for homolog of Drosophila headcase cyclin-dependent kinase inhibitor 2D (p1	2.0 2.0
	115197	R18858	Hs.6749	ESTs	2.0
	102808		Hs.179606	nuclear RNA helicase, DECD variant of DE	2.0
75	128869 111229			hypothetical protein ESTs	2.0 2.0
-	129330	AL079310	Hs.92260	high-mobility group protein 2-like 1	2.0
	105448			BTB and CNC homology 1, basic laucine zi	2.0
	127391 102337		Hs.11039 Hs.170133	hypothetical protein MGC2722 forkhead box O1A (rhabdomyosarcoma)	2.0 2.0
80	121897	7 AA427419	Hs.229162	EST, Weakly similar to ZN91_HUMAN ZINC	2.0
	10790: 12934:			ESTs	2.0
	10109		Hs.11050 Hs.89414	F-box only protein 9 chemoline (C-X-C motif), receptor 4 (fus	2.0 2.0
				91	
				•	

	124864 118485	AW970168 AA508515	Hs.185706	ESTs	2.0
	116715	AL117440	Hs.291049 Hs.170263	ESTs turnor protein p53-binding protein, 1	2.0
_	130743	AL049266	Hs.18724	Homo saplens mRNA; cDNA DKFZp564F093 (fr	2.0 2.0
5	118877	AW971146	Hs.293187	ESTs	20
	100020				20
	123252	AW968776	Hs.287586	Homo saplens cDNA FLJ13648 fis, clone PL	2.0
	134977 115334	AL044963	Hs.308121	leukocyte receptor cluster (LRC) encoded	2.0
10	111790	AA702972 AW769683	Hs.65300 Hs.6734	ESTs ESTs, Wealdy similar to \$26650 DNA-bindi	2.0
	129101	NM_013403		zinedin	2.0 2.0
	132676	N92589	Hs.261038	ESTs, Wealthy similar to 138022 hypothet	20
	111018	Al287912	Hs.3628	mitogen-activated protein kinase kinase	2.0
15	105933	AF078544	Hs.194686	solute carrier family 25 (mitochondrial	2.0
13	110679	AA004798	Hs.108311	ESTs, Wealdy similar to T00351 hypotheti	2.0
	120861 132430	AA350394 AW973652	Hs.96952 Hs.283105	ESTs ESTs	20
	115026	AA251972	Hs.188718	ESTs .	2.0 2.0
	128660	AA011597	Hs.177398	ESTs	20
20	134554	AI184316	Hs.85273	retinoblastoma-binding protein 6	20
	109592	Al198059	Hs.26370	ESTs .	20
	123636	AA609263	11- 6000	gb:af13c08.s1 Soares_lestis_NHT Homo sap	2.0
	132610 122652	AA160511 AA454641	Hs.5326	arnino acid system N transporter 2; porcu	2.0
25	120467	AW292582	Hs.187628	gb:xx99d05.s1 Soares_NhHMPu_S1 Homo sepi ESTs	2.0 2.0
	126048	AA804957	Hs.119840	ESTs	20
	128179	AW293689	Hs.127116	ESTs	20
	123349	AB033042	Hs.29679	cofactor required for Sp1 transcriptiona	20
30	106208	AK001674	Hs.22630	cofactor required for Sp1 transcriptiona	2.0
50	125832 133317	AA628600 AC005258	Hs.117587 Hs.70830	ESTs	2.0
	132886	AW978168	Hs.5912	U6 snRNA-associated Sm-like protein LSm7 F-box only protein 7	2.0 2.0
	127447	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	2.0
26	133149	AA370045	Hs.6607	AXIN1 up-regulated	2.0
35	120468	AW967675	Hs.96487	ESTs, Highly similar to S08228 ribosomal	2.0
	106487 126770	A1697340	Hs.135265	Homo saplens clone FLB8436 PRO2277 mRNA,	2.0
	120592	AI292320 AA830664	Hs.81361 Hs.143974	heterogeneous nuclear ribonucleoprotein ESTs	2.0
	100944	L07518	Hs.159593	mucin 6, gastric	2.0 2.0
40	101887	AW987413	Hs.83958	transducin-like enhancer of split 4, hom	2.0
	125324	R07785		gb:yf15c06.r1 Soares fetal liver spleen	2.0
	133906	BE386038	Hs.77492	haterogeneous nuclear ribonucleoprotein	2.0
	113408 115613	NM_005908 AW136951		mannosidase, beta A, lysosomal	20
45	107468	AA740979	Hs.173948 Hs.91389	hypolhetical prolein FLJ 10486 ESTs	2.0
	100554	M95923	1.0.01000	gb:Human 12-lipoxygenase mRNA, partial c	2.0 2.0
	120476		Hs.104305	death effector filament-forming Ced-4-II	. 2.0
	117160	AA322302	Hs.183302	PCTAIRE protein kinase 2	2.0
50	115582 125536	AW245047	Hs.136164	cutaneous T-cell lymphoma-associated tu	2.0
50	100842	F08266 U05597	Hs.77948	ESTs, Wealthy similar to ALU1_HUMAN ALU 8	2.0
	133207	AI561173	Hs.67688	gb:Human anlon exchanger 3 cardiac isofo ESTs	2.0 2.0
	122053	AI637498	Hs.98745	ESTs	2.0
E E	121080	AA617830	Hs.28310	ESTs	2.0
55	113316	T70318	Hs.268581	ESTs	2.0
	113137 100416	AW952129	Hs.293225	ESTs, Weakly similar to FLDED-1 [H.sapie	1.9
	133975	AW505086 C18358	Hs.196914 Hs.295944	minor histocompatibility antigen HA-1 tissue factor pathway inhibitor 2	1.9
	103872		Hs.21756	translation factor suit homolog	1.9 1.9
60	132439	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	1.9
	126082		Hs.269571	ESTs	1.9
	124677		11. 40000	gb:ye84c03.s1 Soares fetal liver spleen	1.9
	123385 103138		Hs.17767	KIAA1554 protein	1.9
65	104867	AA278898	Hs.225979	gb:H.seplens SOD-2 gene for manganese su hypothetical protein similar to small G	1.9
	128668		Hs.103422	Homo sapiens cDNA FLJ14630 fis, clone NT	1.9 1.9
	125826		Hs.7594	solute cerrier family 2 (facilitated glu	1.9
	113701		Hs.18026	EST8	1.9
70	134447		Hs.83428	nuclear factor of kappa light polypeptid	1.9
70	128895 112719			ESTs	1.9
	102552		Hs.19301 B Hs.44585	Homo saplens, Similar to Nedd-4-like ubl tumor protein p53-binding protein, 2	1.9
	131186		Hs.246112	KIAA0788 protein	1.9 1.9
75	133347	BE257758	Hs.71475	acid cluster protein 33	1.9
75	133388	AW245631	Hs.182447	heterogeneous nuclear ribonucleopratein	1.9
	112266		Hs.25934	ESTs, Wealdy similar to HSHU11 histone H	1.9
	100336		Hs.8127	KIAA0144 gene product	1.9
	113479 135231		Hs.10739 Hs.74280	ESTs	1.9
80	123783		· 74,00	hypothetical protein FLJ22237 gb:af19g05.s1 Soares_lotal_fetus_Nb2HF8_	1.9 1.9
	113016	NM_01400	7 Hs.127649	KIAA0414 protein	1.9
	132761	AI815537	Hs.323502	nuclear RNA export factor 1	1.9
	128536	AW955085	Hs.101150	Homo septens, clone IMAGE:4054156, mRNA,	1.9

	126663	AW518478	Hs.181297	ESTs	1.9
	103973 106742	AA305729 AW591428	Hs.18272	amino acid transporter system A1	1.9
_	129793	AW207000	Hs.27556 Hs.126857	hypothetical protein FLJ22405 Homo septens cDNA FLJ12935 fis, clone NT	1.9 1.9
5	105888	AW970872	Hs.9247	protein kinase, AMP-activated, alpha 1 c	1.9
	101892 125511	AJ271379	Hs.75206	protein phosphatase 3 (formerly 2B), cat	1.9
	126751	Al378328	Hs.76194 Hs.77258	ribosomal protein S5 enhancer of zeste (Drosophila) homolog 2	1.9 1.9
. ^	129111	AL080155	Hs.226372	DKFZP434J154 protein	1.9
10	128750	T80270	Hs.104788	hypothetical protein LOC55565	1.9
	133531 125704	BE276738 R55094	Hs.74578 Hs.26239	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.9
	100157	D14661	Hs.119	Human DNA sequence from clone RP11-438B2 Wilms' tumour 1-associating protein	1.9 1.9
15	125845	AK001440	Hs.131840	hypothetical protein FLJ10578	1.9
IJ	134682 106565	AW882645 NM_014892	Hs.88044	sprouty (Orosophila) homolog 1 (antagoni	1.9
	106708	AB037810	Hs.18760	KIAA1116 protein KIAA1389 protein	1.9 1.9
	125761	R68351		gb:yh99b03.r1 Soares placenta Nb2HP Homo	1.9
20	116470 123264	AI272141 AI681270	Hs.83484	SRY (sex determining region Y)-box 4	1.9
-0	126096	F08208	Hs.99824 Hs.283844	BCE-1 protein similar to rat tricarboxylate carrier-li	1.9 1.9
	104995	AK001690	Hs.16390	hypothetical protein FLJ10035	1.9
	133424 132450	AA350994	Hs.20281	KIAA1700	1.9
25	131803	AA100012 U73737	Hs.48827 Hs.284289	hypothetical protein FLJ12085 vililigo-essociated protein VIT-1	1.9
	116548	D20433		gb:HUMGS01407 Human promyelocyte Homo sa	1.9 1.9
	113815 100245	AA386192	Hs.193482	Homo saplens cDNA FLJ11903 fis, clone HE	1.9
	113877	AL039248 270200	Hs.3094 Hs.246112	KIAA0083 gene product KIAA0788 protein	1.9 1.9
30	134470	X54942	Hs.83758	CDC28 protein kinase 2	1.9
	134937 134506	AI251449	Hs.171939	ESTs	1.8
	128469	AW247364 BE384361	Hs.84285 Hs.182885	ubiquilin-conjugating enzyme E2i (homolo ESTs, Weakly strnitar to JC5024 UDP-gatac	1.9
26	115261	AA938293	Hs.60088	hypothetical protein MGC11314	1.9
35	125198	W69474	Hs.323140	ESTs	1.9
	115317 112342	AA303799 AW410273	Hs.300141 Hs.92614	ribosomal protein L39	1.9
	117329	AA524065	Hs.93670	longavity assurance (LAG1, S. cerevisiae Homo sapiens cDNA: FLJ22664 fis, clone H	1.9 1.9
40	116353	AB032968	Hs.131728	KIAA1140 protein	1.9
+0	114459 133903	AW445217 X63692	Hs.103362 Hs.77482	ESTS DNA (adapting E.) mathyltografiance 4	1.9
	116083	AA455706	Hs.44581	DNA (cytosine-5-)-methyltransferase 1 heat shock protein hsp70-related protein	1.9 1.9
	130037	A1498631	Hs.111334	ferritin, light polypeptide	1.8
45	102273 120452	BE391815 AL022328	Hs.75981 Hs.104335	ubiquitin specific protease 14 (tRNA-gua	1.9
	116432	BE271922	Hs.71243	hypothetical protein IMAGE3510317 ESTs, Weakly similar to zinc finger prot	1.9 1.9
	115916	AI052731	Hs.91910	ESTs	1.9
	120827 129602	AA382525 Al282193	Hs.132967	Human EST clone 122887 mariner transposo	1.9
50	105693	BE250951	Hs.198298 Hs.181368	v-src avian sarcoma (Schmidt-Ruppin A-2) U5 snRNP-specific protein (220 kD), orth	1.9 1.9
	102316	U34301		gb:Human nonmuscle myosin heavy chain II	1.9
	131422 128434	AW607731	Hs.26670	Human PAC clone RP3-515N1 from 22q11.2-q	1.9
	117086	Al190914 AA581602	Hs.143880 Hs.41840	ESTs ESTs	1.9 1.9
55	102006	AL048967	Hs.172207	non-POU-domain-containing, octamer-bindi	1.9
	121335 105905	AA404418 AA401533	Un 10110	gb:zw37e02.s1 Soares_total_fetus_Nb2HF8_	1.9
	125165	W45350	Hs.19440	ESTs gb:zc81h08.s1 Pancreatic Islet Homo sapi	1.5
6 0	109875	H03260	Hs.30385	ESTs	1.5 1.5
60	109152	AW380723	Hs.73451	ESTs, Weakly similar to S55024 nebulin,	1.9
	126203 122530	AK001035 AW959741	Hs.130881 · Hs.40368	B-cell CLL/lymphoma 11A (zinc finger pro adaptor-related protein complex 1, sigma	1.9
	124508	BE273688.	Hs.182447	heterogeneous nuclear ribonucleoprotein	1.5 1.5
65	130525	AA361850	Hs.322149	Human clone 137308 mRNA, partial cds	1.9
J.J	127226 106465	AL036559 AA971576	Hs.3463 Hs.225951	ribosomal protein S23 topolsomerase-related function protein 4	1.5
	106970	AA521368	Hs.24252	ESTs	1.5 1.5
	134275	AJ878910	Hs.3688	cisplatin resistance-associated overexpr	1.
70	126825 132443	AA100230 AW246148	Hs.268371	gb:zi81c01.s1 Stratagene colon (937204)	1.
. •	104631	AA002064	Hs.18920	hypothetical protein FLJ20274 ESTs	1. 1.
	111468	H62647	Hs.205481	ESTs	1.
	114317 126158	AA524839 N55989	Hs.469	succinate dehydrogenase complex, subunit	1.
75	113782	AK001567	Hs.16390 Hs.311002	hypothetical protein FLJ 10035 Homo sapiens cDNA FLJ 10705 fis, clone NT	1.
	119229	T03229		gb:FBSC2 Fetal brain, Stratagene Homo sa	1. 1.
	105930 127245	AF016371 AA323958	Hs.9880	peptidyl prolyl isomerase H (cyclophilin	1.
	100967	8E011845	Hs.251064	gb:EST26810 Cerebellum II Homo sapiens c high-mobility group (nonhistone chromoso	1.
80	105149	BE089288	Hs.8958	Homo saplans cDNA FLJ 12024 fis, clone HE	1. 1.
	104542	R29657		gb:F1-1179D 22 week old human fetal live	i.
	124238 127155	AF086006 AA284993		gb:Homo sapiens full length insert cDNA gb:zi23e10.r1 Soares ovary turnor NbHOT H	1.
					1.
				· 93	

	126854	AJ275986	U- 71414	harrien e communication de la communication de	
	107021	AK001342	Hs.71414	transcription factor (SMIF gena)	1.8
	110023	AW294701	Hs.14570	hypothetical protein FLJ22530	1.8
	114899	AKD00342	Hs.31040	ESTs	1.8
5	127315	AF116622	Hs.77846	Homo sapiens mRNA; cONA DKFZp761M0223 (1	1.8
•	110384	H45282	Hs.268798	gb:Homo sepiens clone FLB4217 mRNA seque ESTs	1.8
	132693	BE244200	Hs.55075	and the second s	1.8
	127684	AA568631	Hs.32556	KIAA0410 gene product KIAA0379 protein	1.8
	127297	AW629485	Hs.140720		1.8
10	104249	AF004231	Hs.22405	GSK-3 binding protein FRAT2	1.8
	112652	BE269699	Hs.235782	teukocyte immunoglobulin-like receptor,	1.8
	110312	BE256986	Hs.11896	solute carrier family 21 (organic anion hypothetical protein FLJ12089	1.8
	100417	NM_014003		pre-mRNA splicing factor similar to S. c	1.8
	120532	AA262354	Hs.186648	ESTs, Weakly similar to 138022 hypotheti	1.8
15	127629	AA293279	Hs.29173	hypothetical protein FLJ20515	1.8
	100739	M59287	Hs.2083	CDC-like kinase 1	1.8
	110636	H72868	Hs.19110	ESTs .	1.8
	132957	BE244044	Hs.61469	hypothetical protein	1.8
	115467	Al368784	Hs.48820	TATA box binding protein (TBP)-essociate	1.8
20	132161	W31634	Hs.180799	hypothetical protein FLJ22561	1.8
	129510	AW968504	Hs.123073	CDC2-related protein kinase 7	1.8
	126805	F32658	Hs.101359	chromosome 6 open reading frame 32	1.8
	129295	U63127	Hs.110121	SEC7 homolog	1.8
0.5	127823	AW972893	Hs.78869	transcription elongation factor A (SiI),	1.8 1.8
25	104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m	1.8
	111959	R40978	Hs.271498	ESTs, Moderately similar to ALU1_HUMAN A	1.8
	109303	AA199857	Hs.269291	ESTs	1.8
	112501	AA972447	Hs.288833	Homo septens mRNA; cDNA DKFZp434K087 ((r	1.8
20	127303	AA366951		gb:EST77963 Pancreas tumor III Homo sapi	1.8
30	115982	W92113		gb:zh48e01.r1 Soares_fetal_liver_spleen_	1.8
	123331	AA497013		gb:ae32g02.s1 Gessler Wilms turnor Homo s	1.8
	111598	R11505	Hs.268912	ESTs	1.8
	121643	AA640987	Hs.193767	ESTa	1.8
35	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	1.8
33	118761	AW799109	Hs.226755	ESTs	1.8
	128765	AF073310	Hs.143648	Insulin receptor substrate 2	1.8
	118103	AA401733	Hs.184134	ESTs	1.8
	134595	NM_002401		mitogen-activated protein kinase kinase	1.8
40	134212 128033	AA654353	Hs.17719	EBP50-PDZ Interactor of 64 kD	1.8
70		AI248705	Hs.149321	ESTs	1.8
	126972	NM_016255		Autosomal Highly Conserved Protein	1.8
	111122 114798	N63753	Hs.16492	DKFZP564G2022 protein	1.8
	108349	AA159181	Hs.54900	serologically defined colon cancer anlig	1.8
45	135358	AW954310	Hs.127270	KIAA1545 protein	1.8
	116223	BE622827 AF045458	Hs.99488	hypothelical protein FLJ13044	1.8
	116654	Z26324	Hs.47061 Hs.79204	unc-51 (C. elegans)-like kinase 1	1.8
	124554	N65961	113.7 3204	ESTs, Weakly similar to 138022 hypotheti	1.8
	120259	AW014786	Hs.192742	gb:zaZ7d03.s1 Scares fetal liver spleen	1.8
50	123044	AK001035	Hs.130881	hypothetical protein FLJ12785	1.8
	125261	W90351	Hs.110134	B-cell CLL/lymphoma 11A (zinc finger pro ESTs, Highly similar to CREB-binding pro	1.8
	135026	N92165	Hs.93231	ESTs County strikes to CACE-during pro	1.8
	129951	AL110282	Hs.268024	Homo saplens, clone IMAGE:3873720, mRNA	1.8
	125768	AI557486	Hs.119122	ribosomai protein L13a	1.8
55	114122	R46128	Hs.12751	ESTs	1.8
	133047	AA310600	Hs.63657	peplide:N-glycanase similar to yeast PNG	1.8
	133589	L37388	Hs.75104	RNA-binding protein S1, serine-rich doma	1.8
	130872	U61084	Hs.226307	phorbolin (similar to apolipoprotein B m	1.8 1.8
4 0	133498	BE299587	Hs.85301	calcium binding protein P22	1.8
60	131144	AA305255	Hs.23528	HSPC038 protein	1.8
	104261	AW248364	Hs.5409	RNA polymerase I subunit	1.8
	115507	AI083568	Hs.50601	hypothetical protein MGC10986	1.8
	109073	T05003	Hs.10056	hypothetical protein FLJ14621	1.8
65	115363	AA214618	Hs.152759	activator of S phase kinase	1.8
UJ	112657	AW844878	Hs.19769	hypothetical protein MGC4174	1.8
	102960	A1904738	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.8
	125549	R20215		gb:yg18b09.r1 Soares infant brain 1NIB H	1.8
	133797	AL133921	Hs.76272	retinoblastoma-binding protein 2	1.8
70	125048 103403	AW440068	Hs.59425	hypothetical protein FLJ23323	1.8
/ •	123546	X95406	II- 449C07	gb:H.sapians cyclin E gena.	1.8
	124694	AA608817	Hs.112597	EST	1.8
	102406	R06108 U43177		gb:ye94h05.s1 Soares fetal liver spleen	1.8
	130695	197205	U- 17009	(NONE)	1.8
75	123951	AB012922	Hs.17998	ESTs. Weakly similar to 2109260A B cell	1.8
· -	118533	N71861	Hs.173043	metastasis-associated 1-like 1	1.8
	123197	AA489250	Hs.49413	ESTS CONTROL C	1.8
	125658	AW516428	Hs.78687	gb:ss57h12s1 NCI_CGAP_GCB1 Homo saplens	1.8
	100154	H80720	Hs.81892	neutral sphingomyelinase (N-SMase) activ KIAAD101 gene product	1.8
80	106876	N52821	Hs.269412	ESTs, Moderately similar to ALU7_HUMAN A	1.8
	128339	AL121087	Hs.298406	KIAA0685 gane product	1.8
	105939	AL137728	Hs.12258	Homo saplens mRNA; cONA OKFZp434B0920 (f	1.8
	102495	NM_006762	Hs.79356	Lysosomal-associated multispanning membr	1.8
					1.8
				- 4	

	100221	D20202		Author Survey and the	
	101741	D28383 NM_003199	We 336108		1.8
	101701	NM_002438			1.8
_	107119	Al375499	Hs.27379		1.8 1.8
5	134362	U47742	Hs.82210	zinc finger protein 220	1.8
	127964	F06298		gb:HSC13F081 normalized Infant brain cDN	1.8
	101437	M20681	Hs.7594		1.8
	106204 112716	AA188734 AW590680	Hs.21479 Hs.110802		1.8
10	109779	AB029396	Hs.3353		1.8
	111369	AA535740	Hs.170263		1.8 1.8
	135204	AF087515	Hs.183418		1.8
	105788	AB009698	Hs.23965		1.8
15	110997	AW862823	Hs.168052	KIAA0421 protein	1.8
1.5	111620 115618	R14853	Hs.307478		1.8
	115904	H11695 Al167560	Hs.322901 Hs.61297		1.8
	107510	BE613332	Ha.132055		1.8 1.8
•	116435	AA186761	Hs.334812		1.8
20	112399	R60920	Hs.296770		1.8
	127426	AA854756	Hs.124076	ESTs	1.8
	125175 132972	W52355	Hs.303030		1.8
	125982	AA034365 R98091	Hs.288924		1.8
25	115620	AA399997	Hs.211610	gb:yr30e11_r1 Soares fetal liver splean CUG triplet repeat, RNA-binding protein	1.8
	128115	AI435590	Hs.130168	ESTs	1.8 1.8
	106880	A1493206	Hs.32425	ESTs	1.7
	101199	L22075	Hs.1666	guanine nucleotide binding protein (G pr	1.7
30	104159	BE386983	Hs.283685	hypothetical protein FLJ20396	1.7
50	101368 103648	M13058 AW248439	Hs.73952	proline-rich protein Haeili subfamily 2	1.7
	130717	AA334274	Hs.2340 Hs.18368	junction plakoglobin	1.7
	124981	N25485	Hs.330310	DKFZP564B0769 protein maternal G10 transcript	1.7
~ ~	124770	AA984414	Hs.120429	ESTs	1.7 1.7
35	126926	AA179472	Hs.832	ESTs, Highly similar to A41029 Integrin	1.7
	101636	BE392781	Hs.89474	ADP-ribosylation factor 6	1.7
	123553	Al494291	Hs.111977	ESTs	1.7
	127172 130621	AA292208 AW513087	Hs.251278	KIAA1201 protein	1.7
40	116925	H73110	Hs.16803 Hs.260603	LUC7 (S. cerevisiae)-like ESTs, Moderatety similar to A47582 B-ce	1.7
	108845	AW362901	Hs.68864	ESTs, Weakly similar to phosphatidylseri	1.7 1.7
	128092	AA904817	Hs.166229	ESTs	1.7
	128193	AJ224442	Hs.155020	putative methyltransferase	1.7
45	113965	Al268666	Hs.19631	ESTs, Wealdy similar to I38022 hypotheti	1.7
43	106620	D52562	Hs.296317	KIAA1789 protein	1,7
	102926 114964	W28363 BE085271	Hs.239752	nuclear receptor subfamily 2, group F, m	1.7
	101800	NM_008433	Hs.8834 Hs.105806	ring finger protein 3 granulysin	1.7
	130094	NM_001471		gamma-aminobutyric acid (GABA) B recepto	1.7 1.7
50	120112	AA180240	Hs.6083	Homo saplens cDNA: FLJ21028 fis, clone C	1.7
	109978	H09356	Hs.22528	ESTs	1.7
	121252	AA393907	Hs.97179	ESTs	1.7
	127768 125445	AW085002	Hs.156187	EST8	1.7
55	100052	AJ452722	Hs.7709	WW domain binding protein 1	1.7
	119863	AA081218	Hs.58608	Homo sapiens cDNA FL114208 fis, clone NT	1.7 1.7
	134333	AW888411	Hs.81915	teukemia-associated phosphoprotein p18 (1.7
	123541	AW976511	Ha.112592	ESTs	1.7
60	134191	W26632	Hs.7979	KIAA0736 gene product	1,7
JU	103305 112411	X82279	N- 074545	gb:H.saptens Fas, Apo-1 gene (promoter a	1.7
	100598	R43090 AL121734	Hs.271510 Hs.146409	ESTs, Moderately similar to ALU1_HUMAN A	1.7
	113610	T93279	115.140405	cell division cycle 42 (GTP-binding prot gb:ye25f01.a1 Stratagene lung (937210) H	1.7
~~	105593	AA279341	Hs.174151	aldehyde oxidase 1	1,7 1.7
65	125317	Z99348	Hs.112461	ESTs, Wealdy similar to 138022 hypotheti	1.7
	125956	AK000214	Hs.129014	hypothetical protein FLJ20207	1.7
	105105	R61532	Hs.87016	hypothetical protein FLJ22938	1.7
	132791 116996	A8029551	Hs.7910	RING1 and YY1 binding protein	1.7
70	133335	H83935 BE251012	Hs.40535 Hs.263812	ESTs	1.7
. •	120959	BE247692	Hs.102469	nuclear distribution gene C (A_nidulans) putative nuclear protein	1.7
	105621	AL040058	Hs.6375	uncharacterized hypothalamus protein HTO	1.7 1.7
	106181	AI803651	Hs.191608	ESTs	1.7
75	125661	AA491830	Hs.25689	ESTs	1.7
13	127585	AA604144	Hs.190632	ESTs	1.7
	112035	AI955289	Hs.300759	ribosomal protein L38	1.7
	102870 108039	M64437 AA280319	Hs.234799 Hs.288840	brezkpolnt cluster region PRO1575 protein	1.7
	125898	AK001823	Hs.92287	Homo sapiens mRNA; cDNA DKFZp564C2478 (F	1.7
80	114740	N70103		gb:za53e10.s1 Soares felal liver spicen	1.7 1.7
	120304	AA192469	Hs.271838	EST8	1.7
	103433	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	1.7
	116180	AA463902	Hs.13522	ESTs, Weakly similar to I38022 hypothet	1.7
				06	

	105250	AE474400	11- 6364		
	105269 125431		Hs.6764	histone deacelylase 6	1.7
	133579	AW851639 X75346	Hs.75584 Hs.75074	polymyositis/scheroderma autoantigen 2 (1.7
	105355	AL031447	Hs.26938	mitogen-activated protein kinase-activat	1.7
5	129601	AB032964	Hs.115726	Homo sapiens, clone IMAGE:4053044, mRNA, KIAA1138 protein	1.7
_	113739	AA356599	Hs.173904	ESTs .	1.7 1.7
	100840	U04816	Hs.183418	cell division cycle 2-like 1 (PITSLRE pr	1.7
	122878	AAB47744	Hs.99640	ESTs	1.7
10	119495	BE144608	Hs.55533	ESTs	1,7
10	125669	R51308	Hs.333256	ESTs, Wealty similar to ALUS_HUMAN ALU	1.7
	109891	HD4757	Hs.323176	ESTS	1.7
	126884	U49436	Hs.288236	KIAA1856 protein	1.7
	132977	AA093322	Hs.301404	RNA binding motif protein 3	1.7
15	101396	BE257931	Hs.78998	problerating cell nuclear antigen	1.7
13	104730 102205	AW139789 BE242291	Hs.16370	Homo saplens cDNA FLJ11652 fis, clone HE	1.7
	112945	AW138458	Hs.197540 Hs.20787	hypoxia-inducible factor 1, alpha subuni	1.7
	129902	AA076278	Hs.13277	Homo sapians cDNA: FLJ21688 fis, clone C hypothetical protein FLJ22054	1.7
	107157	AW853745	Hs.286035	hypothetical protein FLJ22686	1.7
20	133229	AL137480	Hs.6834	KIAA1014 protein	1.7 1.7
	129912	AF155098	Hs.107213	hypothelical protein FLJ20585	1.7
	119811	AW137640	Hs.231444	Homo sapiens, Similar to hypothetical pr	1.7
	126323	N77584	Hs.68644	Homo saplens microsomal signal peptidase	1.7
25	133134	AF198620	Hs.65648	RNA binding motif protein 8A	1.7
25	115278	AK002163	Hs.301724	hypothetical protein FLI11301	1.7
	133817	AW578718	Hs.7644	H1 histone family, member 2	1.7
	130753	AA205223	Hs.189	phosphodiesterase 4C, cAMP-specific (dun	1,7
	107463	AW952022	Hs.315164	hypothetical protein similar to actin re	1.7
30	121009	NM_001533	Hs.2730	heterogeneous nuclear ribonucteoprotein	1,7
50	125546 129991	H09950 R28386	Un 17000C	gb:ym01d12.r1 Soares infant brain 1NIB H	1.7
	119015	N95490	Hs.179925	ESTs, Weakly similar to ALUS_HUMAN ALU	1.7
	100058	1133430	Hs.29700	hypothetical protein FL120094	1.7
	116655	AF271732	Hs.68090	bridging integrator-3	1.7
35	119898	R93325	Hs.58690	ESTs	1.7
	105021	H07960	Hs.306044	CGI-05 protein	1.7
	102098	N25485	Hs.330310	maternal G10 transcript	1.7 1.7
	126730	AA442429		gb:zv70g02.rl Soares_total_fetus_Nb2HF8_	1.7
40	113427	T85105	Hs.15471	ESTs	1.7
40	122317	T85253	Hs.290874	ESTs, Weakly similar to ALUS_HUMAN ALU S	1.7
	130503	BE208491	Hs.295112	KIAA0818 gene product	1.7
	117348	N24157		gb:yx96b12.s1 Soares melanocyte 2NbHM Ho	1.7
	127033	AF169301	Hs.9098	sulfate transporter 1	1.7
15	128554	AW972147	Hs.101395	hypothetical protein MGC11352	1.7
45	124733	R20547	Hs.100830	ESTs	1.7
	106310	R98185	Hs.17240	ESTs	1.7
	122638	AL137476	Hs.123609	Homo saplens mRNA; cDNA DKFZp43410623 (f	1.7
	101075	L03532	Hs.79024	heterogeneous nuclear ribonucleoprotein	1.7
50	126659 127717	T16245	Us 472200	gb:NIB1005R Normalized Infant brain, Ben	1.7
50	105441	F12209 N28522	Hs.173380 Hs.8935	CK2 interacting protein 1; HQ0024c prote	1.7
	104188	AA478423	Hs.300870	quinolinate phosphoribosyltransferase (n	1.7
	134750	129073	Hs.1139	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	1.7
	106826	BE253927	Hs.24983	cold shock domain protein A hypothetical protein from EUROIMAGE 2021	1.7
55	113511	T89578	Hs.189740	ESTs	1.7
	111070	NM_006201		PCTAIRE protein kinase 1	1.7 1.7
	129091	AA056483	Hs.301463	Human Chromosome 16 BAC clone CIT987SK-A	1.7
	129710	AJ277841	Hs.120963	ELG protein	1.7
60	132833	U78525	Hs.57783	eukaryotic translation initiation factor	1.7
60	125775	AW514585	Hs.29205	alpha integrin binding protein 63	1.7
	113675	T81034	Hs.14841	ESTs	1.7
	100487	AU076640	Hs.15243	nucleolar protein 1 (120kD)	1.7
	119302	T25725	11 470400	gb:ESTDIR152 CD34+DIRECTIONAL Homo saple	1.7
65	128245 130322	AA993101	Hs.170486	ESTs	1.7
00	135363	AW589601	Hs.154545	PDZ domain containing guanine nucleotide	1.7
	125181	R40815	Hs.12396	Wilms' tumour 1-associating protein	1.7
	132347	BE271016	Hs.169850	ESTs, Weakly similar to 2004399A chromos	1.7
	127206	AW816490	Hs.337508	ESTs, Weakly similar to T21554 hypotheti ESTs	1.7
70	121880	AW946155	Hs.7750	hypothetical protein AL133206	1.7
	125797	H03117	Hs.111497	similar to mouse neuronal protein 15.6	1.7
	114601	AA075568		gb:zm88f08.s1 Stratagene ovarian cancer	1.7 1.7
	126278	AA417302	Hs.63042	DKFZp564J157 protein	1.7
75	120964	AA398085	Hs.142390	ESTs	1.7
75	133634	AL035071	Hs.234279	microtubula-associated protein, RP/EB fa	1.7
	107025	AA825523	Hs.21255	ESTs. Wealtly similar to 138022 hypotheti	1.7
•	105538	AA493453	Hs.247817	H2B histone family, member A	1.7
	135398	M16029	Hs.287270	ret proto-oncogene (multiple endocrine	1.7
80	115794	AA424900	Hs.112227	membrane-associated nucleic acid binding	1.7
55	102083	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	1.7
	100188 130868	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.7
	110493	AB037855 Al247707	Hs.171917	hypothetical protein FLJ 11085	1.7
		/44-11VI	Hs.36915	ESTs	1.7
				· 96	

5	128764 / 134065 2 101082 E	AA252457 AW024282 X78992 BE616731 U20582	Hs.86543 Hs.104938 Hs.78909 Hs.80645	ESTs, Moderately similar to T00256 hypot hypothetical protein MGC15906 butyrate response factor 2 (EGF-response interferon regulatory factor 1	1.7 1.7 1.7 1.7
J	106974 126752 133327	AIB17130 AI073373 AL390127	Hs.2149 Hs.9195 Hs.326923 Hs.7104	actin like protein Homo sapiens cDNA FLJ13698 fis, clone PL EST, Weakly similar to 138022 hypothetic Kruppel-like factor 13	1.7 1.7 1.7 1.7
10	105615 116295	T81309 AA281959 AA742596 A1125887	Hs.251664 Hs.5210 Hs.91218 Hs.20734	Insufin-like growth factor 2 (somatomedi glia maturation factor, gamma ESTs, Weakly similar to 2004399A chromos ESTs	1.7 1.7 1.7 1.7
1.5	104570 134752	AW978870 BE246762	Hs.131828 Hs.89499	ESTs arachidonate 5-lipoxygenase	1.7 1.7
15	119244 131152	W27893 AW407564 NM_004380	Hs.23598	putative translation initiation factor ribosomel protein \$18 CREB binding protein (Rubinstein-Taybi s	1.7 1.7 1.7
20	106542	8E242676 AA339541	Hs.73172 Hs.24956	growth factor independent 1 hypothetical protein FLJ22056	1.7 1.7
20		AW207000 AW500131	Hs.126857 Hs.171763	Homo sepiens cDNA FLJ12936 fis, clone NT CD22 antigen	1.7 1.7
	125840	AB028986 AA283893	Hs.12064 Hs.337079	ubiquitin specific protease 22	1.7
0.0	120041	AA830882	Hs.59368	ESTs ESTs	1.7 1.7
25		Al281459 AA449804	Hs.270114 Hs.292154	ESTs stromal cell protein	1.7 1.7
			113.202104	Strainer Cell protein	1.7
	Table 2B: Pkey:		hique Fos omi	eset Identifier number	
30	CAT numb	ber. G	ene cluster nu	mber	
	Accession	r G	Senbank access	ion numbers	
	Pkey 108451	CAT numb		Accession	
35	124236	13766_27 46919_1		AA079195 AA084955 AA126308 AA084956 AF086006 H64722 H65212 H66282	
	115982	173_2		W92113 AA702794 BE044316 W91984 AA679375 T	4184 AA679335 BE503126 AW502118 BE467367 AA584550 AW139964 R93353
				Al124782 AA889402 AA765804 AA765530 AA05569	A447817 AA447667 F13631 AW268271 AA055366 AW629027 AA677404 AA831618 AA594019 Al267368 AA456946 R93354 AF264624 AW668618 AA601493
40	116665 125165	1394292_ 1852047_	1	F04405 BE173130 W45350 W45406	
	125324	1692163_		R07785 T85948 T86972	
	126053 125499	1601238_ 1562851_		H64450 H64464 H10543 R11878	
45	126127	1205826	1	N95428 W24040 AW751366 H81987	
43	125546 125549	356478_1 1702179_		H09950 R18413 AA570553 AW973425 R20215 R18767	
	125761 127155	1744008_	1	R68351 R68364	
50	125957	200358_1 1583542_		AA284993 AA478122 AA477923 H41694 H45213	
50	125982 127245	1766315 226662_1		R98091 W92898 AA323958 AA370268	
	127248	227560_1	1	AA364195 AA325029 AW962050	
	127262 126659	231725_1 1541209_		AA828125 AA834883 AA330555 T16245 R19694 F13545 H10299 T66048 T65279 H1	RANA
55	127303 127315	258778_1		AA366951 AA470999 AA469425	•••
	126730	37938_1 297653_1	1	AF116622 A1114507 AA640834 AA377999 AA442429 T19477	
	103898 126872	187213_; 142696_;		AA24884 AWAENOTO AA13EEE3 AA13EEEE AWA10301 AA09A	358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
60				BE011368 BE011362 BE011215 BE011365 BE0113	
	112540 127705	1605263 966283_		R69751 R70467 H69771 H80879 H80878 AJ003322 AJ003324	
	121335 120734	279548_ 208882_	1	AA404418 AI217248	
65	114620	32062_8		AA299948 AA299949 AA642974 AA084223	
	122652 123638	26401_3i	0 _AA609263	AA454641 AA609263	
	100842	tigr_HT4:	398	U05597	
70	116548 123783	genbank	_D20433 _AA610112	D20433 AA610112	
	125032 123808		T74884 AA620552	T74884 AA620552	
	102316	entrez_U	134301	U34301	
75	102406 134076	entrez_U 40321_1		U43177 AF086215 W02702 AA284288 W25655	
	104542	_		R29657	
	113119 104799		_T47910 _AA029703	T47910 AA029703	
80	127984 120809	135151_		F06298 R18057	
-	113610	genbank	_T93279	AA346495 T93279	
	113947 101045		_W84768 I05614	•	
		_			

	129969	genbank_N57818	
	117031	genbank_H88353	
	101447 124540	entrez_M21305	
5		genbank_N63232	
,	124554	genbank_N65961	
	117348	genbank_N24157	
	117357	genbank_N24829	
	124677	genbank_R01073	
10	124694	genbank_R06108	
10	103138	entrez_X65965	
	103305	entrez_X82279	
	103392	entrez_X94563	
	103403	entrez_X95406	
15	119229	genbank_T03229	
IJ	119302	genbank_T25725	
	126825	430458_1	AA100230 AA100274
	105225	genbank_AA211777	
	121292	genbank_AA401807	1
20	112853	genbank_T02843	T02843
20	121387	genbank_AA405854	
	114601	genbank_AA075566	
	100221	entrez_D28383	D28383
	123197	genbank_AA489250	AA489250
25	114740	379876_1	N70103 N70020 AW383189 AI207469 W00935 W00906 AA551669 AI343837 AA135199
20	123331	genbank_AA497013	
	107794	genbank_AA019255	
	100554	Ugr_HT2241	M95923
	123423	genbank_AA598484	
30	123474 109061	genbank_AA599209	
50	103001	genbank_AA160898	

TABLE 3A: About 1346 Genes Up-regulated in Acute Lymphocytic Leukemia (ALL) Compared to Normal Adult Hernatopoletic Tissues

Table 3A lists about 1346 Genes Up-regulated in acute lymphocytic leukemia (ALL) compared to normal adult hernatopoletic tissues. These were selected from 35403 probesets on the Affymethy/Eos Hut01 GeneChip array such that the ratio of "average" teukemia level was set to the 85° percentile amongst various ALL samples. The "average" normal adult hernatopoletic tissues was greater than or equal to 3.0. The "average" teukemia level was set to the 85° percentile amongst various ALL samples. The "average" normal adult hernatopoletic tissue level was set to the 75° percentile amongst various non-both the numerator and the denominator before the ratio was evaluated.

Piery:

Unique Eos probeset identifier number

EXACC:

Exemplar Accession number, Genbank accession number

UniqueneID:

Unique Eos probeset identifier number

UniqueneID:

Unique Genechip accession number

Unique Genechip accession

35

40

45	Pkey	ExAcon	11-7		
	129498	AA449789	UnigenelD	Unigene Title	R1
	100458	S74019	Hs.75511	connective tissue growth factor	57.88
	133774	X54079	Hs.247979	pre-8 lymphocyle gene 1	49.45
	102564	U59423	Hs.76067	heat shock 27kD protein 1	48.42
50	130650		Hs.79067	MAD (mothers against decapentaplegic, Dr	41.49
50	132922	AB040951	Hs.284208	DKFZP434N161 protein	35.88
		AF249745	Hs.6066	Rho guanina nucleotida exchange factor	35.74
	112254	AA852097	Hs.25829	ras-related protein	33.28
	106706	AB037810	Hs.18760	KIAA1389 protein	32.39
55	101050	AU077324	Hs.1832	nauropeptide Y	30.68
"	102455	U48705	Hs.75562	discoldin domain receptor family, member	26.81
	101838	BE243845	Hs.75511	connective tissue growth factor	25.46
	113374	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	24.69
	134125	NM_014781	Hs.50421	KIAA0203 gene product	24.63
60	106943	AW888222	Hs.9973	tensin	23.14
60	130069	Al754813	Hs.146428	collagen, type V, alpha 1	23.06
	119073	BE245360	Hs.279477	ESTs	22.53
	130444	M12125	Hs.300772	tropomyosin 2 (beta)	21.96
	100420	D86983	Hs.118893	Melanoma associated gene	21.05
65	114324	AF084481	Hs.26077	Wolfram syndrome 1 (wolframin)	18.95
65	101400	M15990	Hs.194148	v-yes-1 Yamaguchi sarcoma viral oncogene	18.48
	102759	NM_605100	Hs.788	A kise (PRKA) anchor protein (gravin)	17.88
	100893	BE245294	Hs.180789	S164 protein	16.75
	131689	AB012124	Hs.30696	transcription factor-like 5 (basic helix	
	106410	AB037787	Hs.26229	neurolioin 2	16.60
70	101304	AA001021	Hs.6685	thyroid hormone receptor interactor 8	16.51
	131524	AB040927	Hs.301804	KIAA1494 protein	15.60
	107794	AA019255	110.001001	gb:ze56e10.s1 Soares reti N2b4HR Homo	15.01
	129213	AJ148494	Hs.109526	CCTo Month - Court IDV2 1784441 DOG14	14.78
	116068	AA328041	Hs.194329	ESTs, Weakly similar to IRX2_HUMAN IROQU	14.76
75	134418	X68264	Hs.211579	hypothetical protein FLJ21174	14.24
	134545	AI902899	Hs.85155	melanoma cell adhesion melecule	14.06
	114009	A)248544	Hs.103000	butyrate response factor 1 (EGF-response	14.03
	115110	AK001671	Hs.11387	KIAA0831 protein	13.93
	130107	AF112977	Hs.172887	KIAA1453 protein	13.75
80	133558	X66945		phytanoyl-CoA hydroxylase (Refsum diseas	13.60
	100871	785231	Hs.748	fibroblast growth factor receptor 1 (frns	13.60
	101462	AL035668	Hs.179661	tubulin, beta 5	13.50
	120809	AA346495	Hs.73853	bone morphogenetic protein 2	13.48
	120003	WW940433		gb:EST52657 Fetal heart II Homo sapiens	13.33

	123340	AA504264	Hs. 182937	peptidylprolyl isomerasa A (cyclophilin	13.25
	103460	Al021993	Hs.14331	S100 calcium-binding protein A13	13.25
	102460	U48959	Hs.211582	myosin, light polypeptide kise	13.14
5	100168 115844	H73444	Hs.394	adrenomedullin	13.09
	130103	Al373062 Y13492	Hs.332938	hypothetical protein MGC5370	13.00
	102407	AW602154	Hs.149098	smoothelin	12.92
	113632	T94907	Hs.82143 Hs.188572	E74-like factor 2 (ets domain transcript	12.03
	118951	NM_000448	Hs.73958	ESTs recombition activating gene 1	11.85
10	100305	NM_004941	Hs.171872	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	11.73
	109737	AA055415	Hs.13233	ESTs. Moderately similar to A47582 B-cel	11.63
	122577	AA829725	Hs.334437	hypothetical protein MGC4248	11.55
	115147	AA745781	Hs.38399	hypothetical protein MGC2454	11.49 11.40
1.5	132303	BE177330	Hs.325093	Homo saplens cD: FLJ21210 ffs, clone C	11.37
15	103176	AL021154	Hs.76884	inhibitor of D binding 3, domint neg	11.17
	108358	MB1933	Hs.1634	cell division cycle 25A	11.15
	104584	AA704538	Hs.193777	ESTs	11.12
	106777	AF037261	Hs.33787	vinexin beta (SH3-containing adaptor mol	11.08
20	121054	AW976570	Hs.97387	ESTs	10.90
20	119400	T92767		gb:ye27d06.s1 Stratagene lung (937210) H	10.83
	126610 134555	AI911353	Hs.191391	ESTs	10.83
	131555	U34879 T47384	Hs.85279	hydroxysteroid (17-beta) dehydrogese 1	10.80
	130979	NM_012446	Hs.278613	Interferon, elpha-inducible protein 27	10.79
25	113783	AL359588	Hs.169833 Hs.7041	single-stranded-D-binding protein	10.70
	123503	AW975051	Hs.293156	hypothetical protein DKFZp7628226	10.65
	117031	H88353	113.233130	ESTs, Weakly similar to 178885 serine/th	10.60
	100752	T81309	Hs.251664	gb:yw21a02.s1 Morton Fetal Cochlea Homo	10.45
	102618	AL037672	Hs.81071	insufin-fike growth factor 2 (somatomed) extracellular matrix protein 1	10.44
30	113089	T40707	Hs.270862	ESTS	10.38
	132089	W22007	Hs.39122	hypothetical protein MGC15737	10.33 10.29
	101663	NM_003528	Hs.2178	H2B histone family, member Q	10.23
	104876	Al933128	Hs.25220	ike-glycosyttransferese	10.23
25	106370	AF039843	Hs.18676	sprouty (Orosophila) homolog 2	10.18
35	129406	AB018255	Hs.111138	KIAA0712 gene product	10.18
	115354	AA281636	Hs.334827	ESTs	10.13
	123077 131273	AA485229	Hs.105649	ESTs	10.05
	126177	AW206008	Hs.283378	Homo sapiens cD: FLJ21778 fis, clone H	9.95
40	133699	AW752782 BE501689	Hs.129750	hypothetical protein FLJ 10546	9.83
	110855	AB007928	Hs.75617 Hs.28169	collagen, type IV, alpha 2	9.80
	111826	R35975	LE: 50 10A	KIAA0459 protein	9.65
	126947	Z40778	Hs.191837	gb:yh91b07.s1 Soares placenta Nb2HP Homo ESTs	9.58
	116674	AI768015	Hs.92127	ESTs	9.50
45	129087	Al348027	Hs.108557	hypothetical protein PP1057	9.48
	114837	BE244930	Hs.166895	ESTs	9.46 9.45
	120009	Al080491	Hs.93270	ESTs, Moderately similar to S65657 atpha	9.45 9.45
	112483	AW989785	Hs.285885	Homo sapiens cD FLJ11321 fis, clone PL	9,40
50	103487	AA743603	Hs.172108	nucleoporin 88kD	9.30
50	105675	AL390083	Hs.271277	hypothetical protein from EUROIMAGE 3636	9.28
	129158 114394	NM_004413	Hs.109	dipeptidase 1 (rel)	9.23
	133331	T34462 Y14487	Hs.103291	neuritin	9.17
	114787	AA156509	Hs.738	ribosomal protein L14	9.11
55	125502	AW977181	Hs.231892 Hs.194718	ESTs, Wealdy similar to S65657 alpha-1C-	9.10
	132325	N37065	Hs.44856	Zinc finger protein 265	9.03
	127968	AA830201	Hs.124347	hypothetical protein FLJ12118 ESTs	9.01
	114605	AL157423	Hs.306478	Homo sapiens mR; cD DKFZp76100511 (f	9.00
60	114875	AA235609	Hs.236443	Homo saplans mR; cD DKFZp564N1063 (f	8.93 8.93
60	129898	AI672731	Hs.13256	ESTs	8.89
	108283	W21493	Hs.28329	hypothetical protein FLJ14005	8.89
	117130	AA748850	Hs.125830	bladder cancer overexpressed protein	8.88
	105553	AA258758	Hs.31178	ESTs	8.85
65	103657 105831	Z73677 AA329449	11. 5	gb:H.sapiens gene encoding plakophilin 1	8.83
00	106375	AW872878	Hs.247302	twisted gastrulation	8.82
	114518	AW163267	Hs.289072 Hs.106469	hypothetical protein FLJ22175	8.80
	123433	AW450922	Hs.112478	suppressor of var1 (S.cerevisiae) 3-like	8.75
	134558	NM_001773	Hs.85289	ESTs CD34 antigen	8.67
70	115893	AI652127	Hs.48419	ESTs	8.67
	128621	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mR, comp	8.67
	122798	AW366286	Hs.145696	splicing factor (CC1.3)	8.60 8.58
	112554	R71489	Hs.29198	EST	8.55
75	129989	N57818		gb:yv59d07.s1 Soares fetal liver spieen	8.53
75	131558	AA453208	Hs.28726	RAB9, member RAS oncogene family	8.45
	134027	Z97630	Hs.226117	H1 histone family, member 0	8.45
	134138	AB023169	Hs.7935	KIAA0952 protein	8.43
	120030 101005	AI076355	Hs.58694	ESTs	8.43
80	115423	NM_005239 AI499516	Hs.85146	v-ets avian erythroblastosis virus E26 o	8.33
	104948	AW242407	Hs.89303	ESTS	8.33
	131965	W79283	Hs.73848 Hs.35962	carcinoembryonic antigen-related cell ad ESTs	8.30
	126426	AA125984	1000000		8.30
				gb:zn27h06.r1 Stratagena neuroepithelium	8.28
				00	

	400000				
	108886 107985	AW248434 T40064	Hs.91521	hypothetical protein	8.26
	114239	AL137667	Hs.71968	Homo sapiens mR: cD DKFZp564F053 (fr	8.25
	124281	Al333756	Hs.267445	Homo seplens mR; cD DKFZp434B231 (fr	8.23
5	117099	H93699	Hs.111801	arsete resistance protein ARS2	8.23
	119432	AL120247	Hs.40109	gb:yv16a11.s1 Soares fetal liver spieen	8.20
	115967	AI745379	Hs.42911	KIAA0872 protein ESTs	8.15
	132355	D67942	Hs.46328	fucosyltransferase 2 (secretor status in	8.15
10	108339	AW151340	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.13
10	131694	NM_000246	Hs.3076	MHC class II transactivator	8.10 8.05
	104897	N33937	Hs.10336	ESTs	8.03
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	8.03
	130404 115729	AJ872727	Hs.78753	endoglin (Osler-Rendu-Weber syndrome 1)	8.00
15	127216	AA417812 AI798703	Hs.38775	ESTS	8.00
	131693	AW983776	Hs.143702	ESTs, Wealty similar to S70029 probable	7.95
	113107	AI821027	Hs.110796 Hs.8429	SAR1 protein	7.93
	122282	BE246331	Hs.98401	ESTS	7.90
	111040	Al435502	Hs.14931	Homo sapiens mR full length insert cON ESTs	7.90
20	127987	AI022103	Hs.124511	ESTs	7.90
	125317	Z99348	Hs.112461	ESTs, Waakly similar to 138022 hypotheti	7.90
	105242	A1554857	Hs.27888	ESTs, Weakly similar to serine/threonine	7.88 7.75
	100421	D86985	Hs.79276	KIAA0232 gene product	7.75 7.71
25	114359	NM_016929	Hs.283021	chloride Intracellular channel 5	7.70
23	119772	AJ250839	Hs.58241	gene for serine/threonine protein kise	7.70
	124040 134361	U23752	Hs.32964	SRY (sex determining region Y)-box 11	7.65
	105476	BE549343 AL117352	Hs.82208	acyl-Coenzyme A dehydrogese, very long	7.57
	113289	T66900	Hs.120828	Human D sequence from clone RP5-876B10	7.55
30	122707	NM_002039	Hs.188446 Hs.239706	ESTs	7.50
	130055	AJ568248	Hs.146355	GRB2-associated binding protein 1	7.50
	108766	AF145713	Hs.61490	wab! Abelson murine leukemia viral onco schwannomin-interacting protein 1	7.49
	107957	Z36842	Hs.57548	ESTs	7.45
26	123116	AW190412	Hs.183738	FERM, RhoGEF (ARHGEF) and pleckstrin dom	7.45
35	123190	AA489212	Hs.105228	EST VANISET / BID PREASURE BOTH	7.38 7.38
	129574	AA026815	Hs.11463	UMP-CMP kise	7.38
	115274	C01568	Hs.86671	ESTs	7.35
	102571	U60115	Hs.239069	four and a half LIM domains 1	7.34
40	116845 134851	AA649530 AB011124		gb:ns44f05.a1 NCI_CGAP_Alv1 Homo saplens	7.33
40	101780	M82882	Hs.90232	KIAA0552 gene product	7.33
	125042	T78906	Hs.154365 Hs.269432	E74-like factor 1 (ets domain transcript	7.28
	118472	AL157545	Hs.42179	ESTs. Moderately similar to ALU1_HUMAN A	7.28
	108700	AA121518	Hs. 193540	bromodomain and PHD finger containing, 3	7.25
45	109411	R98881	Hs.109655	ESTs, Moderately similar to 2109260A B c	7.23
	127692	AI021912	Hs.187983	sex comb on midleg (Drosophila)-like 1 ESTs	7.20
	128501	AL133572	Hs.199009	protein containing CXXC domain 2	7.18
	107727	AA149707	Hs.173091	ubiquitin-like 3	7.18
50	118089	AI762507	Hs.47878	ESTs	7.14 7.12
30	106025	AV653785	Hs.173334	ELL-RELATED R POLYMERASE II, ELONGATIO	7.12
	122111	AW593206	Hs.98785	Ksp37 protein	7.08
	119674 126607	W60379	Hs.57773	ESTs	7.05
	121545	W87425 AA412442	Hs.114688	ESTs	7.05
55	113287	T66847	Hs.98132	ESTs	7.05
-	126672	AA255592	Hs.194040	ESTs. Wealdy similar to 138022 hypotheti	7.03
	132087	H14486	Hs.203631 Hs.3903	ESTs. Weakly similar to altertively sp	7.00
	118697	N22706	Hs.43234	Cdc42 effector protein 4; binder of Rho ESTs	6.97
60	100295	M74782	Hs.172689	interleukin 3 receptor, alpha (low effin	6.97
60	101188	L20320	Hs.184298	cyclin-dependent kise 7 (homolog of Xe	6.95
	121481	AA411931		gb:zu03g05.s1 Soares_lesis_NHT Horno sap	6.95 6.95
	113003	AW292315	Hs.7215	ESTs	6.93
	101851	BE260964	Hs.82045	midkine (neurite growth-promoting factor	6.91
65	113529	AJ190741	Hs.177415	Finkel-Biskis-Reilly murine sarcoma viru	6.90
05	132887	AA195831	Hs.273385	guanine nucleotide binding protein (G pr	6.90
	113560 123440	T91015 AI733692	Hs.268826	ESTs	6.85
	130390	AA490770	Hs.112488	ESTs	6.83
	133889	U48959	Hs.182382 Hs.211582	ESTs	6.83
70	113573	R89379	Hs.15990	myosin, light polypeptide kise	6.83
	112453	R63899	Hs.28455	ESTs ESTs	6.80
	125221	AA236115	Hs.120785	ESTS	6.78
	134081	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t	6.78
75	127610	AA960867	Hs.150271	ESTs, Highly similar to unmed protein	6.77 6.75
75	105486	AW449258	Hs.6187	ESTs & draw and a draw of protess	6.75 6.75
	107796	AA058848	Hs.60797	ESTs	6.75 6.71
	132754	AJ752244	Hs.75309	eukaryotic translation elongation factor	6.71
	105806	AF206019	Hs.110347	REV1 (yeast homolog)- like	6.70
80	110837 117698	H03109 N82293	Hs.108920	HT018 protein	6.65
	128994	AF205849	Hs.45107	ESTs	6.65
	129131	AB026436	Hs.107740 Hs.177534	Kruppel-like factor 2 (lung)	6.65
	108528	AA650558	Hs.325202	dual specificity phosphatase 10	6.65
			15340444	ESTs, Highly stimilar to GBAS_HUMAN GUANI	6.62

	131009	AF169802	Hs.22142	a deshama hiji mdushasa hiji a	
	129389	NM_012445	Hs.288126	cylochrome b5 reductase b5R.2 spondin 2, extracellular matrix protein	6.61 6.60
	125278	AJ218439 .	Hs.129998	enhancer of polycomb 1	6.59
5	124667	W24320	Hs.102941	Homo sepiens cD: FLJ21531 fis, clone C	6.59
5	105640	AA001021	Hs.6685	thyroid hormone receptor interactor 8	6.58
	106474 105808	BE383668 AI133161	Hs.42484	hypothetical protein FLJ 10618	6.58
	120087	AF186780	Hs.286131 Hs.79219	CGI-101 protein	6.53
	100514	AU076887	Hs.28491	Ra/GDS-tike gene; KIAA0959 protein spermidine/spermine N1-acetyltrans/erase	6.52
10	108378	A1368460	Hs.74615	platelet-derived growth factor receptor.	6.50 6.50
	133350	A1499220	Hs.71573	hypothetical protein FLJ10074	6.50
	115673	AA406341	Hs.269908	Homo saplens cD FLJ11991 fis, clone HE	6.48
	133410	Y07847	Hs.73088	RAS-related on chromsome 22	6.48
15	131281 105510	AA251716 Z42047	Hs.25227	ESTs	6.46
	128766	AW160432	Hs.283978 Hs.296460	Homo sapiens PRO2751 mR, complete cds crantofacial development protein 1	6.45
	114530	AA601038	Hs.191797	ESTs, Weakly similar to S65657 sipha-1C-	6.45 6.43
	120120	BE547267	Hs.59791	hypothetical protein MGC13183	6.40
20	120593	AA748355	Hs.193522	ESTs	6.40
20	125832	AA528600	Hs.117587	ESTs	6.38
	129837 115302	NM_004606 AL109719	Hs.1179	TATA box binding protein (TBP)-associate	6.38
	126137	AA312594	Hs.47578 Hs.99115	ESTs hypothetical protein FLJ20689	6.33
	114465	BE621056	Hs.131731	hypothetical protein FLI11099	6.30 6.29
25	125562	A1494372	Hs.98968	hypothetical protein FL123058	6.29
	127380	AF070554	Hs.15535	Homo sapiens clone 24582 mR sequence	6.26
	106958	R06428	Hs.226351	ESTs	6.25
	105962 109416	AW880358 BE268388	Hs.339808	hypothetical protein FLJ 10120	6.25
30	111116	AK002039	Hs.86945 Hs.28243	ESTs, Weakly similar to A45010 X-linked	6.23
	127282	AA347158	Hs.185780	Homo septens cD FLJ11177 fis, clone PL ESTs	6.23 6.23
	113074	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	6.21
	101664	AA436989	Hs.121017	H2A histone family, member A	6.20
35	103317	X83441	Hs.166091	figase IV, D, ATP-dependent	6.20
33	133894 109260	AW021236 AW978515	Hs.180433	rTS beta protein	6.19
	112772	A1992283	Hs.131915 Hs.35437	KIAA0863 protein	6.18
	132050	Al267615	Hs.38022	ESTs, Moderately similar to 138026 MLN 6 ESTs	6.18
40	113009	T23699	Hs.7246	ESTs	6.18 6.17
40	118835	AA535246	Hs.50852	ESTS	6.16
	125626	A1038854	Hs.180789	\$164 protein	6.15
	117086 101960	AA581602 AL036287	Hs.41840	ESTs	6.14
	104488	N58191	Hs.194662 Hs.106511	calponin 3, acidic prolocadherin 17	6.13
45	127695	AA714731	Hs.291457	ESTs, Wealdy similar to heterogeneous ri	6.13 6.13
	127894	AL121053	Hs.5534	Homo saplens cD FLJ12961 fis, clone NT	6.13
	113595	T92058	Hs.290240	ESTs, Moderately similar to ALU2_HUMAN A	6.10
	120784	AW752101	Hs.16580	hypothetical protein FLJ11026	6.10
50	115004 129740	AA329340 BE165866	Hs.4867	mannosyl (alpha-1,3-)-glycoprotein beta-	6.08
50	117483	N72185	Hs.83623 Hs.44189	nuclear receptor subfamily 1, group I, m	6.05
	103815	BE245294	Hs.180789	ESTs S164 protein	6.04
	122040	AA847758	Hs.111030	ESTs	6.03 6.03
55	109638	AW977747	Hs.119120	E3 ubiquitin ligase SMURF1	6.02
33	112727	T91029	Hs.15069	ESTa	6.01
	120273 122127	AA176688	Hs.269284	ESTs	6.00
	126046	AW207175 AA804957	Hs.106771 Hs.119840	ESTs ESTs	6.00
	119774	AB032977	Hs.6298	KIAA1151 protein	5.99
60	106265	AA412176	Hs.236463	Homo sapiens mR; cD DKFZp586I0521 (f	5.98 5.98
	111987	NM_015310	Hs.6763	KIAA0942 protein	5.98
	123619	AA602964		gb:no97c02.s1 NCI_CGAP_Pr2 Homo sapiens	5.96
	128122 128473	Al267491	Hs.160593	ESTs	5.95
65	102283	T78277 AW161552	Hs.100293 Hs.83381	O-linked N-acetylglucosamine (Glcc) tr	5.95
••	122468	AA448172	Hs.137687	guanine nucleotide binding protein 11 ESTs, Highly similar to K6B1_HUMAN RIBOS	5.94
	101801	M88407	Hs.1216	actinin, stpha 3	5.93 5.93
	107059	BE614410	Hs.23044	RAD51 (S. carevisiae) homolog (E coli Re	5.92
70	108908	AA136569	Hs.10848	KIAA0187 gene product	5.90
70	121470	AA558958	Hs.324751	ESTs	5.90
	131938 109613	AF176085 H47315	Hs.34956	neural polypyrimidine tract binding prot	5.89
	109384	AA219172	Hs.27519 Hs.86849	ESTs ESTs	5.89
7.	118559	N68456	Hs.49519	ESTs	5.88
75	102010	U02687	Hs.385	fma-related tyrosine kise 3	5.88 5.88
	105921	AA421973	Hs.169119	ESTs, Wealty similar to T25731 hypotheti	5.85
	124298	H91679		gb:yv04a07.s1 Soares fetal liver spieen	5.85
	120827 103331	AA382525	Hs.132967	Human EST clone 122887 mariner transposo	5.84
80	135052	A1825463 AL136653	Hs.147996 Hs.93675	protein kise, X-linked	5.82
	115219	AA262776	Hs.269314	decidual protein induced by progesterone Homo sapiens cD FLJ14123 fis, clone MA	5.80
	121899	R55341	Hs.50421	KIAA0203 gene product	5.78 5.78
	135217	AA453880	Hs.9658	hypothetical protein FLJ11790	5.78 5.77
				•	

	123973	C14805		gb:C14805 Clontech human aorta polyA+ mR	5.77
	112605 110151	R79374 H18835	Hs.29852 Hs.31608	ESTS	5.76
_	129889	AA810932	Hs.131899	hypothetical protein FLJ20041 ESTs, Wealdy similar to T00370 hypotheti	5 .75 5.75
5	102638	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	5.73
	121501 124921	AA470687 R93082	Hs.104772	ESTs	5.73
	109850	AJ150548	Hs.332635 Hs.23155	ESTs ESTs	5.70 5.70
10	120594	AW136478	Hs.5094	ring finger protein 10	5.70
10	126433 100455	AA325606	11. 2000	gb:EST28707 Cerebellum II Homo sapiens c	5.70
	106565	AW888941 NM_014892	Hs.75789 Hs.227602	N-myc downstream regulated KIAA1116 protein	5.69
	120912	AA376690	Hs.187650	ESTs	5.68 5.68
15	127209	AA305023	Hs.81964	SEC24 (S. cerevisiae) related gene famil	5.68
13	107606 106597	AF207989 Al091277	Hs.330425 Hs.302634	Homo septens, Similar to G protein-coupt frizzled (Drosophila) homolog 8	5.67
	102126	AW950870	Hs.78961	protein phosphatase 1, regulatory (inhib	5.66 5.65
	100064			AFFX control - TrpnX-3	5.63
20	108758 101392	AA127395 NM_002507	Hs.222414 Hs.1827	ESTS	5.63
	102211	BE314524	Hs.78776	nerve growth factor receptor (TNFR super putative transmembrane protein	5.61 5.60
	107427	W26975	Hs.46736	hypothetical protein FLJ23476	5.60
	135175 111764	M91463 AI420368	Hs.95958 Hs.290259	solute carrier family 2 (facilitated glu	5.60
25	119405	T93865	Hs.91085	ESTs, Weakly similar to 138022 hypotheti ESTs	5.58 5.58
	126464	Al990046	Hs.54780	transcription termition factor, R po	5.58
	133865 123255	AB011155 AA830335	Hs.170290 Hs.105273	discs, large (Drosophila) homolog 5 ESTs	5.58
	122881	AA335721	Hs.119394	ESTs	5.57 5.56
30	112046	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	5.55
	132906 109001	BE613337 AI056548	Hs.234896 Hs.72116	geminin	5.55
	115816	BE042915	Hs.287588	hypothetical protein FLJ20992 similar to Homo sapiens cD FLJ13675 fis, clone PL	5.55 5.55
35	128401	R01865	Hs.268586	ESTs	5.53
22	129296 120314	AI051967 T10013	Hs.110122 Hs.221040	ESTs	5.53
	132815	AJ815189	Hs.57475	HBS1 (S. cerevisiae)-like sex comb on midleg homolog 1	5.51 5.50
	113983	W87415	Hs.55296	HLA-B associated transcript-1	5.50
40	105002 132025	- AA224244 AA011117	Hs.182704 Hs.3745	ESTs, Moderately similar to altertivel	5.49
	110732	AW070838	Hs.174174	milk fat globule-EGF factor 8 protein KIAA0601 protein	5.49 5.48
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-lin	5.48
	126758 129426	Al559444 AF077953	Hs.293960	ESTs	5.48
45	103217	NM_001841	Hs.111323 Hs.73037	Protein inhibitor of activated STAT X canbinoid receptor 2 (macrophage)	5.47 5.48
	132261	U80743	Hs.306094	trinucleotide repeat containing 12	5.45
	105586 109454	AA865118 AA232255	Hs.191538 Hs.295232	ESTs	5.43
	113063	W15573	Hs.5027	ESTs, Moderately similar to A46010 X-lin ESTs, Weakly similar to A47582 B-cell or	5.43 5.43
50	134092	AA218558	Hs.7905	sorting nextin 9	5.41
	119316 108019	AJ114630 AJ017773	Hs.208334 Hs.249159	Homo saptens cD: FLJ21874 fis, clone H adrenergic, alpha-2A-, receptor	5.38
	109421	AW604652	Hs.332442	ESTs	5.38 5.38
55	111929	AF027208	Hs.112360	prominin (mouse)-like 1	5.38
73	119718 106154	W69216 BE540255	Hs.92848 Hs.6994	ESTs Homo saplens cD: FLJ22044 fis, clone H	5.38
	108544	W39433	Hs.23971	hypothetical protein DKFZp547N043	5.35 5.35
	119580 126777	AL079310	Hs.92260	high-mobility group protein 2-like 1	5.35
60	112944	AL157491 H18083	Hs.145211 Hs.13254	Homo septens mR; cD DKFZp434K1111 (f ESTs	5.35 5.34
	103149	NM_006201	Hs.171834	PCTAIRE protein kise 1	5.34
	132437 103860	AA152106	Hs.4859	cyclin L ania-Ga	5.33
	104865	AW976877 179340	Hs.38057 Hs.22575	ESTs B-cell CLL/lymphoma 6, member 8 (zinc fi	6.33 5.33
65	129914	NM_012421	Hs.13321	rearranged L-myc fusion sequence	5.33 5.33
	130309	AF067804	Hs.15423	hypothetical protein HDCMC04P	5.31
	116312 124191	T96509	Hs.65403 Hs.248549	hypothetical protein ESTs, Moderately similar to S65657 alpha	5.30 5.28
70	125583	AA195667	Hs.86022	ESTs	5.28
70	130591 116355	N59646	Hs.169745	crumbs (Orosophila) homolog 1	5.28
	115553	AA789133 AJ275988	Hs.88650 Hs.71414	ESTs transcription factor (SMIF gene)	5.26 5.26
	122802	A1687303	Hs.285529	G protein-coupled receptor 49	5.25
75	128495 117667	NM_005904 U59305	Hs.100602	MAD (mothers against decapentaplegic, Dr	5.24
	127890	AA294934	Hs.44708 Hs.293902	Ser-Thr protein kise related to the my ESTs, Weakly similar to ISHUSS protein d	5.23 5.22
	134843	AA428520	Hs.90061	progesterone binding protein	5.21
	120988 102076	AA528283 BE299197	Hs.292737	ESTs	5.21
80	100934	J03019	Hs.179665 Hs.99913	cyclin-dependent kise Inhibitor 1A (p2 adrenergic, beta-1-, receptor	5,20 5.20
	112667	BE538516	Hs.15423	hypothetical protein HDCMC04P	5.20
	119304 131868	AW249268 AW408296	Hs.98493	X-ray repair complementing defective rep	5.20
		7117 100200	Hs.33532	zinc finger protein 151 (pHZ-67)	5.20
				. 102	

5	102258 103850 112516	NM_001546 - AA187101	Hs.9701 Hs.34853	growth arrest and O-damage-inducible,	5.18
5		· AA497404	113.34033	inhibitor of O binding 4, domint neg	5.18
5	112516		Hs.213194	hypothetical protein MGC10895	5.18
,	133640	T83909	11	gb:yd67f10.r1 Soares fetal liver spieen	5.18
	135180	AW246428 D90070	Hs.75355 Hs.98	ubiquitin-conjugating enzyme E2N (homoto	5.18
	135309	AI564123	Hs.42500	phorbol-12-myristate-13-ecetate-induced ADP-ribosylation factor-like 5	5.18
	134801	S76825	Hs.89595	insufin receptor	5.18 5.17
10	133362	AK001519	Hs.7194	CGI-74 protein	5.17
10	135206 111480	AB024703	Hs.98334	ring finger protein 11	5.15
	118466	R06453 N66741	Hs.19706	ESTs	5.15
	125757	Al274908	Hs.166835	gb:yz33g08.s1 Morton Fetal Cochlea Homo ESTs, Highly similar to 1814460A p53-ass	5.15
	127140	AI273507	Hs.303966	ESTs	6.15 5.15
15	109223	AW000714	Hs.65818	ESTs	5.14
	103656	273497	Hs.247802	Human D sequence from clone U240C2 on	5.14
	133388 100511	AW245631 M76676	Hs.182447	heterogeneous nuclear ribonucleoprotein	5.12
	101941	S77583	Hs.116840	ESTS	5.10
20	109937	AI084068	Hs.20072	gb:HERVK10/HUMMTV reverse transcriptase myosin regulatory light chain interactin	5.10 5.10
	122996	Al436216	Hs.191715	ESTs, Wealty similar to ZN91_HUMAN ZINC	5.10
	128242	AA992626	Hs.269755	ESTs, Moderately similar to ALUS_HUMAN A	5.10
	112374 124506	NM_016323	Hs.26663	cyclin-E binding protein 1	5.10
25	104216	BE273688 AB002313	Hs.182447 Hs.3989	heterogeneous nuclear ribonucteoprotein	5.10
	135051	AI272141	Hs.83484	plexin B2 SRY (sex determining region Y)-box 4	5.09 5.08
	131629	Z45794	Hs.238809	EST8	5.08
	111722	R23924	Hs.23596	EST	5.07
30	107034 110243	AF257770	Hs.20930	poly(rC)-binding protein 4	5.06
50	125837	H26683 AW968123	Hs.333513	gb:yl14g03.s1 Soares breast 2NbHBst Homo	5.05
	130300	X58288	Hs.154151	small inducible cytokine subfamily E, me protein tyrosine phosphatase, receptor t	5.05
	103967	AL120051	Hs.144700	ephrin-B1	5.05 5.04
25	112678	AJ418456	Hs.33665	ESTs	5.03
35	124963	F06600	Hs.101375	Homo sapiens mR; cD DKFZp434H205 (fr	6.03
	131379 109451	AK001123 N32264	Hs.26176	hypothelical protein FU10261	5.03
	101396	BE267931	Hs.44330 Hs.78996	ESTs proliferating cell nuclear antigen	5.02
40	131038	W87778	Hs.169388	hypothetical protein DKFZp761H2024	5.02 5.01
40	101208	L25081	Hs.179735	ras homolog gene family, member C	5.01
	104973	NM_015310	Hs.6763	KIAA0942 protein	4.99
	103141 111260	X66113 AB033035	Hs.75584	polymyositis/scleroderma autoantigen 2 (4.98
	128142	T67162	Hs.51965 Hs.135127	KIAA1209 protein ESTs, Weakly similar to unmed protein	4.98
45	113857	AW243158	Hs.5297	DKFZP564A2416 protein	4.98 4.96
	105292	AF128542	Hs.166846	polymerase (D directed), epsilon	4.96
	114341	AF270491	Hs.28249	hepatocellular carcinoma-associated anti	4.95
	100615 103208	W32474 AW411340	Hs.301746	RAP2A, member of RAS oncogene family	4.95
50	121121	AA399371	Hs.31314 Hs.189095	retinoblastoma-binding protein 7	4.95
	125321	T86652	Hs.178294	similar to SALL1 (sel (Drosophila)-like ESTs	4.95 4.95
	101145	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	4.95
	100551	M73980	Hs.129053	Homo sapiens NOTCH 1 (N1) mR, complete	4.93
55	126182 127925	AA721331 AA805151	Hs,293771 Hs,3628	ESTs	4.93
••	133969	AA669112	Hs.78	mitogen-activated protein kise kise GA-binding protein transcription factor,	4.93
	120873	AA358015		gb:EST66864 Fetal lung till Homo saplens	4.93 4.92
	125219	AI804331	Hs.99423	ATP-dependent R helicase	4.91
60	102790 129486	BE245277	Hs.154196	E4F transcription factor 1	4.90
•	130381	NM_005754 L47345	Hs.220689 Hs.155202	Ras-GTPase-activating protein SH3-domain	4.90
	132389	AA310393	Hs.190044	transcription elongation factor B (SIII) ESTs	4.89 4.88
	100260	D38491	Hs.322478	KIAA0117 protein	4.88
65	109585	N59650	Hs.27252	ESTS	4.88
UJ	111603 120514	R11529 AA258335	Hs.20634	EST	4.88
	130314	NM_014874	Hs.154332	gb:zr59b02.s1 Sozres_NhHMPu_S1 Homo sapi	4.88
	108958	AF142482	Hs.203846	KIAA0212 gene product TEA domain family member 3	4.86
70	126603	W86610	Hs.185738	ESTs	4.88 4.85
70	100406	A1962060	Hs.118397	AE-binding protein 1	4.85
	116238 105288	AV560717 N99673	Hs.47144	DKFZP586N0819 protein	4.84
	118753	AA346206	Hs.3585 Hs.50471	ESTs, Weakly similar to AF126743 1 DJ	4.83
-	113070	AB032977	Hs.6298	ESTs, Wealdy similar to T14267 Xin prote KIAA1151 protein	4.82
75	107908	AF087999	Hs.42826	ESTs	4.81 4.80
	119678	A1658666	Hs.6106	R binding motif protein 4	4.80
	100415 128360	D86970 E12374	Hs.75822	TGFB1-induced anti-apoptotic factor 1	4.79
	133101	F12374 AK000299	Hs.180952	gb:HSC39B101 normalized infant brain cDN	4.78
80	103507	AJ000512	Hs.295323	dyclin 4 (p62) senum/glucocorticold regulated kise	4.78
	107666	AA010611	Hs.60418	EST	4.78 4.78
	108030	Al378523	Hs.62011	ESTs	4.78
	131479	D86181	Hs.273	galactosylceramidase (Krabbe disease)	4.78
				103	
				103	

	133140	AF180581	Hs.6582	Rho guanine exchange factor (GEF) 12	4.78
	134654	AK001741	Hs.8739	hypothetical protein FLJ 10879	4.78
	106288 101524	AB037742	Hs.24336	KIAA1321 protein	4.76
5	113095	NM_000448 AA828380	Hs.73958 Hs.126733	recombition activating gene 1	4.75
•	114924	Al338053	Hs.87329	ESTs HSPC072 protein	4.75
	127543	AK000787	Hs.157392	Homo sapiens cD FLJ20780 fis, clone CO	4.75 4.75
	115866	AW062829	Hs.52081	KIAA0867 protein	4.75
10	101382	AU076772	Hs.1279	complement component 1, r subcomponent	4.74
10	126509 127930	R47400 AA809572	Hs.23850	ESTs	4.74
	127824	AI911518	Hs.123304 Hs.127811	ESTs ESTs	4.73
	110049	H12449	Hs.31159	EST, Weakly similar to ALUB_HUMAN IIII A	4.73 4.73
1.5	127115	H77859	Hs.65450	reticulon 4	4.73
15	104727	N81203	Hs.20047	zinc finger protein, subfamily 2A (FYVE	4.72
	127532	AJ003429		gb:AJ003429 Selected chromosome 21 cD	4.71
	127304 105409	AI741577 AW505076	Hs.99962 Hs.301855	proteoglycan 2, bone marrow (tural kil	4.70
	114969	AW162998	Hs.24684	DiGeorge syndrome critical region gene 8 KIAA1376 protein	4.70
20	115125	AA193588	Hs.85888	ESTS	4.70 4.70
	118348	AW408586	Hs.91052	ESTs, Moderately similar to ALUS_HUMAN A	4.70
	123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H	4.70
	130881 132074	AA809875	Hs.25933	ESTs	4.70
25	106897	AA478486 AF039023	Hs.3852 Hs.167498	KIAA0368 protein	4.70
	131121	AA120865	Hs.23136	RAN binding protein 6 ESTs	4.69 4.69
	116046	BE395293	Hs.94491	hypothetical protein FLJ20297	4.68
	112868	AW388359	Hs.10667	ESTs	4.68
30	116877 131241	AA708958	Hs.168732	ESTs	· 4.68
50	132027	BE501914 AF151020	Hs.24654 Hs.181444	Homo saplens cD FLJ11640 fis, clone HE	4.68
	133323	BE336654	Hs.70937	hypothetical protein H3 histone family, member A	4.68
	114269	AA176769	Hs.23450	mitochondrial ribosomal protein S25	4.68 4.67
25	122713	A1089443	Hs.99436	ESTs	4.67
35	133571	BE515037	Hs.177556	melanoma entigen, family D, 1	4.66
	134453 115510	AJ272141 BE299339	Hs.83484 Hs.72249	SRY (sex determining region Y)-box 4	4.66
	115322	L08895	Hs.78995	three-POZ containing protein similar to MADS box transcription enhancer factor 2	4.66
40	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	4.66 4.65
40	104674	AJ935962	Hs.26289	ESTs	4.65
	105276	AA625947	Hs.25750	ESTs	4.65
	108216 120376	AA524743 AA227469	Hs.44883	ESTs	4.65
	121743	AA397636		gb:zr18a07.s1 Stratagene NT2 naurol pr	4.65
45	128011	AI347067	Hs.124636	gb:zi79e09.r1 Soares_testis_NHT Homo sap ESTs	4.65 4.65
	123454	AA868510	Hs.112496	ESTs	4.64
	103409	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	4.64
	120484 127046	AA253170	Hs.96473	EST	4.63
50	133184	AA321948 AA001021	Hs.293968 Hs.6685	ESTs	4.63
-	123184	BE247767	Hs.18166	thyroid hormone receptor interactor 8 KIAA0870 protein	4.63 4.62
	106627	AK000708	Hs.15125	hypothetical protein FLJ20699	4.62
	115476	AB033085	Hs.40193	hypothetical protein KIAA1259	4.61
55	119468 133662	AI911535	Hs.6657	hypothetical protein bK1048E9.5	4.59
55	113941	BE409053 AA531016	Hs.299629 Hs.22399	peroxisomal long-chain acyl-coA thioeste	4.58
	131590	R46277	Hs.250638	hypothetical protein FLJ14824 Homo saptens mR full length Insert cDN	4.58
	128795	AA531287	Hs.105805	ESTs	4.58 4.58
60	116480	C14088	Hs.169476	glyceraldehyde-3-phosphate dehydrogese	4.58
OO	111713	C75253	Hs.220950	ESTs	4.58
	113721 111657	AF143885 R07364	Hs.18190 Hs.268667	EST	4.57
	102009	BE245149	Hs.82643	ESTs, Weakly similar to ALU1_HUMAN ALU S protein tyrosine kise 9	4.56
<i>C E</i>	135242	Al583187	Hs.9700	cyclin E1	4.55 4.55
65	127580	BE548749	Hs.148016	ESTs	4.55
	109785	AB011131	Hs.12376	piccolo (presyptic cytomatrix protein)	4.53
	109700 124882	F09809	17- 404500	gb:HSC33H092 normalized infant brain cDN	4.53
	131765	AI698652 AW381270	Hs.101539 Hs.194110	ESTs	4.53
70	115684	NM_006577	Hs.284284	hypothetical protein PRO2730 ESTs, Highly similar to beta-1,3-N-acety	4.53
	102034	Al903474	Hs.230	fibromodulin	4.52 4.52
	109776	R43665	Hs.12257	ESTs	4.50
	111650	R16722	Hs.124246	ESTs	4.50
75	132993 129017	AB023154 AA115333	Hs.62264	KIAA0937 protein	4.49
. •	132902	A1938442	Hs.107968 Hs.59838	ESTs hypothetical protein FLJ10808	4.49
	114814	AB006622	Hs.182536	KIAA0284 protein	4.48 4.48
	120839	AA348913		gb:EST55442 Infant adrel gland II Homo	4.48
80	101434	AV650068	Hs.1430	coagulation factor XI (plasma thrombopla	4.48
50	102018 104619	U03398 AA001635	Hs.1524	tumor necrosis factor (figand) superfami	4.48
	105716	AA931198	Hs.287414 Hs.238928	transcriptiol Intermediary factor 1 ga	4.48
	126020	H79863	Hs.114243	HT002 protein; hypertension-related calc ESTs	4.48
					4.48

	119899	AI057404	Hs.58698	ESTs	4.47
	115582	AW245047	Hs.136164	cutaneous T-cell lymphoma-associated turn	4.46
	125695	W22529	Hs.30942	ephrin-82	4.46
5	105715	BE621800	Hs.29444	putative small membrane protein NID67	4.45
,	117169 102757	R87866 AW955454	Hs.95120	ESTs, Weakly similar to HZHU hemoglobin	4.45
	120637	AA811804	Hs.30942	ephrin-B2	4.45
	131579	N62922	Hs.29088	gbob39a05.s1 NCI_CGAP_GCB1 Homo saptens ESTs	4.45 4.45
	135287	U82670	Hs.9786	zinc finger protein 275	4.45 4.45
10	112540	R69751	11010100	gb.yl40a10.s1 Soares placenta Nb2HP Homo	4.45
	125724	AL360190	Hs.295978	Homo sepiens mR full length Insert cDN	4,44
	115498	AA291070		gbzs46a08.s1 NCL_CGAP_GCB1 Homo sapiens	4.43
	102263	U29171	Hs.75852	caseln kise 1, delta	4.43
1.5	124312	H94647	Hs.102329	ESTS	4.43
15	112366	AF035318	Hs.12533	Homo sapiens clone 23705 mR sequence	4.43
	115955	AF283813	Hs.44198	Intracellular membrane-associated calciu	4.43
	103562	NM_002702	Hs.2815	POU domain, class 6, transcription facto	4.42
	100169	AL037228	Hs.82043	D123 gene product	4.40
20	108928	AA143802	Hs.71781	ESTS	4.40
20	125908 126996	AF265555	Hs.250646	baculoviral IAP repeat-containing 6	4.40
	129512	BE161065 TB8845	Hs.167531 Hs.112200	methylcrotonoyl-Coenzyma A carboxylasa 2	4.40
	134570	U66615	Hs.172280	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.40
	135073	W55956	Hs.94030	SW/SNF related, matrix essociated, acti Homo sapiens mR; cD DKFZp586E1624 (f	4.40
25	105011	BE091926	Hs.16244	milotic spindia coiled-coil related prot	4.40 4.40
	128793	AB011125	Hs.105749	KIAA0553 protein	4.40
	107292	BE168479	Hs.4789	Homo sapiens serologically defined breas	4.38
	126144	H84455	Hs.40639	ESTs	4.38
20	130783	X07282	Hs.171495	refinoic acid receptor, beta	4.38
30	135192	U83993	Hs.321709	purinergic receptor P2X, ligand-gated to	4.38
	100284	D43767	Hs.66742	small inducible cytokine subfamily A (Cy	4.37
	117269	N21621	Hs.91142	KH-type splicing regulatory protein (FUS	4.36
	104261	AW248364	Hs.5409	R polymerase I subunit	4.35
35	108609 126319	BE409857 D81689	Hs.69499	hypothetical protein	4.35
55	127445	AA906286	Hs.193942	gb:HUM184E058 Human fetal brain (TFujiwa	4.35
	130772	BE270640	Hs.19192	ESTs	4.35
	134625	AA977638	Hs.184389	cyclin-dependent kise 2 ESTs	4.35
	135397	L14922	Hs.166563	replication factor C (activator 1) 1 (14	4.35 4.35
40	128070	AA886944	Hs.303908	ESTs	4.35
	135046	Al494054	Hs.93589	hypothetical protein DKFZp564B1162	4.33
	101881	NM_004957	Hs.754	folytpolyglutamate synthase	4.33
	129838	AB007863	Hs.185140	KIAA0403 protein	4.33
AF	130974	NM_003528	Hs.2178	H2B histone family, member Q	4.33
45	107763	AA018220	Hs.106730	chromosome 22 open reading frame 3	4.32
	129818	T71092	Hs.172572	hypothetical protein FLJ20093	4.31
	129407 110846	AL137597	Hs.11114	hypothetical protein dJ1181N3.1	4.30
	111433	BE277343 R01452	Hs.297875	endoplasmic reticulum chaperone SIL1, ho	4.30
50	114860	AL157545	Hs.40193 Hs.42179	hypothetical protein KIAA1259	4.30
-	115853	AW978561	Hs.191548	bromodomain and PHD finger containing, 3 ESTs	4.30
	116165	AI184751	Hs.75874	pregnoy-associated plasma protein A	4.30 4.30
	126911	AA428049	Hs.1501	syndecan 2 (heparan sulfate proteoglycan	4.30
	131230	NM_005865	Hs.274407	protesse, serine, 16 (thymus)	4.30
55	100349	D64110	Hs.77311	BTG family, member 3	4.29
	100175	BE258769	Hs.32500	acetyl-Coenzyme A acyltransferase 2 (mil	4.29
	105335	AW291165	Hs.25447	ESTs	4.29
	122507	BE567620	Hs.99210	ESTs	4.28
60	105397	AA814807	Hs.7395	hypothetical protein FLI23182	4.28
oo	133574	AW851121	Hs.75497	Homo sapiens cD: FLJ22139 fis, clone H	4.28
	102826 103272	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	4.28
	111887	NM_006680 R38635	Hs.2838 Hs.12328	malic enzyme 3, DP(+)-dependent, mitoc	4.28
	120338	N85785	Hs.181165	KIAA 1005 protein	4.28
65	133736	D49958	Hs.75819	eukaryotic translation elongation factor stycoprotein M6A	4.28
•••	130356	AF127577	Hs.155017		4.28
	119830	AW054922	Hs.53478	nuclear receptor interacting protein 1 Homo sapiens oD FLJ12368 fis. clone MA	4.27 4.27
	106758	AB014564	Hs.22616	KIAA0664 protein	4.25
~~	109709	F09749	Hs.187405	ESTs	4.25
70	110463	H52931	Hs.165067	ESTs	4.25
	124472	N52517	Hs.102670	EST	4.25
	109770	R40322	Hs.248420	ESTs, Moderately similar to A47582 B-cel	4.24
	131487	F13036	Hs.27373	Homo seplens mR; cO DKFZp564O1763 (I	4.23
75	107216	D51069	Hs.211579	melanoma cell adhesion molecule	4.23
13	123562	AA177088	Hs.190085	ESTs	4.23
	125988	W02410	Hs.205555	ESTs	4.23
	126221 127092	N20514 T26085	Hs.172965	ESTs	4.23
	132349	T26985 AW975654	Un 404900	gb:NIBT065H01R Infant brain, LLNL array	4.23
80	118946	N92834	Hs.181286	serine protease inhibitor, Kazel type 1	4.23
	101531	Al199711	Hs.576	gb:zb87f03.s1 Soares_fetal_lung_NbHL19W fucosidase, alpha-L-1, tissue	4.22
	105322	T87179	Hs.16346	ESTs, Weakly similar to \$57447 HPBRII-7	4.21 4.21
	104219	AB002323	Hs.7720	dynein, cytopiasmic, heavy polypeptide 1	4.20
			· —	A .	7.40

	102825	BE262386	Hs.7137	A 80003 4 00375 1 A	
	103571	A1675749	Hs.21,1608	ctones 23667 and 23775 zinc finger prote nucleoporin 153kD	4.20
	106942	AA995351	Hs.31314	refinoblastoma-binding protein 7	4.20 4.20
_	112685	R87650	Hs.33439	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.20
5	123107	AA225048	Hs.104207	EST8	4.20
	132659	275190	Hs.54481	low density Opoprotein receptor-related	4.20
	130084	AI929377	Hs.173724	creatine kise, brain	4.19
	114553 129628	BE219860 U38945	Hs.22505 Hs.1174	hypothetical protein FLJ10159	4.18
10	102266	U29725	Hs.3080	cyclin-dependent kise inhibitor 2A (me mitogen-activated protein kise 7	4.18
	110637	Al241470	Hs.268982	ESTs	4.18 4.18
	127520	T51239		gb:yb20d12.s1 Stratagene fetal spieen (9	4.18
	130322	NM_014247	Hs.154545	POZ domain containing guanine nucleotide	4.17
15	104768	D82319	Hs.11056	RALBP1 protein	4.17
13	123360 133110	AA532718 AA808177	Hs.178604	ESTs	4,17
	130923	H96115	Hs.65228 Hs.21293	ESTs	4.16
	109878	BE620775	Hs.4866	UDP-N-acteylglucosamine pyrophosphorylas Homo sapians cD FLJ14387 fis, ctona HE	4.16 4.16
	119265	BE539706	Hs.285363	ESTs	4.16
20	124214	H58608	Hs.151323	ESTs	4.15
	106193	AA057478	Hs.23272	ESTs	4.15
	105169 132304	BE245294	Hs.180789	S164 protein	4.15
	131600	AA610002 NM_004377	Hs.44296 Hs.29331	hypothetical protein FLJ22324	4.15
25	131365	M93415	Hs.26014	camitine palmitoyltransferase I, muscle activin A receptor, type II	4.14 4.14
	121993	AW297880	Hs.98661	ESTs	4.14
	110779	Al391472	Hs.12561	ESTs, Highly similar to C212_HUMAN 28.3	4.13
	126383	AB032977	Hs.6298	KIAA1151 protein	4.13
30	104445	AF084555	Hs.7351	cyclic AMP phosphoprotein, 19 kD	4.13
50	131475 128933	AA992841 NM_002050	Hs.27263 Hs.334695	KIAA1458 protein	4.13
	113141	AJ493276	Hs.9187	GATA-binding protein 2 ESTs	4.12
	134833	L20965	Hs.89901	phosphodiesterase 4A, cAMP-specific (dun	4.11 4.11
2.5	106461	AI630759	Hs.17481	Homo sapiens clone 24606 mR sequence	4.10
35	128058	A1990131	Hs.276973	potassium large conductance calcium-acti	4.10
	114757	AW970579	Hs.291031	ESTs	4.10
	134653 100472	AI765883 D90084	Hs.87385	ESTs	4.09
	103102	X61177	Hs.1023 Hs.68876	pyruvate dehydrogese (lipoamide) alpha interleukin 5 receptor, alpha	4.08
40	106779	BE276013	Hs.172364	Homo sepiens mR for FLJ00086 protein,	4.08 4.08
	133815	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	4,08
	130178	U20982	Hs.1516	insulin-like growth factor-binding prote	4.07
	124659	AI680737	Hs.289068	Homo sapiens cD FLJ11918 fls, clone HE	4.07
45	127861 112129	AW295020	Hs.198529	ESTs	4.07
73	100918	AB037715 AK001335	Hs.183639 Hs.31137	hypothetical protein FLJ10210	4.07
	124677	R01073	113.51151	protein tyrosine phosphatase, receptor t gb:ye84c03.s1 Soares fetal liver spleen	4,06 4.05
	102722	F13271	Hs.79981	Human clone 23560 mR sequence	4.05
50	111117	AB037721	Hs.173871	KIAA1300 protein	4.05
50	122506	AA449120	Hs.99209	ESTs	4.05
	126392 130760	Al356294	Hs.3280	caspase 6, apoptosis-related cysteine pr	4.05
	104220	AW379130 AB002324	Hs.18953 Hs.301094	phosphodiesterase 9A	4.05
	112774	R95770	Hs.35455	KIAA0326 protein ESTs	4.05 4.04
55	111128	AW505364	Hs.19074	LATS (large turnor suppressor, Drosophila	4.04
	113146	BE151985	Hs.5722	hypothetical protein FLJ23316	4.04
	124940	AF068846	Hs.103804	heterogeneous nuclear ribonucleoprotein	4.03
	105498 112631	H68279 R82040	Hs.24937	transformer-2 alpha (htra-2 alpha)	4.03
60	118244	N62518	Hs.48556	gb:yj06b06.s1 Soares placenta Nb2HP Homo ESTs	4.03
	118720	N73515	12.4000	gb:za49d07.s1 Soares fetal liver spleen	4.03 4.03
	129232	R98881	Hs.109655	sex comb on midleg (Orosophila)-like 1	4.03
	134192	H01345	Hs.24139	Homo saplens cD: FLJ23137 fis, clone L	4.03
65	131893	B£336886	Hs.3416	adipose differentiation-related protein	4.02
UJ	116793 125674	T77781 AL036166	Hs.323378	gb:yd20a11.s1 Soares fetal liver spleen	4.02
	116640	X89984	Hs.211563	coated vesicle membrane protein B-cell CLL/lymphoma 7A	. 4.01
	105057	AA134233	Hs.336942	Homo sepiens cD: FLJ21488 fis, clone C	4.01 4.00
~~	105158	AW976357	Hs.234545	hypothetical protein NUF2R	4.00
70	116245	AB033107	Hs.42796	KIAA1281 protein	4.00
	119946	AA932283	Hs.58925	ESTs	4.00
	121975 132037	AA740679	Hs.98631	ESTs	4.00
	133669	AA352702	Hs.332541	Homo sapiens, Similar to RIKEN cD 2700	4.00
75	109468	NM_006925 NM_015310	Hs.166975 Hs.6763	splicing factor, arginine/sertne-rich 5 KIAA0942 protein	4.00
	106829	AW959893	Hs.27099	hypothetical protein FLJ23293 similar to	3.99
	134682	AW882645	Hs.88044	sprouty (Orosophila) homolog 1 (antagoni	3.99 3.98
	105966	AA142984	Ha.5344	adaptor-related protein complex 1, gamma	3.98
80	100448	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	3.98
οU	102589	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61	3.98
	104148 111465	AW880614 Al968256	Hs.146381	R binding motif protein, X chromosome	3.98
	126499	AK001779	Hs.15470 Hs.110445	putative ring zinc finger protein NY-REN CGI-97 protein	3.98
	-40100		10.110770	Contract biorem	3.98

	124200	*****			
	134388 105564	AW405434	Hs.82575	small nuclear ribonucleoprotein polypept	3.98
	115208	BE616694	Hs.288042	hypothetical protein FLJ14299	3.97
	103853	AW183695 AF272390	Hs.186572	ESTs	3.96
5	110542	H58373	Hs.111782	myosin 5C	3.96
	106797	Al768801	Hs.332938 Hs.169943	hypothetical protein MGC5370	3.96
	130589	AL110226	Hs.16441	Homo sapiens cD FLJ13569 fis, clone PL DKFZP434H204 protein	3.98
	122788	AI828638	Hs.99514	hypothetical protein FLJ20574	3.95
10	104518	H20816	Hs.112423	Homo sapiens mR; cD OKFZp586I1420 (f	3.95
	130640	NM_004753	Hs.17144	short-chain dehydrogese/reductase 1	3.95
	110847	N30169	Hs.279807	ESTs, Westly similar to 2004399A chromos	3.95 3.95
	115156	AA461045	Hs.50701	ESTs	3.95
	122096 122160	AA431162 AI769281	Hs.98690	ESTs	3.95
15	123930	AA740878	Hs.97439	ESTs	3.95
	126280	Z19417	Hs.112982	ESTs	3.95
	126547	U47732	Hs.84072	gb:HSB26B122 STRATAGENE Human skeletal m	3.95
	134757	AA913267	Hs.211576	transmembrane 4 superfamily member 3 IL2-inducible T-cell kise	3.95
20	117296	AL133427	Hs.42506	Homo saplens mR full length insert cDN	3.95
20	112261	AL050297	Hs.300861	ESTs, Highly similar to T08701 hypotheti	3.95
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	3.95
	131844	Al419294	Hs.324342	ESTs	3.94 3.94
	101607 121613	X60111	Hs.1244	CD9 entigen (p24)	3.94
25	115815	AA416879 AW905328	Hs.193195	ESTs, Wealty similar to 2109260A B cell	3.93
	125684	AW589427	Hs.180842	ribosomal protein L13	3.93
	126783	AA083531	Hs. 158849	Homo septens cD: FLJ21663 ffs, clone C	3.93
	129201	H18359	Hs.109390	gb:zn09d10.s1 Stratagene hNT neuron (937	3.93
20	128954	AA346839	Hs.209100	ESTs	3.93
30	122939	AA477141		DKFZP434C171 protein gb:zu37g08.s1 Soares ovary tumor NbHOT H	3.92
	130348	AB032957	Hs.210850	KIAA1131 protein	3.92
	125847	AW161885	Hs.249034	ESTs	3.92
	120452	AL022328	Hs.104335	hypothetical protein IMAGE3510317	3.91 3.91
35	123143 105729	AA487595		gb:aa95e02.s1 Stratagene fetat reti 93	3.91
55	106605	H46612	Hs.293815	Homo saplens HSPC285 mR, partial cds	3.91
	126714	AW772298 AF114491	Hs.21103	Homo saplens mR; cD DKFZp564B076 (fr	3.90
	121611	M31669	Hs.137354 Hs.1735	egi-tike modute containing, mucin-like.	3.90
40	120468	AW967675	Hs.964B7	inhibin, beta 8 (activin AB beta polypep	3.90
40	101356	AW878229	Hs.80642	ESTs, Highly similar to S08228 ribosomal	3.90
	133668	L77984	Hs.271980	sigi transducer and activator of trans mitogen-activated protein kise 6	3.89
	109114	BE622787	Hs.84045	hypothelical protein FLJ20288	3.89
	115134	AW968073	Hs.194331	ESTs, Highly similar to A55713 inositol	3.88
45	107850	AA022910	Hs. 295446	ESTs, Moderately similar to 810024C cyto	3.88 3.88
	130907 101879	AA322866	Hs.21107	neuroligin	3.88
	104267	AA 176374 AFD43244	Hs.243886	nuclear autoantigenic sperm protein (his	3.88
	112232	BE253927	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.88
	113248	T63857	Hs.24983	hypothetical protein from EUROIMAGE 2021	3.88
50	114044	BE327427	Hs.79953	gb:yc16e01.s1 Stratagene lung (937210) H ESTs	3.88
	115414	AA662240	Hs.283099	AF15q14 protein	3.88
	129598	N30436	Hs.11656	Homo sapiens cD FLJ12566 fis, clone NT	3.88
	102134	AL036967	Hs.2324	protamine 2	3.68 3.87
55	108310	R98185	Hs.17240	ESTs	3.87
55	116470 110947	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.86
	115839	AW298410 BE300266	Hs.21475	ESTS	3.85
	103534	AW970872	Hs.28935	transducin-like enhancer of split 1, hom	3.85
	105209	AB023197	Hs.9247 Hs.227743	protein kise, AMP-activated, alpha 1 c	3.85
60	108749	AA127017	Hs.71052	KIAA0980 protein ESTs	3.85
	110565	A1884970	Ha.4983	ESTs	3.85
	110799	AI089660	Hs.323401	dpy-30-like protein	3.85
	117068	H91257	Hs.41391	EST	3.85
65	130956 102273	NM_001135	Hs.2159	aggrecan 1 (chondroffin sulfate proteogl	3.85 3.85
00	112960	BE391815	Hs.75981	ubiquitin specific protease 14 (IR-gua	3.85
	114414	AL110209 AW152166	Hs.6770	LCAT-like lysophospholipase	3.84
	109865	AA249439	Hs.182113	ESTs	3.84
=-	108208	AK001674	Hs.27027 Hs.22630	hypothetical protein DKFZp762H1311	3.84
70	122311	NM_014913	Hs.131915	cofactor required for Sp1 transcriptio	3.84
	124271	AW293223	Hs.8928	KIAA0883 protein hypothetical protein Ft. 120291	3.84
	106650	ALD49951	Hs.22370	Homo sapiens mR; cD DKFZp56400122 (f	3.83
	112187	N99591	Hs.25587	ESTs, Weakly similar to T00329 hypotheti	3.83
75	122354	AL157579	Hs.153610	KIAAD751 gene product	3.83
13	111462	R05296		gb:ye91e08.s1 Soares fetal liver spleen	3.83 3.81
	128109 127003	AW269421	Hs.128093	£518	3.81
	109210	AW816515 AA669722	Hs.173540	ATPase, Class V, type 10D	3.81
	132543	BE568452	Hs.272137	ESTS	3.81
80	106827	AA457456	Hs.5101 Hs.11408	protein regulator of cytokinesis 1	3.80
	124232	H63391	Hs.339677	hypothetical protein FLJ20435	3.80
	126039	AL137523	Hs.181102	ESTs, Wealdy similar to 136022 hypotheti p30 DBC protein	3.80
	128022	AW195569	Hs.125906	ESTs ESTS	3.80
					3.60

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	400005		11. 488444		2.70
	132005 131392	AA149707	Hs.173091 Hs.26320	ubiquiin-like 3	3.79 3.79
	131775	AA235153 AB014548	Hs.31921	TRABID protein KIAA0648 protein	3.79
	126257	N99838		gbzga39g11.r1 Soares (etal liver spleen	3.79
5	121950	AA429515		gb:zw75c05.s1 Soares_tastis_NHT Homo sap	3.79
	116067	AA454827	Hs.293637	ESTs	3.78
	104658	AA360954	Hs.27268	Homo sapiens cD: FLJ21933 fs, clone H	3.78
	104493 100163	AW960427 W44671	Hs.79059 Hs.124	transforming growth factor, beta recepto gene predicted from cD with a complete	3.77 3.77
10	116223	AF045458	Hs.47061	unc-51 (C. elegans)-like kise 1	3.77
- •	120588	AL031778	Hs.797	nuclear transcription factor Y, etpha	3.76
	128764	AW024282	Hs.104938	hypothetical protein MGC15906	3.75
	111574	AI024145	Hs.188526	ESTs	3.75
15	117396	W20128	Hs.296039	ESTs	3.75
15	119052 121806	R10889 AA424313	Hs.98402	gb:yf38d02.s1 Soares fetat liver spleen ESTs	3.75 3.75
	122410	AA446854	Hs.271004	ESTs. Weakly similar to I38022 hypotheti	3.75
	126638	AA649257	Hs.188602	ESTS	3.75
00	127879	AA768098	Hs.189079	ESTs	3.75
20	121095	AA320134	Hs.196029	Homo saplens mR for KIAA1657 protein,	3.75
	103430 101230	8E564090 AW504300	Hs.20716	translocase of inner mitochondrial membr mannosidase, alpha, class 2A, member 2	3.74 3.74
	100200	H94688	Hs.295605 Hs.173737	ras-related C3 botulinum toxin substrate	3.73
	106913	Al219346	Hs.86178	M-phase phosphoprotein 9	3.73
25	110975	H17012	Hs.14633	ESTs	3.73
	117314	N32498	Hs.42829	ESTs	3.73
	118737	AA199686	41- 074000	gb:zq75g09.r1 Stratagene hNT neuron (937	3.73
	124169 124580	8E079334 N68420	Hs.271630 Hs.107992	ESTs ESTs	3.73 . 3.73
30	125747	NM_002884	Hs.865	RAP1A, member of RAS oncogene tamily	. 3.73 3.73
	124879	R73588	Hs.101533	ESTs	3.72
	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	3.72
	103644	M13305	Hs.247787	opsin 1 (cone pigments), long-wave-sensi	3.72
35	106044	N90344	Hs.149436	Idnesin family member 58	3.71 3.71
55	127867 133828	C18530 T28472	Hs.7655	gb:C18530 Human placenta cD (TFujiwara U2 small nuclear ribonucleoprotein auxil	3.71
	107387	D86983	Hs.118893	Melanoma associated gene	3.71
	104160	AA455706	Hs.44581	heat shock protein hsp70-related protein	3.71
40	106098	BE278344	Hs.7970	DKFZP434B027 protein	3.70
40	133891	M85289	Hs.211573	heparan sulfate proteoglycan 2 (perfecan	3.70
	120717 119263	AA904581 T15977	Hs.154434	ESTs, Weakly similar to unknown [H.sapie gb:182328 Infant brain, Bento Soares Hom	3.70 3.70
	102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	3.70
	106566	8E298210	13.55.0	gb:601118016F1 NIH_MGC_17 Homo saplens c	3.70
45	110708	N33878	Hs.306117	KIAA0306 protein	3.70
	114357	R41677	Hs.6107	Homo sapiens cD FLJ14839 fis, clone OV	3.70
	115285 123034	AW972872 AL359571	Hs.293736 Hs.44054	ESTs ninein (GSK3B Interacting protein)	3.70 3.70
	126396	T06298	Hs.153326	EST	3.70
50	132597	Y11192	Hs.5299	aldahyda dehydrogese 5 family, member	3.70
	105823	A1559444	Hs.293960	ESTs	3.70
	102644	T59816	Hs.173311	C18B11 homolog (44.9kD)	3.70
	133513 116450	AF136407 Al654450	Hs.7448 Hs.47274	chromosome 6 open reading freme 5 Homo saplens mR; cD DKFZp564B176 (fr	3.70 3.69
55	104596	AF067804	Hs.15423	hypothetical protein HDCMC04P	3.69
	133579	X75346	Hs.75074	miliogen-activated protein kise-activat	3.68
	124556	N29317	Hs.236463	Homo sepiens mR; cD DKFZp586I0521 (f	3.68
	120534	AI635113	Hs.270368	ESTs, Weakly similar to 178885 serine/th	3.68
60	103156 134992	BE259039 AA464444	Hs.129953 Hs.5831	Ewing sarcoma breakpoint region 1 tissue inhibitor of metalloproteise 1	3.68 3.68
00	106730	BE467313	Hs.260707	ESTs	3.68
	120880	AA360240	Hs.97019	EST	3.68
	123731	AA609839		gb:ee62f01.s1 Stratagene lung carcinoma	3.68
65	126973	W48653	Hs.251928	nuclear pore complex interacting protein	3.67
65	103646	AW248439	Hs.2340	junction plakoglobin	3.67
	116333 120922	AF155827 AA481003	Hs.203963 Hs.97128	hypothetical protein FLJ 10339 ESTs	3.67 3.67
	127407	AW089514	Hs.279681	heterogeneous nuclear ribonucleoprotein	3.67
	106578	AA838381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	3.67
70	123000	AI584156	Hs.105640	Homo saplans, clone IMAGE:4139775, mR,	3.87
	101464	AA852431	Hs.51299	Did dehydrogese (ubiquinone) flavopro	3.67
	101397 131135	M26380 NM_016569	Hs.180878 Hs.267182	lipoprotein lipase TBX3-iso protein	3.67 3.66
	106112	AL117518	Hs.3688	KIAA0978 protein	3.66
75	123974	NM_015678	Hs.3821	neurobeachin	3.66
	127742	AW293496	Hs.180138	ESTs	3.66
	112908	BE281000	Hs.3530	TLS-essociated serine-arginine protein 2	3.66
	131802 135162	AL137406	Hs.296358	Homo sapiens mR; cD DKFZp434M162 (fr	3.65 3.65
80	124984	A1187925 BE313210	Hs.95667 Hs.223241	F-box protein 30 eukeryolic translation elongation factor	3.65 3.65
	118844	AL035364	Hs.50891	hypothetical protein	3.65
	125429	AI023654	Hs.114191	ESTs	3.65
	125598	R25698	•	gb:yg44h11.r2 Soares Infant brein 1NiB H	3.65

	125792	AA495205	Hs.193700	Homo saplens mR; cD DKFZp58610324 (1	
	126965	A1470523	Hs.139335	ATP-binding cassette, sub-family C (CFTR	3.65 3.65
	130776	AF167706	Hs.19280	cysteine-rich motor neuron 1	3.65
5	131949	AK000010	Hs.258798	hypothetical protein FLJ20003	3.65
,	116612 123749	C14904 AA609949	Hs.45184	Homo sapiens cD FLJ12284 fls, clone MA	3.65
	134203	AA161219	Hs.112790 Hs.799	EST diphtheria toxin receptor (heperin-bindi	3.65
	133605	AL038165	Hs.75187	translocase of outer miliochondrial membr	3.64
10	109235	AI381800	Hs.300684	calcitonin gene-related peptide-receptor	3.64 3.64
10	125447	Al582222	Hs.128686	ESTs	3.63
	122942 122748	Al277829	Hs.111862	KIAA0590 gene product	3.63
	103840	AA458822 AW975861	Hs.193815 Hs.47367	ESTs	3.63
	105333	AA234831	Hs.246112	KJAA1785 protein KJAA0788 protein	3.63
15	108807	Al652236	Hs.49376	hypothetical protein FLJ20644	3.63 3.63
	114699	AA127386		gb:zn90d09.r1 Stratagene lung carcinoma	3.63
	126040 131028	728444	Hs.24119	Homo sapiens mR; cD DKFZp588G2222 (f	3.63
	131710	AI879165 NM_015368	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	3.63
20	100164	AW372032	Hs.30985 Hs.173714	pannexin 1 MORF-related gene X	3.63
	120837	BE149656	Hs.306621	Homo sapiens cD FLJ11963 fis, clone HE	3.62
	131089	Z42645	Hs.22870	Homo saplens mR full tength insert cDN	3.62 3.62
	126428	AA412436	Hs.301985	ESTs	3.62
25	129148 102337	AW501216 AJ814663	Hs.108945	KIAA0515 protein	3.61
	104520	AI702384	Hs.170133 Hs.76925	forkhead box O1A (rhabdomyosarcoma)	3.61
	112954	AA928953	Hs.6655	hypothetical protein FLJ14981 Homo saplens EST from clone 208499, full	3.60
	125197	AF086270	Hs.278554	heterochromatin-like protein 1	3.60 3.60
30	128124	Al125748	Hs.130194	ESTS	3.60
30	129553 123998	AW015763	Hs.113065	ESTs	3.60
	128835	AA203429 AK001731	Hs.79474	tyrosine 3-monooxygese/typtophan 5-mo	3.60
	129226	BE222494	Hs.106390 Hs.180919	Homo saplens mR; cD DKFZp586H0924 (f inhibitor of D binding 2, domint neg	3.59
25	135131	AI582743	Hs.94953	Homo sapiens, Similar to complement comp	3.59
35	128955	AA775076	Hs.185807	Homo saplens, Similar to PRO0478 protein	3.59 3.58
	100225	D28539	Hs.167185	glutamata receptor, metabotropic 5	3.58
	101572 102277	AA437199 U31099	Hs.656	cell division cycle 25C	3.58
	103667	280788	Hs.158326 Hs.247815	prostaglandin D2 receptor (DP)	3.58
40	112373	AW963357	Hs.7847	H4 histone family, member L ESTs	3.58
	119284	AL041224	Hs.65379	ESTS	3.58 3.58
	125422	AA903228	Hs.153717	ESTs	3.58
	126381	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogese 1	3.58
45	129168 123133	A1132988 AA487264	Hs.109052	chromosome 14 open reading frame 2	3.58
	128789	AW368576	Hs.154974 Hs.139851	Homo sapiens mR; cD DKFZp667N084 (fr caveolin 2	3.57
	104172	AA476418	113.103031	gb:zx02a12.s1 Soares_total_fetus_Nb2HF8_	3.57
	134263	AW973443	Hs.8086	R (guanine-7-) methyltransferase	3.57 3.57
50	101759	M80244	Hs.184601	solute carrier family 7 (cationic amino	3.57
50	104942 123443	NM_016348 BE244537	Hs.10235	chromosome 5 open reading frame 4	3.56
	110707	Al239832	Hs.167382 Hs.15617	triurelic peptide receptor A/guanylate	3.56
	106787	Al492261	Hs.32450	ESTs, Weakly similar to ALU4_HUMAN ALU S ESTs	3.55
E E	112940	AK001757	Hs.281348	hypothetical protein FW10895	3.55 3.55
55	115301	T11832	Hs.127797	Homo septens cD FLJ11381 ffs, clone HE	3.55
	125978 128002	N66843 Al985897	Hs.35608	ESTs	3.55
	119847	H81136	Hs.125293 Hs.334604	ESTs	3.55
	134595	NM_002401	Hs.29282	Homo septens mR for KIAA1870 protein, mitogen-activated protein kise kise	3.55
60	121309	AA293834	Hs.97312	ESTs	3.55 3.54
	122679	AA811286	Hs.192837	ESTs. Wealdy similar to ALUS_HUMAN ALU S	3.54
	106061 127207	AA565356 AA377165	Hs.13250	ESTS	3,54
	129563	AF119664	Hs.44833 Hs.27299	ESTs	3.54
65	105951	R48700	Hs.20733	transcriptiol regulator protein Homo saplens cD: FLJ22358 fis, clone H	3.54
	115643	AA404276	Hs.123253	hypothetical protein FLJ22009	3.53 3.53
	130473	U11690	Hs.1572	faciogenital dysplasia (Aarskog-Scott sy	3.53
	104246 120562	AF016032	Hs.201377	lysosomal	3.53
70	101211	BE244580 AA355357	Hs.302267 Hs.283429	hypothetical protein FLJ10330	3.53
	100774	J05581	Hs.89603	SMC (mouse) homolog, X chromosome mucin 1, transmembrane	3.53
	108407	AA075519		gb:zm87h09.s1 Stratagene overlan cancer	3.53
	113538	A1554947	Hs.15167	ESTs, Weakly similar to 837482 finger pr	3.53 3.53
75	113876	Al799751	Hs.5635	ESTs	3.53
	110731 125845	NM_014899 AK001440	Hs.188006	KIAA0878 protein	3.52
	112945	AW138458	Hs.131840 Hs.20787	hypothetical protein FLJ10578	3.51
	131586	NM_012296	Hs.30687	Homo septens cD: FLJ21686 fis, clone C GRB2-associated binding protein 2	3.51
00	125413	Al887951	Hs.74566	dihydropyrimidise-like 3	3.51 3.51
80	129360	AJ000534	Hs.110708	sarcoglycan, ension	3.50
	128819	R38007	Hs.77578	ubiquitin specific amtease 9. X channes	3.50
	101973 103616	U41514 NM_002647	Hs.80120 Hs.32971	UDP-N-acetyl-atcha-D-galactosamine:oolyo	3.50
			ri3.a28/ I	phosphoinosilide-3-kise, class 3	3.50
				. 109	

	105535	AJ459519	Hs.297681	serine (or cysteine) proteise inhibito	
	118767	AI038653	Hs.50500	ESTs	3.50 3.50
	126634 130851	AW361109 R66282	Hs.43627	SRY (sex determining region Y)-box 22	3.50
5	134353	AL138201	Hs.20247 Hs.82120	ESTs, Weakly similar to \$65657 alpha-1C- nuclear receptor subfamily 4, group A, m	3.50
	111394	AA412227	Hs.16131	hypothetical protein FLJ12876	3.50 3.50
	102696 113037	BE540274 R17268	Hs.239	forkhead box M1	3.49
4.0	111028	H59346	Hs.259873 Hs.30151	exol transport of syptic vesicles ESTs, Weakly similar to (38022 hypotheti	3.49
10	131688	AI935413	Hs.30692	p21 (CDKN1A)-activated kise 2	3.49 3.49
	115613 116975	AW136951	Hs.173946	hypothetical protein FLJ10486	3.48
	100210	H81076 D26381	Hs.269001 Hs.3104	ESTs	3.48
16	110147	H18700	Hs.268799	KIAA0042 gena product ESTs	3.48
15	115600	AA081395	Hs.42173	Homo sapiens cD FLJ10366 fis, clone NT	3.48 3.48
	119088 120347	R39261 AA211068	Hs.90790	Homo saplens cD: FLJ22930 fis, clone K	3.48
	122702	AI220089	Hs.120247 Hs.99439	nuclear fragile X mental retardation pro ESTs	3.48
20	125552	H09701	Hs.278366	ESTs, Weakly similar to 138022 hypotheti	3.48 3.48
20	126461 128572	AI381659	Hs.267086	ESTs	3.48
	118397	AA933022 BE139479	Hs.256583 Hs.161492	Interleukin enhancer binding factor 3, 9	3.48
	127999	AW978827	Hs.69851	ESTs nucleolar protein family A, member 1 (H/	3.47
25	132066	A1929392	Hs.181195	DJ (Hsp40) homolog, subfamily B, membe	3.47 3.47
23	105693 128874	BE250951 H06245	Hs.181368	U5 snRNP-specific protein (220 kD), orth	3.47
	119984	AA230228	Hs.106801 Hs.59197	ESTs, Weakly similar to PC4259 territin ESTs	3.48
	104000	Al146527	Hs.80475	polymerase (R) ii (D directed) polyp	3.46 3.46
30	101488 101045	BE547216 J05614	Hs.181128	ELK1, member of ETS oncogene family	3.46
	120149	AA227609	Hs.94834	gb:Human proliferating cell nuclear anti ESTs	3.46
	107025	AA825523	Hs.21255	ESTs, Wealdy similar to 138022 hypotheti	3.46 3.45
	101716 102899	AF050658	Hs.2563	tachykinin, precursor 1 (substance K, su	3.45
35	123075	Al815559 AW293133	Hs.75730 Hs.101340	sigl recognition particle receptor ("d	3.45
	124695	AA594979	Hs.239307	ESTs, Wealdy similar to A42442 integrin tyrosyl-tR synthetase	3.45
	127669	N28989	Hs.22891	solute carrier family 7 (cationic amino	3.45 3.45
	129793 120095	AW207000 AA693774	Hs.126857	Homo saplens cD FLJ12936 fis, clone NT	3.44
40	110915	BE092285	Hs.59601 Hs.29724	ESTs hypothetical protein FLJ13187	3.44
	130542	U64675	Hs.179825	RAN binding protein 2-like 1	3.43 3.43
	100488 115027	BE273749 AA743331	Hs.752	FK506-binding protein 1A (12kD)	3.43
	119298	NM_001241	Hs.272572 Hs.155478	hemoglobin, sipha 2 cyclin T2	3.43
45	126486	AI065133	Hs.152316	hypothetical protein PRO0971	3.43
	130021 127166	M24470	Hs.1435	guanosine monophosphate reductase	3.43 3.43
	114988	AW954605 AA251089	Hs.283395	sema domain, transmembrane domain (TM),	3.42
50	133817	AW578716	Hs.7644	gb:zsD4f05.s1 NCL_CGAP_GCB1 Homo sapiens H1 histone family, member 2	3.42
50	133562	M60721	Hs.74870	H2.0 (Orosophila)-like homeo box 1	3.41 3.41
	105610 129007	AA280072 AK001521	Hs.99872	fatel Alzheimer antigen	3.41
	100662	Al368680	Hs.107882 Hs.816	hypothetical protein FLJ10659 SRY (sex determining region Y)-box 2	3.41
55	120159	R60781	Hs.92927	putative 47 kDa protein	3.41 3.41
23	134966 100369	AW402389 D79988	Hs.920	modulator recognition factor I	3.41
	104260	AF008192	Hs.115778 Hs.194283	KIAA0166 gene product putative GR6 protein	3.41
	100134	AA305746	Hs.49	macrophage scavenger receptor 1	3.40
60	116015 119251	AA338648	Hs.50334	testes development-related NYD-SP22	3.40 3.40
00	127176	715753 BE387162	Hs.65250 Hs.280858	EST	3.40
	123422	AA598484	10.200030	ESTs, Highly similar to A35661 D excis gb:ae38f04.s1 Gessler Wilms tumor Homo s	3.40
	123094 105289	AA761073	Hs.146847	TRAF family member-associated NFKB activ	3.39 3.39
65	111219	AB020638 N68838	Hs.103000	KIAA0831 protein	3.39
-	127963	Al299013	Hs.19247 Hs.87779	ESTs, Moderately similar to ALUC_NUMAN (Homo saplans c0: FLJ23087 fis. clone (3.38
	109412	BE543313	Hs.209473	hypothelical prolein FLJ 10520	3.38 3.38
	118794 112040	AW517051 R43286	Hs.118210	ESTs	3.38
70	111180	A1798851	Hs.283108	gb;yg17e11.s1 Soares infant brain 1NIB H	3.38
	117329	AA524065	Hs.93670	hemoglobin, gamma G Homo saplens cD: FLJ22664 fis, clone H	3.38
	104371	A1288698	Hs.194081	ESTs, Wealdy similar to 138022 hypotheti	3.38 3.38
	109265 109557	AA 195285 AW 452405	Hs.85982	ESTs	3.38
75	120753	AA312551	Hs.6427 Hs.230157	ESTs ESTs	3.38
	120970	AA398118	Hs.97579	ESTs, Wealthy similar to A46010 X-linked	3.38 3.38
	127094 127746	F13215 Al239495	Hs.287849	ESTs, Weakly similar to T22074 hypotheti	3.38
00	123553	A1494291	Hs.120189 Hs.111977	ESTs ESTs	3.38
80	130652	M31689	Hs.1735	es rs inhibin, beta B (activin AB beta polypep	3.37
	135101	U82275	Hs.94498	eukocyte immunoalobulin-like recenter	3.37 3.37
	121799 112278	A1885670 Z41698	Hs.124027	SELENOPHOSPHATE SYNTHETASE: Human selen	3.37
		-	Hs.26039	Homo septens cD FLJ13937 fis, clone Y7	3.36
				. 110	
			•		

	113401	AA610175	Hs.179847	Homo saplens cD FLJ12195 fis, clone MA	3.36
	109292	AW975746	Hs.188662	KIAA1702 protein	3.38
	135026 118210	N92165 N49233	Hs.93231	ESTs	3.38
5	123476	AA384564	Hs.46914 Hs.108829	ESTs, Wealthy similar to A46010 X-linked	3.35
	111076	N59129	Hs.20851	ESTs ESTs	3.35 3.35
	111520	Al985369	Hs.301134	ESTs	3.35 3.35
	133383	8E313555	Hs.7252	KIAA1224 protein	3.35
10	103731 11082B	AA070545 AK002114	Hs.23495	gb:zm70c03.r1 Stratagena neuroepithelium	3.35
	112520	R68654	Hs.30814	hypothetical protein FLJ11252 ESTs	3.35
	115725	AW899053	Hs.76917	F-box only prolein 8	3.35 3.35
	125867	H13331	Hs.123721	ESTs	3.35
15	127719 129863	AI242163	Hs.22670	chromodomain helicase D binding protei	3.35
13	130816	BE379765 M61877	Hs.129872 Hs.1985	sperm associated antigen 9	3.35
	130888	AL044315	Hs.173094	spectrin, aipha, erythrocytic 1 (ellipto Homo saplens mR for KIAA1750 protein.	3.35
	133377	AJ131245	Hs.7239	SEC24 (S. carevistae) related gene famil	3.35 3.35
20	118986	AF148713	Hs.125830	bladder cancer overexpressed protein	3.35
20	101723	U34304		gb:Human nonmuscle myosin heavy chain !!	3.34
	134693 102856	N70361 M26150	Hs.8854	Human transcription unit PVT gene, exons	3.34
	105593	AA279341	Hs.248177 Hs.174151	H3 histone family, member L aldehyde oxidase 1	3.34
25	134748	L34059	Hs.89484	cadherin 4, type 1, R-cadherin (retii)	3.34 3.34
25	109149	AA831179	Hs.40065	hypothetical protein MGC4825	3.33
	115026 103548	AA251972	Hs.188718	ESTs	3.33
	111189	Z14244 N87603	Hs.75752 Hs.272130	cytochrome c oxidase subunit VIIb	3.33
	127078	Al422951	Hs.146162	ESTs, Weakly similar to S65824 reverse t ESTs	3.33
30	124949	AI903210	Hs.336780	tubulin, beta polypeptide	3.33 3.33
	111012	A1077389	Hs.269818	ESTs, Weakly similar to Z195_HUMAN ZINC	3.33
	113412 116351	AW628660 AL133623	Hs.44131	KIAA0974 protein	3.33
	121633	AA417011	Hs.82501 Hs.98175	similar to mouse Xm1 / Dhm2 protein EST	3.33
35	124591	N69243	Hs.192974	hypothetical protein FLJ12735	3.33 3.33
	130225	AB021179	Hs.15299	HMBA-inducible	3.33
	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.33
	132581 105726	AK000631 NM_012068	Hs.52256 Hs.9754	hypothetical protein FLJ20624	3.33
40	101867	M96132	FIS.97.34	activating transcription factor 5 gb:Human MHC class II HLA-DR-beta-1*0901	3.32
	105004	BE616023	Hs.25298	KIAA1813 protein	3.32 3.32
	100288	AL039103	Hs.153834	pumilio (Drosophila) homolog 1	3.32
	118349 103352	N63786 H09366	Hs.94149	ESTs. Weakly similar to ALU1_HUMAN ALU S	3.32
45	107436	W27720	Hs.78853 Hs.12450	uracil-D glycosylase protocadherin 9	3.30
	109062	AA160941	110.12400	gb:zq40d12.s1 Stratagene hNT neuron (937	3.30 3.30
	110379	Al300505	Hs.33130	Homo sapiens cD: FLJ23486 fis, clone L	3.30
	111221 117903	AB037782	Hs.15119	KIAA1361 protein	3.30
50	123265	AA768283 AA491209	Hs.47111	ESTs	3.30
	128226	AJ284940	Hs.289082	gb:aa47a08.s1 NCI_CGAP_GCB1 Horno saplens GM2 ganglioside activator protein	3.30
	111945	R40663	Hs.124944	EST8	3.30 3.30
	126214	AW748338	Hs.168052	KIAA0421 protein	3.30
55	121073 102083	146199 135901	Hs.112184	DKFZP586J0819 protein	3.30
	100992	NM_007289	Hs.75117 Hs.1298	interleukin enhancer binding factor 2, 4 membrane metallo-endopepildase (neutral	3.30
	134021	L13720	Hs.78501	growth arrest-specific 8	3.30 3.30
	126452	R26867		.gb:yh52e01.s1 Soares placenta Nb2HP Homo	3.29
60	117195 127663	AJ798425	Hs.42710	ESTs	3.29
00	113677	AK000452 270200	Hs.10340 Hs.246112	hypothelical protein FLJ20445 KIAA0768 protein	3.29
	132398	AA876616	Hs.16979	ESTs, Weakly similar to A43932 much 2 p	3.28
	109533	AL043979	Hs.259729	KIAA0596 protein	3.28 3.28
65	102915	X07820	Hs.2258	matrix metalloproteise 10 (stromelysin	3.28
05	104348 113047	H05405 A1571940	Hs.19221	hypothetical protein DKFZp566G1424	3.28
	113203	AA743563	Hs.7549 Hs.10305	ESTs ESTs	3.28
	114503	AL040600	Hs.188083	ESTS	3.28 3.28
70	122100	AA431220	Hs.41086	pleckstrin homology domain-containing, f	3.28
,,	123073 130253	AA485061	Hs.105652	ESTs	3.28
	130365	AI078570 W56119	Hs.167473	phosphoglucomutase 5	3.28
	130762	D84371	Hs.155103 Hs.1898	eukaryotic translation initiation factor paraoxose 1	3.28
75	132360	AW893660	Hs.46440	solute carrier family 21 (organic anion	3.28 3.28
75	110763	AI928445	Hs.92254	syptotagmin-like 2	3.27
	103437 114840	AV655598 AA447591	Hs.184211	peptidase (milochondrial processing) bet	3.27
	106888	AA020964	Hs.87359 Hs.24734	ESTs, Highly similar to RB18_HUMAN RAS-R cxysterol binding protein	3.27
90	129896	BE295568	Hs.13225	UDP-Gal:betaGlcc beta 1,4- galactosyll	3.27 3.26
80	113459	T80206	Hs.14716	ESTs	3.26
	134332 117048	D86962 H89732	Hs.81875	growth factor receptor-bound protein 10	3.26
	109249	AA194730	Hs.230113 Hs.268189	EST hypothetical protein FLJ20438	3.26
				Andreas de Proposit Le Parageon	3.26

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	40.4000	1100.000			
	134663 114440	W73428	Hs.8750	uncharacterized bone marrow protein BM04	3.26
	102196	AL046511 BE266830	Hs.106525 Hs.75238	hypothetical protein FLJ12567	3.25
	109581	R45584	Hs.23025	chromatin assembly factor 1, subunit B (ESTs, Wealdy similar to ALUS_HUMAN ALU S	3.25
5	120814	AW887798	Hs.95860	ESTs, Weakly similar to 138022 hypotheti	3.25
	122391	AA446316	Hs.191622	EST8	3.25 3.25
	122553	AA451884	Hs.190121	ESTs	3.25
	124755	R38087	Hs.267690	KIAA1228 protein	3.25
10	130943	U20760	Hs.272429	calclum-sensing receptor (hypocalcluric	3.25
10	115185 114297	BE299677	Hs.105461	hypothetical protein FLJ20357	3.25
	106657	AA149707 AW854339	Hs.173091 Hs.33476	ubiquifin-like 3	3.25
	124320	H95749	Hs.102342	hypothelical protein FLJ11937 EST	3.25
	124087	H08773	Hs.288590	Homo sapiens cD FLJ11454 fis, clone HE	3.25 3.24
15	110705	AB007902	Hs.32168	KIAA0442 protein	3.24 3.24
	106508	AI205785	Ha.30348	ESTs	3.24
	112538	AA908813		gb:og77h06.s1 NCI_CGAP_Ov8 Homo septens	3.24
	100130	NM_000304	Hs.103724	peripheral myelin protein 22	3.24
20	106017	AA477956	Hs.26268	ESTs 🦟	3.24
20	113921 121520	AW976530 AA412163	Hs.28355	hypothetical protein FLJ22402	3.23
	129255	Al961727	Hs.164785 Hs.109804	ESTs	3.23
	125069	H81306	Hs.194485	H1 histone family, member X ESTs	3.23
~ ~	119863	AA081218	Hs.58608	Homo saplens cD FLJ14206 fis, clone NT	3.23 3.23
25	111273	N70934		gb:za33f06.s1 Soares fetal liver splean	3.23
	102971	X16609	Hs.183805	ankyrin 1, erythrocytic	3.23
	103937	AA934083	Hs.13836	ESTs, Weakly similar to 138022 hypotheti	3.23
	121770	NM_015902	Hs.278428	progestin induced protein	3.23
30	128972 132528	AA528140 T78738	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	3.23
	134835	L04569	Hs.50758 Hs.89925	SMC4 (structural maintence of chromoso	3.23
	103158	8E242587	Hs.118651	calcium channel, voltage-dependent, L ty hematopoletically expressed homeobox	3.23
	118405	AL117518	Hs.3686	KIAA0978 protein	3.22 3.22
26	104631	AA002064	Hs.18920	ESTs	3.22
35	114253	BE149866	Hs.14831	Homo saplens, Similar to zinc finger pro	3.22
	134607	Al675881	Hs.86538	EST\$	3.22
	135114 120191	AW340493	Hs.175043	ancient conserved domain protein 4	3.22
	105029	BE407106 AI122691	Hs.65907	Homo sapiens, clone IMAGE:3959816, mR,	3.22
40	128550	AA418276	Hs.13268 Hs.170142	ESTs	3.21
	119873	Al660149	Hs.44865	lysosomal	3.21
	130115	T47294	Hs.149923	X-box binding protein 1	3.21 3.21
	133916	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.21
4.5	120259	AW014788	Hs.192742	hypothetical protein FLJ12785	3.21
45	110721	H97678	Hs.31319	EST8	3.21
	130052	AL049415	Hs.278679	a disintegrin and metalloproteise doma	3.21
	100255 100624	D38521	Hs.112398	KIAA0077 protein	3.20
	122275	AB001025 AA437124	Hs.9349	ryanodine receptor 3	3.20
50	127099	AA347668	Hs.187247	ESTS	3.20
	134321	BE538082	Hs.8172	gb:EST54026 Fetal heart II Homo sapiens ESTs, Moderately similar to A46010 X-lin	3.20
	132809	AF036144	Hs.5734	meningloma expressed entigen 5 (hyaluron	3.20 3.20
	101125	AJ250582	Hs.82749	transmembrane 4 superfamily member 2	3.20
55	128339	AL121087	Hs.296406	KIAA0685 gene product	3.19
33	117121	H95044	Hs.321388	EST	3.19
	124760 132232	AW408586 Al522273	Hs.91052	ESTs, Moderately similar to ALU5_HUMAN A	3.19
	125919	W26713	Hs.42640 Hs.256972	ESTs	3.19
	123324	AB018352	Hs.105399	ESTs K1AA0809 protein	3.19
60	100157	D14861	Hs.119	Wilms' tumour 1-associating protein	3.19 3.19
	101447	M21305		gb:Human alpha satellite and satellite 3	3.19
	124345	NM_014487	Hs.120766	nucleolar cysteine-rich protein	3.18
	122583 128961	NM_012447	Hs.20132	stromal antigen 3	3.18
65	111321	AL133014 Al569766	Hs.107387	CGI-20 protein	3.18
•	134977	AL044963	Hs.13205	ESTs	3.18
	131535	N22120	Hs.306121 Hs.75277	leutocyte receptor cluster (LRC) encoded hypothetical protein FLJ13910	3.18
	109950	H08200	Hs.268770	ESTs, Weakly similar to 2004399A chromos	3.18
70	129875	AA181018	Hs.13056	hypothetical protein FLJ 13920	3.18 3.18
70	101654	M60298	Hs.733	erythrocyte membrane protein band 4.2	3.18
	104732	AL079294	Hs.29952	Homo saplens mR full length insert cDN	3.18
	106867	AB037744	Hs.34892	KIAA1323 protein	3.18
	108301 118042	AA069728 AJ432389	Hs.184582	ribosomal protein L24	3.18
75	120900	AA830712	Hs.161465 Hs.291931	ESTs ESTs	3.18
	129312	T97579	Hs.110334	ESTs, Weakly similar to 178885 serine/th	3.18
	116291	AW410377	Hs.41502	hypothetical protein FLJ21276	3.18 3.17
	110672	AW612890	Hs.191178	ESTs	3.17 3.17
80	115665	BE072425	Hs.44579	hypothetical protein FLJ20199	3.17
80	127581	AK000680	Hs.266175	phosphoprotein associated with GEMs	3.17
	129584	AV656017	Hs.184325	CGI-76 protein	3.16
	108830 124443	AA131743 AI857519	Hs.193352	ESTs	3.16
	,		Hs.302031	zinc finger protein, subfamily 1A, 4 (Eo	3.16
				. 112	
					

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	106290	AW961393	Hs.16364	hypothetical protein FLJ 10955	3.16
	122787	Al209093	Hs.99512	ESTS	3.16
	133112	T15465	Hs.182231	thyrotropin-releasing hormone	3.16
	116435	AA186761	Hs.334812	hypothetical protein DKFZp586K0717	3.16
5	109121	BE389387	Hs.49767	DH dehydrogese (ubiquinone) Fe-S pro	3.16
_	126721	AW579621	Hs.125359	Thy-1 cell surface antigen	3.15
	102526	AA203429	Hs.79474	tyrosine 3-monooxygese/tryptophan 5-mo	3.15
	100512	D13317	Hs.78915	GA-binding protein transcription factor,	3.15
	105299	AF098951	Hs.194720	ATP-binding cassette, sub-family G (WHIT	3.15
10	117842	AI984505	Hs.161121	ESTs	3.15
10					
	123049	BE047680	Hs.211869	dickkopf (Xenopus tasvis) homolog 2	3.15
	128839	AW582962	Hs.102897	CG1-47 protein	3.15
	130343	AB040914	Hs.278628	KIAA1481 protein	3.15
1.5	115706	AB004849	Hs.50748	chromosome 21 open reading frame 18	3.15
15	120673	AW968634	Hs.105093	ESTs	3.15
	132116	AW960474	Hs.40289	ESTs	3.15
	116217	AU076474	Hs.123178	translocase of Inner milochondrial membr	3.15
	104926	BE298808	Hs.33363	DKFZP434N093 protein	3.14
	105297	NM_015905	Hs.183858	transcriptiol intermediary factor 1	3.14
20	125343	A1475495	Hs.304101	ESTs, Wealdy similar to ALU7_HUMAN ALU S	3.14
	115618	H11695	Hs.322901	disrupter of silencing 10	3.14
	124893	AA830185	Hs.269680	ESTS	3.13
	105481	BE539071	Hs.69388	hypothetical protein FLJ20505	3.13
	126165	AJ741818	Hs.125897	ESTs	3.13
25	105212	AA205334	Hs.324278	Homo sapiens mR; cD DKFZp566M063 (fr	3.13
	101528	M57508	Hs.72918	small inducible cytokine A1 (1-309, homo	3.13
	107951	AI300077	Hs.61590	ESTs	3.13
	109166	AA219691	Hs.73625	RABS interacting, kinesin-like (rabkines	3.13
	117299	N75768	112.0025	gb:yw30b07.r1-Morton Fetal Cochlea Homo	3.13
30	119694	AA041350	Hs.57847	ESTs, Moderately similar to ICE4_HUMAN C	3.13
50	124840	R56146	Hs.164515	EST, Weakly similar to AF090930 1 PRO047	3.13
	127433	AW979155			3.13
			Hs.298275	amino acid transporter 2	
	128337	A1123529	Hs.166592	ESTs	3.13
35	134053	AW628686	Hs.78851	KIAA0217 protein	3.13
33	134475	NM_014733	Hs.83790	KIAA0305 gene product	3.13
	128761	BE300341	Hs.104925	ectodermal-neural cortex (with BTB-like	3.12
	124971	T23800	Hs.151001	hypothetical protein FU14728	3.12
	128314	T87479	Hs.291797	ESTs	3.12
40	134695	AB036829	Hs.178347	SKIP for sketatal muscle and kidney enri	3.12
40	131333	BE244603	Hs.25726	transposon-derived Buster1 transposase-I	3.12
	119781	AJ278016	Hs.55565	ankyrin repeat domain 3	3.12
	131824	U28838	Hs.32935	TATA box binding protein (TBP)-associate	3.11
	124595	AW194851	Hs.111801	arsete resistance protein ARS2	3.11
	116115	AL042355	Hs.70202	WD repeat domain 10	3.11
45	129415	AI907084	Hs.111243	MADS box transcription enhancer factor 2	3.11
	111552	T97939	Hs.191185	ESTs	3.10
	134861	NM_000937	Hs.171880	polymerase (R) II (D directed) polyp	3.10
	104971	BE311926	Hs.15830	hypothetical protein FLJ12691	3.10
	126536	AA156151		gb:zo46c06.r1 Stratagene endothelial cel	3.10
50	128246	AJ990612	Hs.214818	DMRT-like family C2	3.10
	106412	AA453734	Hs.10198	ESTs	3.10
	107902	AA026827	Hs.61358	ESTs	3.10
	112495	A1346487	Hs.28739	ESTs	3.09
	131870	NM_014874	Hs.3363	KIAA0214 gene product	3.09
55	105301	AW352357	Hs.7457	MAGE1 protein	3.09
	123670	Al189844	Hs.112708	ESTs, Moderately similar to ZN91_HUMAN Z	3.09
	116474	AW160774	Hs.159154	tubulin, beta, 4	3.09
	112064	AL049390	Hs.22689	Homo sapiens mR; cD DKFZp586O1318 (f	3.09
	130525	AA361850	Hs.322149	Human clone 137308 mR, partial cds	3.08
60	120398	AL133649		retinoic acid induced 1	3.08
50	102735	AF111106	Hs.110953 Hs.3382		3.08
	124748	R34617	10.3302	protein phosphatase 4, regulatory subuni	3.08
			LL 100745	gb:yh85h12.s1 Soares placenta Nb2HP Homo	
	120755	AA312934	Hs.190745	Homo saplens cD: FLJ21326 fis, clone C	3.08
65	118895	BE304917	Hs.31097	hypothetical protein FLJ21478	3.08
05	107463	AW952022	Hs.315164	hypothetical protein similar to actin re	3.08
	114290	R51383	Hs.25793	ES15	3.08
	119005	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	3.08
	125676	BE612918	Hs.151973	hypothetical protein FLJ23511	3.08
70	127768	AA723659	Hs.290607	EST	3.08
70	132693	BE244200	Hs.55075	KIAA0410 gene product	3.07
	106812	BE251590	Hs.239370	DKFZP727I051 protein	3.07
	125654	X96753	Hs.9004	chondroitin sulfate proteoglycan 4 (mela	3.07
	111836	R58394	Hs.25119	ESTs, Wealdy similar to YEXQ_YEAST HYPOT	3.06
~-	101682	AF043045	Hs.81008	filamin B, beta (actin-binding protein-2	3.08
75	110004	H10413	Hs.268774	ESTs	3.06
	117591	N64777	Hs.44656	ESTs	3.06
	110737	AA335609	Hs.7589	ESTs. Wealdy similar to A46010 X-linked	3.06
	134337	NM_004922	Hs.81964	SEC24 (S. cerevisiae) related gene famil	3.06
	132450	AA100012	Hs.48827	hypothetical protein FLJ 12085	3.06
80	125556	AB033054	Hs.334806	KIAA1238 protein	3.06
	101811	NM_002556	Hs.24734	oxysterol binding protein	3.06
	131530	AA574309	Hs.283402	TCR eta	3.06
	105049		Hs.172506	myosin VB	3.06
	.00010	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	1 No. 1 7 ZAJUU		9.00

	126614	AA701941	Hs.187555	ESTs	2.00
	130960	AF035621	Hs.21611	kinesin family member 3C	3.05
	105503	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	3.05
_	107361	U72513	Hs.159486	Luman DDI 12 2 accordance - D	3.05
5	107575	D81886	Hs.59908	Human RPL13-2 pseudogene mR, complete ESTs	3.05
	116999	H84644	Hs.40707	EST	3.05
	119554	W38188	113.70707		3.05
	120934	AA226198		(NONE)	3.05
	125805	Al160594	Hs.166656	gb:nc25a07.s1 NCI_CGAP_PrI Homo sapiens	3.05
10	127263	AA331156	113.100030	ESTs, Highly similar to S49460 glutamate	3.05
	128025	T64877	No. 400470	gb:EST35034 Embryo, 6 week, subtracted (3.05
	131090	Al143139	Hs.108479	ESTs	3.05
	112197	NM_003655	Hs.2288	visinin-like 1	3.05
	133492		Hs.5637	ESTs .	3.05
15	118485	L40397	Hs.74137	transmembrane trafficking protein	3.04
10		AA508515	Hs.291049	ESTs	3.04
	113893	Al373741	Hs.59384	hypothetical protein MGC3047	3.04
	116911	AW205577	Hs.308435	ESTs, Moderately similar to KIAA0745 pro	3.04
	132833	U78525	Hs57783	eukaryotic translation initiation factor	3.04
20	124724	H20816	Hs.112423	Homo sapiens mR; cD DKFZp586I1420 (f	3.04
20	105894	Al904740	Hs.25691	receptor (catcitonin) activity modifying	
	129991	R28386	Hs.179925	ESTs, Weakly similar to ALUS_HUMAN ALU S	3.04
	128714	T85231	Hs.179661	tubulin, beta 5	3.04
	134650	U76378	Hs.87247	harakiri, BCL2-Interacting protein (cont	3.04
0.0	106851	AI458623		gb:lk04g09.x1 NCI_CGAP_Ln24 Homo saptens	3.04
25	133445	AC005262	Hs.73797	guanine nucleotide binding protein (G pr	3.04
	102581	AU077228	Hs.77258		3.04
	127542	AA703684	Hs.245474	enhancer of zesta (Orosophila) homolog 2 ESTs, Moderately similar to ALU5_HUMAN A	3.04
	113043	AI528789	Hs.7483	ESTs MODELANDY SITTING TO ALUS_MUMAN A	3.03
	134710	Al433797	Hs.8889		3.03
30	119245	Al815733	Hs.114360	serine hydroxymethyltransferase 1 (solub	3.03
	106391	AW959538	Hs.321214	transforming growth factor beta-stimutat	3.03
	114607	AF041260	Hs.129057	hypothetical protein OKFZp564D0478	3.03
	116083	AA455706		breast carcinoma amplified sequence 1	3.03
	132079	AJ701457	Hs.44581	heat shock protein hsp70-related protein	3.03
35	103825	AI571835	Hs.38694	ESTs	3.03
	108438		Hs.55468	ESTs .	3.03
	124359	AI141031	Hs.21342	ESTs .	3.03
	126384	N22508	Hs.139315	Homo sapiens cD: FLJ21479 fls, clone C	3.03
	127995	AW090198	Hs.4779	KIAA1150 protein	3.03
40		AA970953	Hs.128709	ESTs	3.03
40	127981	AA837029	Hs.157463	ESTs	3.02
	124417	N34059		gb:yv28h09.s1 Soares fetal liver spleen	3.02
	124357	N22401		gb:yw37g07.s1 Morton Fetal Cochlea Horno	3.02
	105437	AF151076	Hs.25199	hypothetical protein	3.02
45	101158	AW327723	Hs.76122	splicing factor, arginine/serine-rich 4	3.02
43	113897	R91601	Hs.4947	hypothetical protein FLJ22584	
	100159	AA285268	Hs.23488	KIAA0107 gene product	3.02
	108487	A1697340	Hs.135265	Homo septens clone FLB8436 PRO2277 mR	3.02
	124977	F04819	Hs.190452	KIAA0365 gene product	3.02
EΛ	131631	AA022569	Hs.29802	slit (Drosophila) homolog 2	3.02
50	102259	AL041219	Hs.82222	sema domain, immunoglobulin domain (tg),	3.01
	104399	AL022316	Hs.301947	kraken-like	3.01
	116536	8E218027	Hs.89969	ESTs	3.01
	125889	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.00
	102233	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	3.00
55	102628	U90322	Hs.27812	G protein-coupled receptor 23	3.00
	112812	H55977	Hs.35810	ESTs	3.00
	114654	AA101840	Hs.103679	ESTs	3.00
	118555	N68372	***************************************		3.00
	120005	W90105	Hs.94942	gb:ze68c10.s1 Soares_fetat_lung_NbHL19W EST	3.00
60	123596	AA421130	Hs.112640	EST	3.00
	126134	AL133033	Hs.4084		3.00
	126194	H98755	Hs.302975	KIAA1025 protein	3.00
	129778	AK001676	Hs.12457	ESTs, Weakly similar to Z195_HUMAN ZINC	3.00
_			113.12407	hypothetical protein FLJ10814	3.00
65	Table 38:				
	Pkey:	Holoup Co	a menhanat idantifan ausuban		
	CAT numbe	Coso elve	s probeset identifier number ter number		
	Accession:		er number scession numbers		
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70	Pkey	CAT number			
. •	123619		Accession		
	124417	371681_1 1642364_1	AA602964 AA609	200	
	117299		N34059 N46979		
		1632586_1	N75768 N22543		
75	116845	393481_1	AA649530 AA6593	316 HB4973	
, ,	124748	17150801	R34617		
	125596	1708455_1	R25698 R56582 R	256018	
	126257	182217_1	N99638 AW97375	0 AA328271 H90994 AA558020 AA234435 N59599 R94815	
	126280	1572221_1	Z 10417 11ZUQUQ		
80	126319	1528523_1	D81689 D81802		
UV	104172	273499_1	AA476418 AA393:	338 AA398747 AA476518	
	126426	110687_1	AA125984 AA127	189 AA065075 AA070377 AA100017 AA070891 AA113255 AA	M75160 AA097764 AA097700 MATERIA
	400/00	407440			
	126433	127143_1	AA325608 AA0999	517 N89423	
				· · · · · · · · · · · · · · · · · · ·	

	127092	1779998_1	T26985 Z44165
	127099	244301_1	AA347668 AW956810 Z44271 F07065 F07064 R13508
	126536	149206_1	AA156151 Z25109 C05177
5	103731	112052_1	AA070545 AA131490 AA131373
)	127283	232161_1	AA331156 AA331157 AA331155
	126783	113388_1	AA083531 AA126047 AA074915 AA148849
	118946 127520	1683457_1	N92834 W25061
	127532	6561701 353907_1	T51239
10	112516	1744223_1	AJ003429 AJ003367 AA564825 T83909 R68566
- •	112538	504579_1	AA908813 R70255
	112540	1605263 1	R69751 R70467 H69771 H80879 H80878
	113248	328626_1	T63857 AW971220 AA493469 T63699
1.5	112631	1746257_1	R82040 R70934
15	128360	1540098_1	F12374 T74059
	120514	25532_3	AA258335 AA258499
	127887 120637	1511945_1	C18530 T63953
	121481	200885_1 123001_1	AA811804 AA809404 AA286907 AW977624
20	120934	177521_1	AA41931 AA411930 AA226108 AA226108 AA22610
	106566	120358_1	AA226198 AA226513 AA383773
		12.000_1	BE298210 AI672315 AW086489 BE298417 AA455921 AA902537 BE327124 R14963 AA085210 AW274273 AI333584 AI369742
	121743	274582_1	A039658 A1885095 A1476470 A1287650 A1885299 A1985381 AW592624 AW340136 A1266556 AA456390 A1310815 AA484951 AA397636 AA421144
0.5	114699	135322_1	AA127386 R15844 AA127404
25	106851	322947_1	A458623 AA639708 AA485409 R22065 AA485570
	123731	genbank_AA609839	AA609839
	123973	5063691	C14805
	116793	74964_1	T77781 AW014157 D12422 AI918246 AA452599 AA628404 N35886 AA464593 AW301738 T77780 AI042309 AI095302 H60603
30	109700	genbank_F09809	AWS10376 H37614 W61360 AL373286 AL702287 AA152465 AW169067 AW169012 AW340355 AL289311
50	118466	genbank_N68741	LC3003
	111273	genbank_N70934	N56741 N70934
	118555	genbank N68372	N68372
~ ~	111462	genbank_R05296	R05296
35	118720	genbank N73515	N73515
	118737	382979_1	AA199686 N73861
	111826		· R35975
	120376	genbank_AA227469	AA227469
40	120809 120839	genbank_AA346495	A346495
	120873	genbank_AA348913 genbank_AA358015	AA348913
	115498	genbank_AA291070	AA358015 AA291070
	101045	entrez_J05614	J05614
	129969	genbank_N57818	N57818
45	108407	genbank_AA075519	AA075519
	122939	genbank_AA477141	AA477141
	117031	genbank_H88353	H88353
	124298	genbank_H91679	H91879
50	117099 101447	321871_1	H93699 H97976 H80036
50	124357	entrez_M21305 genbank_N22401	M21305
	101723	2603_1	N22401
		2000_1	U34304 AA355800 M69181 AA375523 AA093590 AA365595 S87247 AI371761 AW351920 AW181991 H28934 W79172 AA653543
			AA122005 W95572 AF086505 C02448 W57668 T11988 W95465 AA425179 F05724 F12205 F06285 R16384 T66222 F08515 F07288 AA150346 H83264 T88770 N38366 AA337253 H12001 H82899 H69395 H69380 N29054 N30920 T97385 T96819
55			AAA63807 AL079850 T11987 AA305048 AA149133 T82813 AA029555 AA035109 AAA49123 AA340297 AA724155 W05196
			AB59528 AA149134 C16426 C16097 C16587 C16138 C16107 AW021754 C16500 N30019 R55718 R60552 N84522 A1143322
			100 IDZ U1030Z AVVUZZ4Z5 AANIJZNYN AANYANIT W77755 W7/43ER C16366 A1490964 A1047000 A169969 A1690000 A1690007
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			1976/3 PV13910/ T11/30 RIQUIZOS MXZXIII BIA74575 NEE71R EDAQIA A AEREATO A ARROSO A ERIOTO A LICOSOTO CO ATROCIO CARROSO
			77791 7 199 777425079 773007490 7030127 1257.559 ADA90A77 DIRECRES ALSONOGE A ANGEENT ALSONOGO ALSONOGO A ANGEOTOE
			NW/3341 NYV233 MIGGUISH NGO196 AA.5611h5 17X6V7 NX17AG A13R7173 AIDEEN33 AIDEEN44 AIDEEE9 AIGGEEG AIGGEEG AIGGE
65			AW197337 A1168323 A1336930 A1094099 A1351490 AA268563 A1634763 AA492374 AA983970 A1123565 T72559 F09890
			AA669531 AI445824 T07180 AW084799 AA306254 R60606 W28367 R55928 WZ7995 AL044845 AA501890 N84045 T97274 N87532 AL135219 AA116056 T06000 AA116057 T07181 R08126
	124677	genbank_R01073	R01073
	110243	genbank_H26683	H26683
70	101867	entrez_M96132	M98132
70	101941	entre2_\$77583	\$77583
	119052	149538_1	R10889 R10888
	126452 119263	209811_1 genbank_T15977	R26867 R27438
_	112040	genbank_R43286	T15977
75	103657	entrez_273677	R43286 273877
-	119400	genbank_T92767	130/7 192767
	119554	NOT_FOUND_entrez_W38188	W38188
	123130	genbank_AA487200	AA487200
80	123143	genbank_AA487595	AA487595
OV.	121950	genbank_AA429515	AA429515
	123265 114988	genbank_AA491209	AA491209
	107794	genbank_AA251089 genbank_AA019255	AA251089
		P	AA019256

123422	genbank_AA598484	AA598484
109062	genbank_AA160941	AA160941
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Pkey	ExAcct	UnigeneiD	Unigene Title	Ri	R2
412719 428321	AW016610	Hs.129911	ESTs	117.8	3.3
455601	A1699994 A1368680	Hs.301347 Hs.816		108.9	39
431917	D16181	Hs.2868	SRY (sex determining region Y)-box 2 peripheral myelin protein 2	107.5	9.9
415817	U88967	Hs.78867	protein tyrosine phosphalase, receptor-t	99.0	11.8
449494	AW237014	Hs.288650	aquaporin 4	72.0	11.3
439285	AL133916	Hs.298998	ESTs	60.0 58.2	2.2 2.2
447072 456759	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	54.2	7.1
427343	BE259150 AI880044	Hs.127792 Hs.176977	delta (Orosophila)-lika 3	53.5	2.5
425088	AA663372	Hs.169395	protein kinase C binding protein 2 Homo saplens cDNA FLJ12015 fis, clone HE	49.6	2.2
412959	D87458	Hs.75090	KIAA0282 protein	49.5	3.1
447004	AW296968	Hs.157539	EST8	46.3	3.0
436878	BE465204	Hs.47448	ESTs	43.7 39.8	3.2 10.8
433551 425842	Al985544	Hs.289048	ESTs	39.7	4.3
407034	AI587490 UB4540	Hs.159823	NK-2 (Drosophila) homolog B	39.3	26.2 .
431725	X65724	Hs.2839	gb:Human dystrobrevin Isoform DTN-3 (DTN	39.1	39.1
453392	U23752	Hs.32964	Norrie disease (pseudogliome) SRY (sex determining region Y)-box 11	38.4	3.7
447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	37.5	22.1
439415	F05538	Hs.12825	ESTs	37.5 35.4	13.9 3.1
409395	U46745	Hs.54435	dystrobrevin, atpha	34.3	3.0
449539 408582	W80363 A1436323	Hs.58446	ESTs	33.6	33.6
431019	NM_005249	Hs.31141 Hs.2714	Homo saplens mRNA for KIAA 1568 protein,	32.8	5.9
427540	R12014	Hs.20976	forkhead box G18 ESTs	32.4	17,0
425057	AA826434	Hs.96944	ESTs	32.1	2.0
431941	AK000106	Hs.272227	Homo seplens cDNA FLJ20099 fis, clone CO	31.0 30.8	2.3
416829	AB013805	Hs.80220	catenin (cadherin-associated protein), d	30.4	30.B 2.2
420807 444190	AA280627	Hs.57846	ESTs	30.4	30.4
429466	A1876918 MB5835	Hs.10526	cysteine and glycine-rich protein 2	30.4	30.4
444471	AB020684	Hs.12827 Hs.11217	ESTs KIAA0877 protein	30.2	7.2
451678	AA374181	Hs.26799	DKFZP564D0764 protein	29.5	29.5
439979	AW600291	Hs.6823	hypothetical protein FLJ 10430	28.8 27.7	3.0
433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	27.1	3.2 27.1
440435 411078	AL042201	Hs.21273	ESTs	26.9	26.9
407808	A1222020 AA683559	Hs.182384 Hs.289109	ESTs, Weakly similar to 25 kDa trypsin i	26.0	26.0
416155	A1807264	Hs.205442	dimethylerginine dimethyleminohydrolase ESTs, Wealdy similar to AF117610 1 inner	25.8	2.2
421659	· NM_014459	Hs.106511	protocadherin 17	25.5	25.5
430132	AA204686	Hs.234149	hypothetical protein FLJ20647	25.0	3.3
433332	AJ367347	Hs.127809	ESTs	24.7 24.6	24.7 24.6
452744 419271	A1267652 N34901	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	23.8	23.8
447397	BE247676	Hs.238532 Hs.18442	ESTs	23.6	5.5
439039	A1656707	Hs.48713	E-1 enzyme ESTs	23.1	3.2
414175	Al308876	Hs.103849	ESTs	23.0	7.2
451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	22.2	2.0
410102	AW248508	Hs.279727	Homo sepiens cDNA FLJ14035 fis, clone HE	22.0 21.6	7.6 2.3
415910 451468	U20350	Hs.78913	chamokine (C-X3-C) receptor 1	21.2	3.0
454117	AW503398 BE410100	Hs.210047 Hs.40368	ESTs	21.0	4.7
443850	AW014723	Hs.134719	adaptor-related protein complex 1, sigma ESTs	20.8	20.8
418738	AW388633	Hs.6682	ESTs	20.4	38.5
449433	A1672096	Hs.9012	ESTs	20.2	2.2
435706	W31254	Hs.7045	GL004 protein	19.9 19.7	16.6
407192 416892	AA609200	11- 00400	gb:af12e02.s1 Soares_testis_NHT Homo sap	19.7	19.7 19.7
442562	L24498 BE379584	Hs.80409 Hs.34789	growth arrest and DNA-damage-inducible	19.6	19.6
439451	AF086270	Hs.278554	ESTs heterochromatin-like protein 1	19.4	19.4
426320	W47595	Hs.169300	transforming growth factor, beta 2	19.1	17.4
412986	X81120	Hs.75110	cannabinoid receptor 1 (brein)	18.7	5.4
452106	AJ141031	Hs.21342	ESTs	18.6 18.6	18.6
431173		Hs.294068	ESTs	18.6 18.6	10.3 18.6
422583 419088	AA410506 Al538323	Hs.118578	Haspiers mRNA for ribosomal protein L18	18.5	18.5
443547	AWZ71273	Hs.77498 Hs.23767	small nuclear ribonucleoprotein polypept	18.5	18.5
451592	A1805416	Hs.213897	Homo seplens cDNA FLJ12666 fis, clone NT ESTs	18.5	5.1
450313	AI038989	Hs.24809	hypothetical protein FLJ 10826	18.4	18.4
			-Abar order bramer i et innett	18.3	18.3

	422544	AB018259	Hs.118140	KIAA0716 gene product	18.2	4.7
	408096 418027	BE250162	Hs.83765	dihydrofolate reductase	18.0	18.0
	414117	AB037807 W88559	Hs.83293 Hs.1787	hypothetical protein proteolipid protein (Pelizaeus-Merzbache	18.0	8.2
5	429418	Al381028	Hs.99283	ESTs	18.0 17.8	18.0 17.8
	432527	AW975028	Hs.102754	ESTs	17.7	4.2
	447609	AW207605	Hs.164230	ESTs, Highly similar to phosphodiesteras	17.5	4.3
	419704 436476	AA429104	Hs.45057	ESTs	17.4	4.6
10	445133	AA326108 AW157648	Hs.53631 Hs.153506	ESTs, Weakly similar to enhancer-of-spill ESTs, Weakly similar to AF150755 1 micro	17.4	21
	446659	Al335361	Hs.226376	ESTs	17.3 17.2	18.8 2.8
	409049	AJ423132	Hs.146343	ESTs	17.2	3.8
	443672	AA323362	Hs.9657	butyrobetaine (gamma), 2-oxoglutarate di	17.2	11.0
15	407748 438527	AL079409	Hs.38178	KIAA0606 protein; SCN Circadian Oscillat	17.0	6.3
13	417791	AI969251 AW965339	Hs.143237 Hs.111471	ESTs ESTs	16.9	18.9
	417355	D13168	Hs.82002	endothelin receptor type B	16.8 16.4	10.5 18.4
	427897	NM_017413	Hs.181060	spelln; peptide ligand for APJ receptor	16.3	4.2
20	419721	NM_001650		aquaporin 4	16.2	4.4
20	427701	AA411101	Hs.221750	ESTs	16.1	3.9
	432435 426809	BE218886 BE313114	Hs.282070 Hs.29706	ESTs ESTs	16.1	5.7
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	16.0 15.9	10.0
0.5	400859			makes an equate (Bracecaniste) a constant	15.7	15.9 15.7
25	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblest	15.6	15.6
	420092	AA814043	Hs.88045	ESTs	15.6	5.4
	449605 422365	AW138581 AF035537	Hs.198416 Hs.115521	ESTs REV3 (yeast homolog)-like, catalytic sub	15.5	3.0
	449611	A1970394	Hs.197075	ESTs	15.3 15.2	4.6 15.2
30	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	15.2	5.6
	405238				15.1	2.8
	429007 409638	D80642	11-04005	gb:HUM092E09B Human fetal brain (TFujiwa	15.0	3.5
	445888	AW450420 AF070564	Hs.21335 Hs.13415	ESTs	14.9	7.1
35	416737	AF154335	Hs.79691	Homo saplens clone 24571 mRNA sequence LIM domain protein	14.8 14.7	5.7 4.2
	429163	AA884768		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	14.6	3.0
	436870	AW204219	Hs.43879	E515	14.6	2.6
	443181 436281	Al039201 AW411194	Hs.54548	ESTs	14.6	3.5
40	449448	D60730	Hs.120051 Hs.57471	ESTS ESTS	14.5	8.5
	422564	AJ148006	Hs.222120	ESTs	14.4 14.4	4.8 14.4
	448243	AW369771	Hs.77496	small nuclear ribonucleoprotein polypept	14.3	2.4
	428748	AW593206	Hs.98785	EST _B	14.2	14.2
45	452578 452461	AB023177	Hs.29900	KIAA0960 protein	14.1	8.1
75	449670	N78223 F07693	Hs.108106 Hs.23869	transcription factor Homo saplens mRNA; cDNA DKFZp434K2172 (t	14.1	12.8
	436837	AI783629	Hs.26768	ESTs	14.1 14.0	14.1 2.3
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	13.9	13.9
50	419078	M93119	Hs.89584	Insulinoma-associated 1	13.9	29
50	410889 452355	X91662 · N54926	Hs.66744 Hs.29202	twist (Drosophila) homolog (acrocephalos	13.9	4.1
	421452	AJ925946	Hs.104530	G protein-coupled receptor 34 fetal hypothetical protein	13.9 13.9	13.9 13.9
	430290	Al734110	Hs.136355	ESTs	13.8	13.8
55	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	13.6	13.6
22	415875 416795	AA894876	Hs.5687	protein phosphatase 18 (formerly 2C), ma	13.5	13.5
	422025	AM97778 BE348774	Hs.168053 Hs.122554	ESTs, Highly similar to AF227948 1 HBV p ESTs	13.5 13.3	13.5
	400992		1101122007	2010	13.3	13.3 5.5
60	413174	AA723564	Hs.191343	EST ₅	13.2	2.5
60	425187	AW014486	Hs.22509	ESTs	13.1	8.2
	456965 419852	AW131888 AW503756	Hs.172792 Hs.286184	ESTs, Weakly similar to hypothetical pro	13.1	27
	409327	L41162	Hs.53563	hypothetical protein dJ551D2.5 collagen, type IX, atpha 3	13.0	24
	439519	AA837118	Hs.118366	ESTs	12.9 12.9	4.0 7.6
65	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	12.7	3.1
	445657	Al335191	Hs.260702	ESTs, Moderately similar to ALU7_HUMAN A	12.6	12.6
	423073 424278	BE252922 AK000723	Hs.123119 Hs.144517	MAD (mothers against decapentaplagic, Dr hypothetical protein FLJ20716	12.6	12.6
	451996	AW514021	Hs.245510	ESTs	12.6 12.6	128
70	400860				12.5	7.0 23.1
	439579	AF086400		gb:Homo saplens full length insert cDNA	12.4	12.4
	408312 419948	AF263813	Hs.44198	intracellular membrane-associated calciu	12.4	12.4
	427304	AB041035 AA761526	Hs.93847 Hs.163853	NADPH oxidase 4 ESTs	124	24
75	419498	AL036591	Hs.20887	hypothetical protein FLJ10392	12.3 12.2	12.3
	428137	AA421792	Hs.170999	ESTs	12.2	12.2 12.2
	432683	AW995441	Hs.10475	ESTs	12.2	2.0
	408622 453884	AA056060 AA355925	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	12.1	12.1
80	441440	AI807981	Hs.38232 Hs.30495	KIAA0188 gene product ESTs	12.0	5.2
	414217	Al309298	Hs.279898		12.0 12.0	3.6 62.7
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	11.9	2.9
	439444	Al277652	Hs.54578	ESTs	11.9	16.5

	433309 439170	AA807060 AA332365		ESTS	11.7 11.6	9.0 9.7
	417160	N76497	Hs.1787	proteolipid protein (Pelizaeus-Merzbache	11.5	7.2
_	424668	D83702	Hs.151573	cryptochrome 1 (photolyase-like)	11.5	5.8
5	410811	AW954134	Hs.20924	KIAA1628 protein	11.5	28.2
	437124 418858	AA554458 AW961605	Hs.204200 Hs.21145	ESTs Homo saplens cDNA: FLJ22489 fls, clone H	11.5 11.3	11.5 11.3
	423600	A1633559	Hs.29076	Homo saplens cDNA: FLJ21841 fis, clone H	11.3	2.8
	429393	AA383024	Hs.201603	ESTs, Highly similar to hypothetical pro	11.3	11.3
10	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	11.3	3.4
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	11.3 11.3	11.7 2.6
	431701 429399	AW935490 AA452244	Hs.14658 Hs.16727	ESTs ESTs	11.2	22
	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	11.2	27.8
15	442671	A1005668	Hs.134779	EST	11.1	11.1
	402524 415558	A A005443	LL 125710	ESTs	11.1 11,1	11.1 11.1
	422390	AA885143 AW450893	Hs.125719 Hs.121830	ESTs, Weakly similar to KIAA0924 protein	11.0	8.8
	418475	AI858732	Hs.30443	sentrin/SUMO-specific protease	11.0	6.1
20	458809	AW972512	Hs.20985	sin3-essociated polypeptide, 30kD	11.0	5.6
	410297	AA148710 U04840	Hs.159441 Hs.214	ESTS	11.0 11.0	3.3 11.0
	444017 437814	AI088192	Hs.135474	neuro-oncological ventral antigen 1 ESTs, Weakly similar to DDX9_HUMAN ATP-D	10.9	3.3
~-	427194	AA399018	Hs.250835	ESTs	10.8	8.0
25	432060	AW971364		gb:E8T383453 MAGE resequences, MAGL Homo	10.8	10.0
	453861 408829	AI026838 NM_006042	Hs.30120	ESTs	10.8 10.6	10.8 3.3
	416913	AW934714	FIS.40-304	heparan sullate (glucosamine) 3-O-sulfot gb:RC1-DT0001-031299-011-e11 DT0001 Homo	10.6	3.4
• •	418049	AA211467	Hs.1904B8	hypothetical protein FLJ10120	10.6	10.6
30	413063	AL035737	Ha.75184	chilinase 3-like 1 (cartilage glycoprote	10.6	27.2
	425264 434408	AA353953 Al031771	Hs.20369 Hs.132586	ESTs, Weakly similar to gonadotropin ind ESTs	10.5 10.5	2.0 10.5
	451697	AW449774	Hs.257208	ESTs	10.5	6.2
	436754	AI061288	Hs.133437	ESTs, Moderately similar to gonadotropin	10.3	10.3
35	410298	A1693821	Hs.182185	ESTs	10.3	2.9
	412766 450689	BE544475 Al369275	Hs.54347 Hs.243010	ESTs ESTs, Moderately similar to RTC0_HUMAN G	10.3 10.3	10.3 10.3
	408331	NM_007240		dual specificity phosphatase 12	10.3	4.5
40	442007	AA301118	Hs.142838	Homo sapiens cDNA: FLJ23444 ffs, clone H	10.3	10.3
40	410386	W26187	Hs.3327	Home saplens cDNA: FLJ22219 fis, clone H	10.2	2.1
	440684 420892	Al253123 AW975076	Hs.127356 Hs.172589	ESTs, Highly similar to NEST_HUMAN NESTI nuclear phosphoprotein similar to S, cer	10.1 10.0	10.1 10.0
	419594	AA013051	Hs.91417	topolsomerase (DNA) il binding protein	9.9	15.8
4.5	419972	AL041465	Hs.294038	ESTs, Moderately similar to ALU2_HUMAN A	9.7	23.2
45	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	9.6	6.5
	434851 436306	AA806164 AA805939	Hs.116502 Hs.117927	ESTs ESTs	9.6 9.5	6.5 4.7
	453331	A1240665	Hs.8895	EST8	9.2	5.8
	414429	R51494	Hs.71818	ESTs	9.0	6.2
50	424998	U58515	Hs.154138	chitinase 3-like 2	8.9	18.1
	446936 410276	H10207 Al554545	Hs.47314 Hs.68301	ESTS ESTS	8.9 8.8	3.6 3.8
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	8.8	3.8
	448321	NM_00588	3 Hs.20912	adenomatous polyposis coli like	8.8	20
55	414783	AW069569		zinc finger protein 6 (CMPX1)	8.7	3.0
	441079 437517	AW150697 A1927675	' Hs.107418 Hs.99858	ESTs ribosomal protein L7a	8.7 8.6	2.2 4.5
	409062	AL157488	Hs.50150	Homo sapiens mRNA; cDNA DKFZp564B182 (fr	8.6	12.2
C O	429630	AL133101	Hs.99508	Homo sapiens mRNA; cDNA DKFZp43400921 (f	8.6	10.4
60	409260	AW242407		ESTs	8.5 8.4	11.6 4.6
	442343 416439	AA992480 AA180363			8.4	7.2
	428054	Al948688	Hs.266619		8.2	9.2
65	421633	AF121860			8.2	26
03	433285	AW97594			8.1	3.3
	433226 424800	AW50373: AL035588		KIAA1488 protein MyoD family inhibitor	8.0 8.0	13.4 2.5
	425681	AB018297			7.9	4.8
70	445034	AW29337			7.9	3.7
70	435020	AW50507 AL038704			7.6	6.4
	446985 446619	AU07664		 ESTs, Wealthy similar to ALU1_HUMAN ALU S secreted phosphoprotein 1 (osteopontin, 	7.5 7.5	7.8 3.9
	418522	AA605038		Homo sapiens cDNA: FLJ21950 fis, clone H	7.5	2.2
75	439864	AI720078		7 ESTs	7.4	6.9
75	419723 447896	AL120193 Al436124			7.4 7.3	3.5 22.1
	404210	M430124	FIS. 234UQ	LOIS WOOM BRIDE W OFFE CORRORS &	7.3 7.3	40.8
	436671	AW13715			7.2	11.8
80.	439231	AW58193			7.2	2.5
90.	418030 459290	8E20757	3 Hs.B3321 146 Hs.34853		7.1 7.0	6.4 6.7
	423869	BE40930			7.0 7.0	4.9
	414825	X06370	Hs.77432		6.9	6.4

	420018	U56387	Hs.94376	proprotein convertase subtilisin/kexin t	6.9	8.6
	428600		Hs.15036	ESTs, Highly similar to AF161358 1 HSPC0	6.9	7.7
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	6.9	3.1
_	402504				6.8	7.0
5	417022	NM_014737		Ras association (RalGDS/AF-6) domain fam	6.8	25
	405239	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	6.8	29
	433577	AW007080	Hs.8817	ESTs	6.6	26
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	6.6	13.9
10	413886	AW958264	Hs.103832	ESTs, Wealthy similar to TRHY_HUMAN TRICH	6.6	2.2
10	451460	AI797550	Hs.209652	ESTs	6.5	13.7
	442145 437273	AI022650	Hs.8117	erbb2-interacting protein ERBIN	6.5	15.6
	418365	AL137451 AW014345	Hs.120873 Hs.161690	ESTs, Highly similar to hypothetical pro	6.5	24
	421684	BE281591	Hs.106768	ESTs hypothetical protein FLJ10511	6.4 6.4	12.8 4.3
15	449458	AI805078	Hs.208261	ESTs	6.4	23
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo saplen	6.3	13.2
	426423	NM_012446	Hs.169833	single-stranded-DNA-binding protein	6.3	10.9
	417709	D87434	Hs.82426	KIAA0247 gene product	6.3	23.3
	448499	BE613280	Hs.250655	prothymosin, alpha (gene sequence 28)	6.2	29 .
20	444880	AW118683	Hs.154150	ESTs	6.2	19.4
	432715	AA247152	Hs.200483	ESTs, Wealty similar to KIAA1074 protein	6.2	12.7
	444864	AW965446	Hs.46637	ESTs, Weakly similar to cONA EST yk289g5	6.2	4.1
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	6.2	3.4
25	431962	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	6.1	2.6
25	424232	AB015982	Hs.143460	protein kinase C, nu	6.1	14.6
	436443	AW138211	Hs.128746	ESTA	6.1	2.8
	433647	AA603367	Hs.222294	ESTs	6.1	15.0
	449961	AW265634 AW080932	Hs.133100	ESTs	6.1	3.4
30	448704 408393		Hs.249247	heterogeneous nuclear protein similar to	6.1	6,1
20	450693	AW015318 AW450461	Hs.23185 Hs.203965	ESTs	6.1	21.6
	407846	AA426202	Hs.40403	ESTs Cbp/p300-interacting transactivator, wit	6.1 6.0	2.2 2.4
	445817	NM_003642		histone acetyltransferase 1	6.0	10.9
	440650	R44692	Hs.6640	ESTs	6.0	2.1
35	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	6.0	2.4
	411083	N41340	Hs.68318	hypothetical protein FLJ20344	6.0	3.6
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	6.0	6.0
	402855			•	6.0	26
40	445594	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	6.0	11.6
40	418791	AA935633	Hs.194628	ESTs	5.9	6.7
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	5.9	2.3
	435677	AA694142	Hs.293726	ESTs	5.9	11.8
	430334	AI824719	Hs.47557	ESTs	5.9	7.5
45	452834 427315	AI838627	Hs.105685	ESTs	5.9	26
43	428250	AA179949 AWB09208	Hs.175563	Homo sepiens mRNA; cDNA DKFZp564N0763 (f	5.8	3.1
	418506	AA084248	Hs.183297 Hs.85339	DKFZP566F2124 protein G protein-coupled receptor 39	5.8	2.0
	417115	AW962792	Hs.1066	small nuclear ribonucleoprotein polypept	5.8 5.8	2.5 16.0
	436758	AW977167	Hs.155272	ESTs	5.B	3.8
50	446332	AK001635	Hs.14838	hypothetical protein FLI10773	5.7	5.1
	423943	AF163570	Hs.135756	polymerase (DNA-directed) kappa	5.7	11.1
	428180	Al129767	Hs.182874		5.6	7.1
	424343	AW956360	Hs.4748	ESTs, Highly similar to JN0902 pitultary	5.6	2.2
EE	417318	AW953937	Hs.12891	ESTs	5.6	25.0
55	423582	BE000831	Hs.23837	Homo seplens cDNA FLJ11812 fis, ctone HE	5.6	4.1
	427472	AA522539	Hs,131250		5.4	3.5
	434701 430147	AA460479	Hs.4096	KIAA0742 protein	5.4	21.2
	411019	R60704 AW993097	Hs.234434 Hs.48617		5.3	2.7
60	424939	AK000059	Hs.153881	Homo septens cDNA FLJ12540 fis, clone NT Homo septens NY-REN-62 antigen mRNA, par	5.3	4.1
••	424028	AF055084	Hs.153692		5.3 5.3	2.4 2.7
	444534	AW271626		ESTs	5.3	21
	426171	Al128606	Hs.301454		5.2	3.8
	431843	AA516420	Hs.183526		5.2	6.2
65	438204	Al589645	Hs.128690		5.2	5.8
	424635	AA420687	Hs.115455	Homo saplens cDNA FLJ14259 fis, clone PL	5.2	8.4
	436223	AK001884	Hs.23799	ESTs	5.2	2.4
	450649	NM_00142			5.2	15.3
70	441689	AI123705	Hs.106932		5.2	2.2
70	443392	AI055821	Hs.293420		5.1	3.3
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	5.1	16.7
	452167	N75238	Hs.13075	Homo sepiens cDNA: FLI23013 fis, clone L	5.1	18.7
	434001 458435	AW950905 Al418718		serine (or cysteine) proteinase inhibito	5.0	2.4
75	433586	T85301	Hs.144121		5.0	3.9
	452040	AW973242	Hs.293690	gb:yd78d06.s1 Soares fetal liver spleen ESTs	5.0	28
	404029	,			5.0 5.0	4.5 4.3
	421141	AW117281	Hs.125914	ESTs	5.0 5.0	21
	402605			,	4.9	4.2
80	435839	AF249744	Hs.25951	Rho guardne nucleotide exchange factor (4.9	2.5
	416404	AA180138			4.9	2.4
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-lik	4.9	7.2
	448425	A1500359	Hs.233401	EST8	4.9	4.9

PCT/US02/29560

	445773		Hs.13299	Homo saplens mRNA; cDNA DKFZp761M0111 (f	4.9	2.9
	448451 444838	AW015994 AV651680	Lla 2005en	gb:UI-H-BIOp-ebh-g-09-0-UI.s1 NCI_CGAP_S	4.9	22
	452438		Hs.208558 Hs.29595	ESTs JM4 protein	4.8 4.8	6.7
5	443898		Hs.9950	Sec61 gamma	4.8 4.8	2.7 7.2
	452776		Hs.13522	ESTs	4.8	3.4
	426108		Hs.166458	programmed cell death 5	4.8	16.7
	416774		Hs.28274	Homo sapiens cDNA: FLJ22049 (is, clone H	4.8	3.2
10	427704		Hs.292882	ESTS	4.8	23.8
10	433588 410108	Al056872 AA081659	Hs.133386 Hs.191098	ESTs	4.8	12.8
	433556	W56321	Hs.111460	KIAA1479 protein Homo saptens cDNA: FLJ21715 fis, clone C	4.7 4.7	2.1 11.2
	418962	AA714835	Hs.271863	ESTs	4.7	2.2
4.5	404049				4.7	3.0
15	435222	Al208737	Hs.122810	Homo sapiens cDNA FLJ11489 fis, clone HE	4.7	3.3
	425234	AW152225	Hs.165909	ESTs	4.7	3.1
	426490 426514			aryl hydrocarbon receptor	4.7	9.1
	428722	BE616833 U76456	Hs.301122 Hs.190787	bane marphogenetic protein 7 (asteogenic tissue inhibitor of metalloproteinase 4	4.7 4.6	2.7
20	451989	AF169797	Hs.27413	adaptor protein containing pH domain, PT	4.6	6.7 13.4
	412490	AW803564	Hs.288850	Homo sepiens cDNA: FLJ22528 fts, clone H	4.6	18.4
	422488	A1679968	Hs.152060	ESTs	4.6	7.7
	428862	NM_000346	Hs.2316	SRY (sex-determining region Y)-box 9 (ca	4.6	4.6
25	413724	AA131466	Hs.23767	Homo sapiens cONA FLJ12666 fis, clone NT	4.5	11.9
23	442495 403549	AJ184717		gb:qd64b01.x1 Soares_testis_NHT Homo sap	4.5	4.5
	456209	W60633	Hs.297792	ESTs	4.5 4.5	11.6 5.1
	421181	NM_005574		LIM domain only 2 (rhombotin-like 1)	4.5	10.6
••	439566	AF086387		gb:Homo saplens full length insert cONA	4.4	2.6
30	446329	NM_013272		solute carrier family 21 (organic anion	4.4	17.2
	446488	AB037782	Hs.15119	KIAA1361 protein	4.4	8.4
	426110 427413	NM_002913 BE547647		replication factor C (activator 1) 1 (14	4.4	2.5
	424340	AA339038	Hs.177781 Hs.7033	superoxide dismutase 2, mitochondrial ESTs	4.4 4.4	14.3 3.9
35	421552	AF026692	Hs.105700	secreted trizzled-retated protein 4	4.3	31.1
	422033	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	4.3	6.1
	434476	AW858520	Hs.271825	ESTs	4.3	4,5
	420582	BE047878	Hs.99093	Homo saplens chromosome 19, cosmid R2837	4.3	3.6
40	419904 407939	AA974411 W05608	Hs.18672	ESTS	4.3	17.1
70	425836	AW955696	Hs.94842	gb:za85e07.r1 Soares_fetal_lung_NbHL19W ESTs	4.3 4.3	9.0
	426304	AA374532	Hs.297985	ESTS	4.3 4.3	3,2 6.6
•	439653	AW021103	Hs.6631	hypothetical protein FLJ20373	4.3	2.3
45	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	4.3	2.5
45	426064	BE387014	Hs.166146	Homer, neuronal immediate early gene, 3	4.2	4.1
	409509	AL036923	Hs.127006	ESTs	4.2	16.4
	424391 425248	BE550112 AW957442	Hs.112712 Hs.252766	ESTs ESTs	4.2	3.8
	418259	AA215404	Hs.137289	ESTS	4.2 4.2	11.1 19.3
50	445525	BE149866	Hs.14831	ESTs	4.2	3.1
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity la, re	4.2	34.8
	430935	AW072916	Hs.115654		4.2	3.0
	442233	AW967149	Hs.28439	ESTs, Weakly similar to ORF2 (M.musculus	4.2	2.4
55	416959 437097	D28459 N45312	Hs.80612 Hs.46506	ubiquitin-conjugating enzyme E2A (RAD6 h ESTs	4.1	15.3
	428189	AA424030	Hs.46627	ESTs	4.1 4.1	15.6 3.6
	434963	AW974957	Hs.288719		4.1	12.2
	425500	AB011541	Hs.158200		4.1	2.8
60	435177	A1018174	Hs.42936	ESTs	4.1	2.1
60	418357	Z44718	Hs.301010		4.1	4.1
	419086 436557	W15573	Hs.89591 Hs.5027	Kallmann syndrome 1 sequence ESTs	4.1	4.1
	425588	F07396	Hs.48751	ESTs	4.0 4.0	21 22
	423905	AW579960	Hs.135150		4.0	3.6
65	437095	D14661	Hs.119	Wilms' tumour 1-associating protein	4.0	10.0
	425332	AA633306	Hs.127279		4.0	10.9
	431558	AF016028	Hs.260039		4.0	3.8
	427209 435468	H06509	Hs.92423	KIAA1566 protein	4.0	3.1
70	416773	AW362803 AK000340	Hs.166271 Hs.79828	ESTs hypothetical protein FLJ20333	4.0	. 22
	440483	AI200836	Hs.150386		4.0 4.D	2.6 2.5
	444821	AA053584	Hs.12040	STE20-like kinase	4.0	10.4
	433873	AW156913			4.0	2.3
75	420028	AB014680	Hs.8786	carbohydrate (chondroitin 6/keratan) sul	3.9	2.8
75	445706	AW807631	Hs.190488		3.9	3.8
	424530 446851	AI632083 AW007332	Hs.28511	ESTs Homo sapiens cDNA: FLJ22063 fis, clone H	. 3.9	2.2
	424720	M89907	Hs.16261 Hs.152292		3.9	16.0
	409456	U34962	Hs.54473	cardiac-specific homeo box	3.9 3.9	4.5 8.0
80	420439	AW270041	Hs.193053		3.9	7.9
	447340	AW981327	Hs.280833	ESTS	3.9	2.1
	430887	N66801	Hs.260287		3.9	2.5
	409381	NM_00598	2 Hs.54416	sine oculis homeobox (Drosophila) homolo	3.9	4.6

	426509	M31166	Hs.2050	pentaxin-related gene, rapidly induced b	3.9	4.0
	410079 426818	U94362	Hs.58589	glycogenin 2	3.9	18.3
	435232	AA554827 NM_001262	Hs.124841 He 4854	ESTs, Weakly similar to ALUS_HUMAN ALU S	3.9	3.0
5	427228	AA115770	Hs.174051	cyclin-dependent kinese Inhibitor 2C (p1 small nuclear ribonucleoprotein 70kD pol	3.8	4.0
	443801	AW206942	Hs.253594	ESTs	3.8 3.8	7.9 3.4
	450746	D82673	Hs.169921	general transcription factor II, i, pseu	3.8	2.2
	443837	A1984625	Hs.9884	spindle pole body protein	3.8	6.5
10	435760 426757	AF231922 AW205640	Hs.213004	chromosome 21 open reading frame 62	3.8	22
10	443101	AV7205640 Al268938	Hs.158206 Hs.129872	ESTs	3.7	3.1
	440118	AB040893	Hs.6968	sperm surface protein KIAA1460 protein	3.7	2.4
	410812	AW502698	Hs.118152	ESTs	3.7 3.7	3.5 22.5
1.5	435869	AF255910	Hs.54650	vascular endothelial junction-associated	3.7	4.2
15	433208	AW002834	Hs.24095	ESTs	3.7	16.0
	432357 413916	AA452506	Hs.274412	similar to yeast Upf3, variant A	3.7	26
	429768	N49813 AA612710	Hs.75615 Hs.146140	epolipoprotein C-II ESTs	3.7	5.4
	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	3.7 3.7	3.2
20	438459	T49300	Hs.35304	Homo saplens cDNA FLJ13655 fis, clone PL	3.7	6.4 10.7
	420361	N92054	Hs.206910	ESTs	3.7	18.7
	408819	AW163483	Hs.48320	DKFZP56681348 protein	3.7	8.8
	411960 435923	R77776 BE301930	Hs.18103 Hs.5010	ESTS	3.7	23
25	440145	AW021433	Hs.250863	Homo sapiens clone 24672 mRNA sequence ESTs	3.7	2.2
	453740	AL120295		gb:DKFZp781M067_s1 761 (synonym; harry2)	3.7 3.6	3.8 3.0
	440975	AW499914	Hs.7579	hypothetical protein FLJ 10402	3.6	20
	443135	Al376331	Hs.156103	ESTs	3.6	12,4
30	419687 451029	A1638859	Hs.227699	ESTs, Weakly similar to Yhr217cp (S.care	3.6	2.7
50	414512	AA852097 AL044338	Hs.25829 Hs.6831	ras-related protein	3.6	29
	410853	H04588	Hs.30469	golgi resident protein GCP60 ESTs	3.6	10.5
	419900	Al469960	Hs.170698	ESTs	3.6 3.6	23.9 3.6
25	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	3.6	7.5
35	428290	Al932995	Hs.183475	Homo saplens clone 25061 mRNA sequence	3.6	9.6
	444381 442104	BE387335 L20971	Hs.283713 Hs.188	ESTs, Weakly similar to CA54_HUMAN COLLA	3.6	4.9
	441269	AW015208	Hs.178784	phosphodiesterase 4B, cAMP-specific (dun ESTs	3.6	2.1
40	447961	W32791	Hs.170405	ESTS	3.6 3.5	2.8
40	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	3.5	4.6 2.1
	437580	AA761075	Hs.293567	ESTs	3.5	3.5
	447710 436446	A1420523	Hs.161282	ESTs	· 3.5	3.5
	448412	AW016809 Al219083	Hs.119021 Hs.42532	ESTS	3.5	2.2
45	409712	AA167385	Hs.13583	ESTs, Moderately similar to ALU8_HUMAN A ESTs	3.5	4.1
	404048			40.0	3.5 3.5	3.8 3.2
	440516	S42303	Hs.161	cadherin 2, type 1, N-cadherin (neuronal	3.5	5.1
	409342 456508	AU077058	Hs.54089	BRCA1 associated RING domain 1	3.5	10.6
50	426101	AA502764 AL049987	Hs.123469 Hs.166361	ESTs, Weakly similar to AF208855 1 BM-01	3.5	3.8
	436252	Al539519	Hs.120969	Homo sapiens mRNA; cDNA DKFZp564F112 (fr Homo sapiens cDNA FLJ11562 fs, ctone HE	3.5	32.2
	433854	AA610649		gb:np95c03.s1 NCI_CGAP_Thy1 Homo sepiens	3.5 3.5	4.6 3.5
	408495	W68796	Hs.237731	ESTs	3.5	6.1
55	418801	AA228366	Hs.115122	ESTs	3.5	5.1
55	422493 428141	AW474183 D50402	Hs.233816	ESTS	3.5	15.2
	414591	AI888490	Hs.182611 Hs.65902	solute carrier family 11 (proton-coupled ESTs	3.5	24
	439627	BE621702	Hs.29076	Homo sapiens cDNA: FLJ21841 fis, clone H	3.5 3.5	8.3 30.2
60	444969	Al203334	Hs.160628	ESTs	3.5	3.1
UU	435370	AI964074	Hs.225838	ESTa	3.5	3.0
	443228 414612	W24781 BE274552	Hs.293798	ESTS	3.4	4.6
	437410	AW023340	Hs.76578 Hs.14880	protein inhibitor of activated STAT3 ESTs	3.4	5.0
	444172	BE147740	Hs.104558	ESTs	3.4 3.4	2.7 12.9
65	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.4	2.8
	437860	AA333083	Hs.279898	Homo saplens cDNA: FLJ 23165 fis, clone L	3.4	4.0
	428776 409493	AW016838	Hs.155847	ESTs, Highly similar to R29144 1 [H.sapt	3.4	2.5
	432559	AA388192 AW452948	Hs.193482 Hs.257631	ESTs ESTs	3.4	3.4
70	451455	A1937227	Hs.8821	liver-expressed entimicrobial peolide	3.4	6.3
	444153	AK001610	Hs.10414	hypothetical protein FU 10748	3.4 3.4	6.1
	422872	BE326786	Hs.187646	ESTs	3.4	2.6 2.2
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.4	26
75	416131 408576	L03532 NM_003542	Hs.79024	heterogeneous nuclear ribonucleoprotein	3.4	9.5
. •	431770	BE221880	Hs.268555	H4 histone family, member G 5'-3' exoribonuclease 2	3.4	3.4
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.4	21,2
	422573	AW297985	Hs.28777	H2A histone family, member L	3.4 3.4	2.1 3.7
80	436865	AW880358	Hs.190488	hypothetical protein FLJ10120	3.4	7.6
50	442091 418699	AW770493	Hs.195904	guarine nucleotide binding protein (G pr	3.4	2.9
	434577	BE539639 R37316	Hs.173030 Hs.179769	ESTs, Weekly similar to ALUS HUMAN ALU S	3.4	5.5
	430314	AA369601	Hs.239138	Homo sapiens cDNA: FLJ22487 fis, clone H pre-B-cell colony-enhancing factor	3.4	3.9
				to a man annual constitution of twenty	3.4	16.8

	447279		Hs.18016	Homo saplens mRNA; cONA DKFZp586H0324 (I	3.3	3.0
	410020	T86315	Hs.728	ribonuclease, RNase A tamily, 2 (liver,	3.3	5.8
	447272		Hs.17969	KIAA0663 gene product	3.3	13.4
_	407656		Hs.37443	Homo saplens mRNA; cDNA DKFZp434B2119 (f	3.3	2.3
5	435354	AA678267	Hs.117115	ESTs	3.3	5.5
	443884	N20617	Hs.226627	leptin receptor	3.3	8.6
	444984	H15474	Hs.12214	Homo sepiens clone 23716 mRNA sequence	3.3	2.0
	431053	S40369	Hs.249141	Glutamate receptor subunit	3.3	24
10	424682	AW604804	Hs.151717	KIAA0437 protein	3.3	13.7
10	457972	AJ419060	Hs.47448	ESTs	3.3	4.2
	424762	AL119442	Hs.183684	eukaryotic translation initiation factor	3.3	3.2
	438666	AW014493	Hs.126727	ESTS	3.3	10.8
	447796	AW953822	Hs.223025	RAB31, member RAS oncogene family	3.3	4.2
15	426751	W92744	Hs.22664	ESTE	3.3	26
13	438251	BE515065	Hs.5092	nucleolar protein (KKE/D repeat)	3.3	3.9
	452688	AA721140	Hs.49930	ESTs, Weakly similar to 834087 hypotheti	3.3	4.9
	416359 424090	AL042210 X99699	Hs.16493	hypothetical protein DKFZp762N2316	3.3	4.2
	434987	AW976114	Hs.139262	XIAP associated factor-1	3.3	2.9
20	428642	NM_014899	Hs.293273	ESTS	3.3	2.2
	420372	AW960049	Hs.293660	KIAA0878 protein	3.3	5.7
	422224	NM_013982		ESTs, Weakly similar to A49618 probable neurogulin 2	3.3	5.5
	432482	L19267	Hs.275924	dystrophia myotonica-containing WD repea	3.2	3.0
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrota	3.2	27
25	428418	Al368826	Hs.30654	ESTs	3.2	2.0
	416728	AB024597	Hs.79658	caseln kinase 1, epsilon	3.2	24
	416224	NM_002902		reticulocalbin 2, EF-hand calcium bindin	3.2 3.2	28
	429803	W81489	Hs.223025	RASS1, member RAS oncogene family	3.2	2.2 4.3
	431387	AJ878854	Hs.252229	v-mai musculoaponeurotic fibrosarcoma (a	3.2	2.8
30	404171			The state of the s	3.2	35.8
	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	3.2	2.6
	426421	AW367884	Hs.169832	zinc finger protein 42 (myeloid-specific	3.2	3.8
	445070	NM_000577	Hs.258	adenosine A3 receptor	3.2	7.6
25	407047	X65965		gb:H.saplens SOD-2 gene for manganese su	3.2	82.0
35	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	3.2	2.2
	430890	X54232	Hs.2699	glypican 1	3.2	4.3
	439807	AA376417	Hs.173501	Homo sapiens mRNA for FLJ00008 protein,	3.2	23
	430412	AW341754	Hs.189305	ESTs	3.2	20
40	442807	AL049274	Hs.8736	Homo saplens mRNA; cDNA DKFZp564H203 (fr	3.2	2.7
40	420253	AI656055	Hs.96200	neighbor of A-kinase anchoring protein 9	3.2	29
	435042	AF284422	Hs.119178	cation-chloride cotransporter-interactin	3.2	4.6
	423422	AC005175	Hs.128425	NY-REN-24 antigen	3.2	4.0
	413020	R98738		gb:yr31h09.r1 Soares fetal liver spleen	3.2	4.1
45	452877	Al250789	Hs.32478	ESTs	3.2	4.0
73	418113 421097	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	3.1	9.0
	450219	Al280112	Hs.125232	Homo saplans cDNA FLJ 13266 fis, clone OV	3.1	20
	434258	A1826999 A1378817	Hs.224624	ESTs	3.1	23,7
	421407	T82331	Hs.191847 Hs.127453	ESTs ESTs	3.1	3.4
50	451198	AW964541	Hs.11500	Homo seplens cDNA: FLJ21127 fis, clone C	3.1	3.9
	445664	AW968638	Hs.237691	EST8	3.1	3.9
	411089	AA456454	Hs.118637	Homo sepiens cONA FLJ13365 fis, clone PL	3.1	7.9
	458050	AA834708	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	gb:od99d04.s1 NCI_CGAP_Ov2 Homo saplens	3.1 3.1	6.0
	454140	AB040888	Hs.41793	hypothetical protein FLJ 10474	3.1	4.4 2.7
55	417270	AA429815	Hs.98593	Homo saplans cDNA: FLJ23233 fis, clone C	3.1	24
	427951	AI826125	Hs.43546	ESTs	31	23
	443693	A1344782	Hs.9683	protein-kinase, interferon-inducible dou	3.1	7.2
	413387	NM_006517	Hs.75317	solute cerrier family 16 (monocarboxylic	3.1	26
CO	429402	AF116571	Hs.201671	SRY (sex determining region Y)-box 13	3.1	6.5
60	447752	M73700	Hs.347	lactotransferrin	3.1	19.4
	408949	AF189011	Hs.49163	putative ribonuclease III	3.1	3.7
	418039	R06859	Hs.193172	ESTs	3.1	3.B
	447343	AA256641	Hs.236894	ESTs, Highly similar to LRP1_HUMAN LOW-D	3.1	2.2
65	424441	X14850	Hs.147097	H2A histone family, member X	3.1	3.2
05	435163	AA668884	Hs.19155	EST8	3.1	21
	428712	AW085131	Hs.190452	KIAA0365 gene product	3.1	2.7
	434542 428147	AA769310	Hs.61260	hypothetical protein FLJ13164	3.1	14.3
		AW629965	Hs.234983	ESTs	3.1	2.7
70	415825 422170	Y18024 Al791849	Hs.78877	Inositol 1,4,5-trisphosphale 3-kinese 8	3.1	25
	448801	N57423	Hs.112432 Hs.179898	anti-Mullerian hormone HSPC055 protein	3.1	8.1
	413542	8E295928	Hs.75424		3.0	2.0
	431562	AI884334	Hs.11637	Inhibitor of DNA binding 1, dominant neg ESTs	3.0	18.3
	410274	AA381807	Hs.61762	hypoxla-inducible protein 2	3.0	3.9
75	458962	NM_005859			3.0	3.0
	436277	R88520	Hs.120917	purine-rich eternent binding protein A ESTs	3.0	3.0
	453288	AW583292	Hs.274412	almilar to yeast Up/3, variant A	3.0	2.7
	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	3.0	3.0
	442554	AW487376	Hs.129640	ESTs	3.0 3.0	4.1
80	441466	AW873081	Hs.54828	ESTs	3.0	4.7
	420297	AI628272	Hs.88323	ESTs	3.0	3.0 8.1
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	3.0	18.7
	453405	AI567972	Hs.49918	ESTs	3.0	9.6
					9.0	5.0

	424534	MA 000007	N- 0000				
	434521 447948	NM_002267 AI620923		karyopherin alpha 3 (Importin alpha 4)		1.0	9.3
	445756	AA290690	Hs.46679 Hs.288493	ESTs		1.0	10.1
	413243	AA769266	Hs.193657	ESTs ESTs		1.0	3.5
5	422845	AA317841	Hs.301838	ESTs, Weakly similar to ALU1_HUMAN ALU S		1.0	5.9
	419409	AW297831	Hs.143792	ESTs		3.0 3.0	2.2 2.1
	446441	AK001782	Hs.15093	hypothetical protein		10	21
	427150	BE616183	Hs.173737	ras-related C3 botulinum toxin substrate		3.0	4.1
10	421043	BE379455	Hs.89072	ESTs		1.0	3.0
10	427239	BE270447	Hs.174070	ubiquitin carrier protein		3.0	4.1
	433312	Al241331	Hs.131765	ESTs	;	3.0	11.0
	415102 414702	M31899 1,22005	Hs.77929	excision repair cross-complementing rode		1.0	6.0
	428673	AW601325	Hs.76932 Hs.274472	cell division cycle 34		3.0	3.3
15	422676	D28481	Hs.1570	high-mobility group (nonhistone chromoso histamine receptor H1		3.0	15.8
	451693	BE220445	Hs.279635	ESTs		3.0	21
	412420	AL035668	Hs.73853	bone morphogenetic protein 2		3.0 3.0	2.3 10.5
	424005	AB033041	Hs.137507	KIAA1215 protein		3.0	3.9
20	440769	8E561793		gb:601346842F1 NIH_MGC_8 Homo septens cD		3.0	5.1
20	428832	AA578229		gbtnl22b12a1 NCI_CGAP_HSC1 Homo sepiens		3.0	2.3
	430293	AI416988	Hs.238272	inositol 1,4,5-triphosphate receptor, ty		3.0	6.3
	450883 407879	NM_001348		death-essociated protein kinese 3		3.0	5.6
	426167	AA045464 AF039023	Hs.6557 Hs.167496	ESTS		2.9	7.0
25	435281	AB020699	Hs.4864	Homo sapiens cDNA FLJ 11120 fis, clone PL KIAA0892 protein		29	26
	432339	AW411259	Hs.25945	ESTs		29 29	3.9
	440524	R71264	Hs.16798	ESTs		29 29	2.9 9.7
	408083	BE383668	Hs.42484	hypothetical protein FLJ10618		2.9	4.4
20	427729	AB033100	Hs.300646	Homo saplens cDNA FLJ11744 fis, clone HE		29	3.1
30	422072	AB018255	Hs.111138	KIAA0712 gene product		2.9	29
	435904	AF261655	Hs.8910	1,2-alpha-mannosidase IC	:	29	3.6
	440100 448356	BE382685	Hs.158549	ESTs		29	3.6
	428005	AL120837 AW302245	Hs.20993 Hs.181390	high-glucose-regulated protein 8		29	13.9
35	403019	AA834626	Hs.66718	caseln kinase 1, gamma 2 RAD54 (S.cerevisiae)-like		29	3.7
_	419175	AW270037	Hs.179507	KIAA0779 protein		2.9 2.9	5.8
	433592	NM_004642		deleted in oral cancer (mouse, homolog)		29	23 23
	413922	AJ535895	Hs.221024	ESTs		2.9	28
40	428593	AW207440	Hs.185973	degenerative spermatocyte (hornolog Droso		29	3.3
40	441789	D52059	Hs.7972	KIAA0871 protein		2.9	2.1
	459107 448560	AA811881	Hs.28505	ubiquitin-conjugating enzyme E2H (homolo		2.9	2.8
	425304	BE613183 AA463844	Hs.23213	ESTs		2.9	3.0
	434846	AW295389	Hs.31339 Hs.119768	fibroblast growth factor 11 ESTs		2.8	3.3
45	408146	R45621	Hs.81057	ESTs, Moderately similar to CL3BC [R.nor		29	5.1
	446644	NM_003272	Hs.15791	transmembrane 7 superfamily member 1 (up		2.9 2.9	5.1
	446808	AA703226	Hs.16193	Homo sapiens mRNA; cDNA DXFZp586B211 (fr		29	2.8 8.5
	433017	Y15067	Hs.279914	zinc finger protein 232		29	2.2
50	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)		2.9	4.5
50	444706	AK000398	Hs.11747	hypothetical protein FLJ20391		29	3.6
	407925 431730	BE002320 AF208856	Hs.287864	Homo sapiens cDNA FLJ14030 fis, clone HE		29	2.1
	447118	AB014599	Hs.268122 Hs.17411	hypothetical protein KIAA0699 protein		2.9	2.5
	453498	AA442103	Hs.33084	solute carrier family 2 (facilitated glu		2.8	2.1
55	425227	H84455	Hs.40639	ESTS		2.8 2.8	7.4
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo		2.8	2.3 76.2
	421465	AK001020	Hs.104627	Homo saplens cONA FLJ 10158 fis, clone HE		28	6.1
	409095	AW337272	Hs.293656	EST8		2.8	34,0
60	424066 432945	Z99348 AL043683	Hs.112461	ESTs		2.8	2.1
•	414079	H19184	Hs.271357 Hs.205230	ESTs, Weakly similar to unnamed protein		2.8	11.9
	414359	M52194	Hs.75929	ESTs cadherin 11, type 2, OB-cadherin (osteob		2.8	21
	438890	AA827756	Hs.135049	ESTs		2.8 2.8	3.9
	430354	AA954810	Hs.239784	human homolog of Drosophila Scribble		2.8	4.9 5.2
65	458367	AA088470	Hs.83135	p53-responsive gene 6		2.8	4.4
	412014	A1620650	Hs.43761	ESTs		2.8	4.8
	428727	AF078847	Hs.191356	general transcription factor IIH, polype		2.8	6.7
	447942 426432	F12628	Hs.155470	zinc finger protein 38 (KOX 25)		28	2.2
70	439189	AF001601 AI951185	Hs.169857	paraoxonase 2		2.8	3.5
	446756	AW028485	Hs.144630 Hs.26136	nuclear receptor subfamily 2, group F, m		2.8	2.5
	432148	AW504912	Hs.81907	ESTs Moderately similar to ALU4_HUMAN A		2.8	4.1
	405649			COTO, INDUCATELY SAILER EL ALDO-INGRAFA		28	26
75	414473	BE302693		gb:ba74c02y1 NIH_MGC_20 Homo saplens c0		2.8 2.8	3.8 2.4
75	443839	AW139834	Hs.143321	ESTs		28	21
	448804	AW512213	Hs.42500	ADP-ribosylation factor-like 5		2.8	27
	426825	AL133415	Hs.2064	vimentin		2.8	25.0
	417528 453657	H47315 W23237	Hs.27519	ESTs		2.8	11.6
80	432714	Y12059	Hs.296162	ESTs		2.8	3.2
	441072	AW275480	Hs.278675 Hs.39504	bromodomain-containing 4 ESTs		28	6.7
	441297	AW403084	Hs.7768	ubiquifin-conjugating enzyme E2E 1 (homo		27	27
	443849	BE566068	Hs.9893	ASB-3 protein		2.7 2.7	2.2 3.0
				•			w

	408243	Y00787	Hs.624	interleukin 8	2.7	3.8
	446243 432238	BE296396 AL133057	Hs.14512 Hs.274135	Homo sepiens cDNA FLJ11761 fis, clone HE	2.7	3.3
	433944	AL117518	Hs.3686	Homo saplens mRNA; cDNA DKFZp434K1815 (f KIAA0978 protein	2.7 2.7	3.0 3.1
5	411400	AA311919	Hs.69851	GAR1 protein	27	16.0
	436840	AW450376	Hs.130803	ESTs, Highly similar to T00367 hypotheti	2.7	4.1
	428281	AA194554	Hs.183434	ATPase, H+ transporting, tysosomal (vacu	2.7	3.2
	426340	Z97989	Hs.169370	FYN oncogene related to SRC, FGR, YES	2.7	20
10	408320 422363	AJ125867 T55979	Hs.20734	ESTs	2.7	4.7
10	436440	AI471862	Hs.115474 Hs.196008	replication factor C (activator 1) 3 (38	2.7	2.2
	408912	AB011084	Hs.48924	Homo sapiens cDNA FLJ11723 fis, done HE KIAA0512 game product	2.7 2.7	4.7 2.1
	419304	A)271326	Hs.146101	ESTs	2.7	3.4
1.5	415045	AA321559	Hs.38270	Homo sapiens cDNA: FLJ20984 fis, clone C	27	2.3
15	441872	BE567100	Hs.154938	hypothetical protein MDS025	2.7	23
	422343	A1628633		gb:ty77d05.x1 NCI_CGAP_Kld11 Homo sapten	2.7	2.5
	415539 443823	A1733881 BE089782	Hs.72472 Hs.9877	ESTs	2.7	2.7
	419881	AA329340	Hs.44649	hypothetical protein ESTs	27 27	4.7 3.3
20	429165	BE242291	Hs.197540	hypoxia-inducible factor 1, alpha subuni	2.7	5.5
	431319	AA873350		gb:oh64h02.s1 NCI_CGAP_Kld5 Homo saplens	27	65.9
	430219	X99209	Hs.235887	HMT1 (hnRNP methyltransferase, S. cerevi	27	3.1
	421016	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	2.7	5.2
25	417259 431747	AW903838	Hs.81800	chondrollin suffate proteoglycen 2 (vers	2.7	10.7
23	408085	AW979134 N25929	Hs.10700 Hs.42500	hypothetical protein	2.7	2.9
	426218	AF119043	Hs. 168005	ADP-ribosylation factor-like 5 transcriptional intermediary factor 1 ga	2.7 2.7	7.8 4.5
	434845	BE267057	Hs.4200	hypothetical protein R32184_1	27	4.6
20	451644	N23235	Hs.30567	ESTs	2.7	2.3
30	428408	W74437	Hs.188757	Homo sapiens mRNA; cDNA DKFZp564M113 (fr	2.7	5.7
	446627	AJ973016	Hs.15725	hypothetical protein SB8I48	2.7	2.9
	450167 408821	AA446404 AL050385	Hs.24563 Hs.48332	NTF2-related export protein 1	2.7	9.9
	452068	W76412	Hs.57877	NIMA (never in mitosis gene a)-related k ESTs	2.7 2.7	21 21
35	431129	AL137751	Hs.263671	Homo sapiens mRNA; cDNA DKFZp434l0812 (f	2.7	6.2
	429025	Al399910	Hs.4842	ESTs	2.7	2.9
	421114	AW975051	Hs.293156	ESTs	2.7	8.8
	428755	D87454	Hs.192966	KIAA0265 protein	2.7	3.0
40	416391 414283	AI878927 AW960011	Hs.79284 Hs.154993	mesoderm specific transcript (mouse) hom ESTs	2.7	5.7
-10	425262	D87119	Hs.155418	GS3955 protein	2.7 2.7	5.9 3.7
	447726	AL137638	Hs.19368	Homo saplens mRNA; cDNA DKFZp434J065 (fr	27	14.3
	424623	AW963062	Hs.165809	EST8	27	5.6
45	444772	AW450800		ESTs	2.7	2.7
45	428419	U49436	Hs.286236	eukaryotic translation initiation factor	2.7	4.6
	441049 412758	W88920	Hs.29341	hypothetical protein FLJ22376	2.7	4.5
	447720	Y07818 AL038765	Hs.74568 Hs.161304	dihydropyrimidinase-like 3 ESTs	2.6 2.6	5.1
	419708	AK000753	Hs.92374	hypothetical protein	2.6	3.2 3.0
50	445502	AW379160		DKFZP434J214 protein	2.6	5.0
	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	2.6	29
	444147	AB002306	Hs.10351	KIAA0308 protein	2.6	6.8
	433193 445439	AB040881	Hs.32580	Homo saplens cDNA FLJ13122 fis, clone NT	2.6	3.2
55	450309	BE243084 W61348	Hs.12719 Hs.4884	regulator of nonsense transcripts 1 KIAA0892 protein	2.6 2.6	3.9
•••	422092	AB007883	Hs.111373	KIAA0423 protein	2.6	3.8 2.3
	424118	BE269041	Hs.140452	cargo selection protein (mannose 6 phosp	26	5.5
	407618	AW054922	Hs.53478	Homo sapiens cDNA FLJ12366 fis, clone MA	2.6	2.9
60	446493	AK001389		hypothetical protein DKFZp5640043	2.6	3.2
UU	442878 448771	A1868648	Hs.22315	ESTs	2.6	4.7
	416611	BE315511 AA568308	Hs.296244 Hs.192789		26	5.0
	409348	A1401535	Hs.146090	ESTs, Weakly similar to ALU7_HUMAN ALU S ESTs	2.6 2.6	7.7 3.5
	439349	A1660898	Hs.195602		26	3.2
65	428433	AA521410		ESTa	2.6	7.9
	436565	BE547674		ESTs	2.6	3.0
	438662	AA223599	Hs.6351	cleavage and polyadenylation specific fa	2.6	2.6
	429362 459035	T25833 AW291109	Hs.200478 Hs.208787		2.6	2.3
70	451814	AA847992			2.6 2.6	2.6
	452331	AA598509		H.sapiens mRNA for pur alpha extended 3'	2.6	19.1 2.2
	438461	AW075485			26	21
	424362	AL137646	Hs.146001	Homo sapiens mRNA; cDNA DKFZp586F0824 (f	26	4.9
75	423599	H41850	Hs.131848	PCAF associated factor 65 alpha	2.6	3.7
13	441226	BE583042			2.6	2.5
	444940 448731	AK002148 Al522273		hypothetical protein FLJ11285	2.6	3.4
	424250	AF073310		ESTs Insufin receptor substrate 2	26	3.2
	433468	AA832055			2.6 2.6	2.5 3.3
80	419925	AA159850		Riporna HMGIC fusion partner	2.6	3.3 4.6
	441384	AW450466	Hs.126830	ESTs .	26	2.8
	425922	AL157466			2.5	2.7
	434974	AA778711	Hs_4310	eukaryotic translation initiation factor	2.5	2.5

	408392	U28831	Hs.44566	KIAA1641 protein	2.5	25.4
	432428		Hs.31050	ESTs	2.5	10.0
	435623	A1417073	Hs.107265	ESTs	2.5	21
5	452683	AI089575	Hs.9071	progesterone membrane binding protein	2.5	2.6
J	410582 441328	AW887197 AI982794	Hs.14562	Homo saplens cDNA: FLJ21616 fis, clone C	2.5	3.7
	453983	H94997	Hs.159473 Hs.16450	ESTs ESTs	25	9.2
	438826	R26709	Hs.10095	hypothetical protein from EUROIMAGE 1669	2.5 2.5	26.1
	427899	AA829286	Hs.181062	serum amyloid A1	25 25	2.3 20.3
10	427820	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg	25	3.5
••	458933	AI638429	Hs.24763	RAN binding protein 1	2.5	3.5
	444871	U46386	Hs.12102	sorting nextn 3	2.5	2.3
	411329	AL360265	Hs.69554	hypothetical protein FLJ20552	2.5	2.9
	424074	AI902456	Hs.210761	ESTs	2.5	4.0
15	438988	H30039	Hs.107674	ESTS	2.5	2.7
	412836	AA121384	Hs.191446	ESTs	2.5	5.7
	430189	AI298841	Hs.135133	ESTs, Wealthy similar to ORF YNL310c (S.c	2.5	3.0
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	2.5	13.4
20	416926	H03109	Hs.108920	HT018 protein	2.5	2.8
20	451429	AA525993	Hs.173699	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.5	3.9
	416388	AJ417358	Hs.73677	ESTs	25	4.2
	421561	Z45399	Hs.105779	protein inhibitor of activated STAT prot	2.5	7.5
	438480	AJ271643	Hs.87469	putative acid-sensing ion channel	2.5	26
25	416273	AW575691	Hs.79123	KIAA0084 protein	2.5	2.6
23	427149	H94888	Hs.173737	ras-related C3 botulinum toxin substrate	2.5	2.6
	453041	AI680737	Hs.289068	transcription factor 4	2.5	2.2
	445899 447301	NM_005397		podocalyxin-like	2.5	4.7
	447769	AW958124 AW873704	Hs.142442 Hs.48764	HP1-BP74 ESTs	2.5	3.2
30	447754	AW073310	Hs.163533	Homo saplens cDNA FLJ14142 fis, clone MA	2.5	24
-0	427087	BE073913	Hs.173515	uncharacterized hypothalamus protein HT0	2.5 2.5	2.5 23.6
	440903	Al468079	Hs.126623	ESTs	2.5	23
	432353	NM_016558		SCAN domain-containing 1	2.5	4.1
	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.5	2.5
35	411373	BE326276	Hs.8861	ESTs	2.5	3.9
	452402	AI138530	Hs.22216	permisome proliferative activated recep	2.5	24
	429998	A1458063	Hs.57841	ESTs	2.5	2.6
	421772	Z24958	Hs.108139	Zinc finger protein 212	2.5	3.7
40	442573	H93366	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H	2,5	2.1
40	444677	AL110212	Hs.9242	purine-rich element binding protein B	2.5	3.4
	441887	AW967865	Hs.92145	ESTs	2.5	3.3
	451031	Al360187	Hs.4254	ESTs .	2.5	4.8
	432450	Al990739	Hs.77868	ORF	2.5	2.4
45	415860	D56051	Hs.78888	dlazepam blinding inhibitor (GABA recepto	2.5	4.8
43	439630	AA313607	Hs.58633	Homo saplens cDNA: FLJ22145 fis, clone H	2.4	2.3
	428607	AB002353	Hs.186840	KIAA0355 gene product	2.4	4.0
	415402 446888	AA164687 AL030996	Hs.297889	ESTS	2.4	2.5
	439208	AK000299	Hs.16411 Hs.180952	hypothetical protein LOC57187	2.4	2.2
50	452900	AA626794	Hs.250655	dynactin p52 subunit prothymosin, alpha (gene sequence 28)	24 24	2.4 3.4
	408657	AA782601	Hs.173328	protein phosphatase 2, regulatory subuni	2.4	3.6
	439143	AJ359214	Hs.179260	ESTs	24	2.5
	439867	AA847510	Hs.161292	ESTs	2.4	9.3
	408138	AA535740	Hs.301967	Homo septens mRNA; cDNA DKFZp434M196 (fr	2.4	5.6
55	428386	R17298	Hs.295923	seven in absentia (Drosophila) homolog 1	2.4	4.2
	417289	D86962	Hs.81875	growth factor receptor-bound protein 10	2.4	2.2
	405268				2.4	3.1
	439734	AC005013	Hs.149	cAMP response element-binding protein CR	2.4	3.6
60	445378	AV653564	Hs.226946	ESTs	2.4	24
00	454085	082418	Hs.29626	ESTs, Wealdy similar to unknown [D.melan	2.4	22.0
-	427354	T57896	Hs.191095		24	3.6
	452906 450085	BE207039 AL050107	Hs.75621	serine (or cysteine) proteinase inhibito	2.4	2.2
	451091	AA810932	Hs.301558 Hs.131899		24	3.6
65	414839	X63692	Hs.77462	ESTs, Wealty similar to coded for by C. DNA (cytosine-5-)-mathyltransferase 1	24	2.7
0.5	420303	AA258282	Hs.278436		2.4	2.6 2.0
	437068	AA743643	Hs.291427		2.4 2.4	2.6
	417446	AL118871	Hs.82163	monoamine oxidese B	24	4.4
	421454	A1660389	Hs.286108		2.4	3.5
70	434943	Al929819	Hs.320	xeroderma pigmentosum, complementation g	24	6.4
	446342	BE298665	Hs.14848	Homo seplens mRNA; cDNA DKFZp564D016 (fr	2.4	3.0
	452847	AK000857	Hs.30783	hypothetical protein FLJ20850	24	21
	422506	R20909	Hs.117816		2.4	22
75	405204				2.4	4.3
75	419441	AW023731			2.4	11.7
	442293	AW292634			24	21
	451484	AV648896		hypothetical protein	24	20
	438545	AB032977		KIAA1151 protein	24	21
80	442724	AA355525	Hs.159604	cysteinyl-tRNA synthetase	2.4	2.8
30	405517 413822	R08950	Un 27204	ESTe Mache della te state to beautiful	2.4	6.6
	445879	AJ343868	Hs.272044 Hs.58800	ESTs, Wealdy similar to ALU1_HUMAN ALU S Homo sapiens cDNA FLJ12488 fis, clone NT	24	3.8
	408838	BE294925		CGI-12 protein	24	23
	.5000		· TOUND	pr	2.4	8.1

	409142	AL136877	Hs.50758	champerome accordated and accorded C		
	422043		Hs.110953	chromosome-essociated polypeptide C Homo septens mRNA; cONA DKFZp434A139 (tr	24 24	24 2.1
	424687		Hs.151738	malrix metalloproteinase 9 (gelatinase B	24	26
•	442560	AA365042	Hs.228598	ESTs	24	4.9
5	418126	T91451	Hs.86538	ESTs	24	11,7
	413313 415167	NM_002047		glycyt-tRNA synthetase	· 24	2.1
	440040	AA160784 BE219431	Hs.26410 Hs.300713	ESTs ESTs	2.4	4.4
	443595	AF169312	Hs.9613	PPAR(gamma) angiopoletin related protein	24 24	3.4 10.7
10	438977	AA482026	Hs.298625	ESTS	24	28
	452068	AA772149	Hs.16979	ESTs	24	5.4
	428500	A1815395	Hs.184641	delta-6 fatty acid desaturase	24	2.2
	408503 433401	AW119059 AF039698	Hs.63163 Hs.284217	ESTs, Weakly similar to UDP-GalNAc:polyp	24	2.7
15	412676	NM_000165		serotogically defined colon cancer antig gap junction protein, alpha 1, 43kD (con	24 24	4.8 2.2
	453753	BE252983	Hs.35086	ubiquitin specific protease 1	24	28
	424050	AA211218	Hs.138381	famesyltransferase, CAAX box, alpha	24	3.9
	440225	BE295782	Hs.159	tumor necrosis factor receptor superfami	24	76.7
20	430512 415156	AF182294 X84908	Hs.241578 Hs.78060	U8 snRNA-associated Sm-like protein LSm8	2.4	12.3
20	435975	AL118990	Hs.41997	phosphorylase kinase, beta alpha-1-8 glycoprotein	2.4 2.4	10.4
	429831	AA564489	Hs.137526	ESTs	24	7.7 4.1
	407373	AA031576	Hs.143812	Homo sepiens cDNA FLJ12956 fis, clone NT	24	3.3
25	422221	AA306649		gb:EST177658 Jurkat T-cells VI Homo sapi	2.4	3.8
23	451351 410082	AW058261	Hs.168213	ESTs, Weakly similar to ALU1_HUMAN ALU \$	24	3.3
	430304	AA081594 AL122071	Hs.158311 Hs.238927	Musashi (Drosophila) homolog 1 Homo sapians mRNA; cDNA DKFZp434H1235 (1	2.4 2.4	2.5
	418863	AL135743	Hs.25566	ESTs	24	6.5 5.2
20	448414	BE391820	Hs.21145	Homo saplens cDNA: FLJ22489 ffs, clone H	24	3.7
30	428351	AK001701	Hs.183779	Homo sapiens cDNA FLJ10530 ffs, clone NT	2.4	6.2
	425750 426295	AL050276	Hs.159458	zinc finger protein 288	24	5.1
	408772	AW367283 W88532	Hs.75839 Hs.254562	zinc finger protein 6 (CMPX1) ESTs	2.4 2.4	113.6
	426307	F24978	Hs.294084	ESTa	2.4	12.3 4.0
35	405203				24	2.5
	453537	AA036755	Hs.283681	ESTs	2.4	3.6
	431427 458021	AK000401	Hs.252748	Homo sapiens cDNA FLJ20394 ffs, clone KA	24	6.2
	453928	AI885190 BE222198	Hs.156089 Hs.143851	ESTs, Wealdy similar to KIAA1339 protein ESTs	2.4	4.3
40	446853	AV660630	Hs.87627	disrupter of silencing 10	2.4 2.3	2.6 9.7
	441626	AA281167	Hs.111911	ESTs	23	23.0
	446138	AW504182	Hs,13999	KIAA0700 protein	2.3	2.2
	452568 417665	AA805634	Hs.3337	transmembrane 4 superfamily member 1	2.3	22.2
45	420088	AW852858 AC006486	Hs.22862 Hs.298033	ESTs Homo sapiens cONA: FLJ22286 fis, clone H	2.3	8.0
	421456	AW579842	Hs.104557	hypothetical protein FLJ 10697	2.3 2.3	5.1 2.5
	412093	BE242691	Hs.14947	ESTs	2.3	31.4
	428172	U09367	Hs.182828	zinc finger protein 136 (clone pHZ-20)	2.3	4.9
50	450447 436001	AF212223 AW903849	Hs.25010	hypothetical protein P15-2	2.3	2.3
20	414786	A1246482	Hs.173840 Hs.249989	HUEL (C4orf1)-interacting protein ESTs	, 23	4.1 2.1
	459284	AF155660	Hs.34401	mitochondrial solute carrier	2.3	2.9
	452701	NM_005110		glutamine-fructose-6-phosphate transamin	2.3	2.6
55	448320	AF126245	Hs.14791	acyl-Coenzyma A dehydrogenase family, me	2.3	3.9
23	446669 434618	AW972832 D79338	Hs.29468 Hs.239720	CCR4 NOT impossible according subscript	2.3	3.8
	452135	AI492175	Hs.301805	CCR4-NOT transcription complex, subunit ESTs	23 23	3.6 2.3
	408696	AW958157	Hs. 18542	ESTs .	23	28
60	436176	AL121422	Hs.184013	ESTs, Highly similar to unnamed protein	23	3.2
60	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	2.3	17.0
	414197 445270	W44877 Al762154	Hs.55501 Hs.54982	ESTS	2.3	11.8
	412247	AF022375	Hs.73793	Homo sapiens cDNA FLJ14014 fis, clone HE vescular endothelial growth factor	2.3 2.3	4.2 5.1
	426494	AL119528	Hs.170098	KIAA0372 gene product	23	4.4
65	405687				23	2.2
	417410	AF063020	Hs.82110	PC4 and SFRS1 interacting protein 1	2.3	20
	450747 433680	AI064821 AI805366	Hs.48306 Hs.199945	ESTs, Highly similar to EWS_HUMAN RNA-BI ESTs	23	3.8
	420025	AF184939	Hs.94392	LDL Induced EC protein	23 23	6.7 2.4
70	413407	Al358293	Hs.75339	inositol polyphosphate phosphatese-like	23	3.1
	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	2.3	3.0
	424414 435791	Al361002	Hs.94814	Homo sapiens cDNA FLJ12168 fis, clone MA	2.3	20
	457635	AA243086 AV660976	Hs.25204 Hs.3569	chondroitin 4-O-sulfotransferase 2	23	24
75	427985	AI770170	Hs.65583	hypothetical protetn ESTs	23 23	6.9 2.3
	445498	AV654019	Hs.180402	Homo saplens cDNA: FLJ23506 fis, clone L	23	23
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.3	4.1
	450388 444614	AU077158	Hs.24930	tubulin-specific chaperone a	2.3	3.5
80	448607	R44284 AL042506	Hs.2730 Hs.21599	heterogeneous nuclear ribonucleoprotein Homo sapiens cDNA FLJ10107 fis, clone HE	2.3	2.6
	447975	BE378418	Hs.127240	ESTs	23 23	2.8 2.2
	429767	AW793022	Hs.218329	hypothetical protein	23	11.5
	408877	AA479033	Hs.130315	ESTs	23	2.3

	448481	W15284	Hs.74832	EST8	2.3	3.3
	452833 421057	BE559681 T58283	Hs.30736	KIAAD124 protein	23	2.8
	408885	C02741	Hs.42679	ESTs	23	11.0
5	427615	BE410107	Hs.48712 Hs.179817	hypothetical protein FLJ20736	2.3	4.6
-	448861	AL049951	Hs.22370	CGI-82 prolein Homo sapiens mRNA; cDNA DKFZp56400122 (r	2.3	2.3
	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	2.3	6.3
	428494	AA233439	Hs.184634	hypothetical protein FLJ20005	2.3	34.6
10	422987	AW407887	Hs.301772	serine/threonine kinase 11 (Peutz-Jegher	23 23	10.2
10	408216	AA741038	Hs.6870	ESTs	23	3.2 3.3
	407862	BE548267	Hs.50724	Homo sapiens cDNA FLJ10934 ffs, clone OV	2.3	5.7
	432215	AU076609	Hs.2934	ribonucleotide reductase M1 polypeptide	2.3	21
	410086 444853	A1268405	Hs.13487	Homo saplens BAC clone RP11-121A8 from 7	2.3	2,2
15	413284	AW576245 AU077055	Hs.149740	Homo saptens mRNA for FLJ00028 protein,	23	4.5
	445547	086181	Hs.289107 Hs.273	bacufoviral IAP repeat-containing 2	2.3	4.8
	420258	AA477514	Hs.96247	galactosylcenamidase (Krabbe disease) translin-associated factor X	23	2.5
	437223	C15105	Hs.107884	ESTS	23	3.5
20	437353	AA749195	Hs.143746	ESTs	23 23	2.7
20	426224	BE085860	Hs.168075	karyopherin (importin) beta 2	23	2.6 36.1
	402575	Z23024	Hs. 138860	Rho GTPase activating protein 1	2.3	3.1
	430712	AW044647	Hs.196284	ESTs	23	2.4
	452036	NM_003966	Hs.27621	sema domain, seven thrombospondin repeat.	2.3	2.4
25	425180 441848	U00115 H05734	Hs.155024	B-cell CLL/lymphoma 6 (zinc finger prote	2.3	4.3
	424130	AL050136	Hs.30559 Hs.140945	ESTS	2.3	2.1
	414682	AL021154	Hs.76884	Homo sapiens mRNA; cDNA DKFZp586L141 (fr inhibitor of DNA binding 3, dominant neg	23	29
	423814	AF105020	Hs.132989	putstive protein O-mannosyltransferase	2.3	12.2
••	421641	AI638184	Hs.106334	Homo sapiens clone 23838 mRNA sequence	23	3.7
30	427882	AA640987	Hs.193767	ESTs	2.3 2.3	2.3
	442159	AW163390	Hs.8123	chromobox homolog 3 (Drosophila HP1 gamm	23	10.2 4.4
	412541	BE009398	Hs.74002	nuclear receptor coactivator 1	2.3	2.4
	447217	BE465754	Hs.17778	neuropilin 2	2.3	3.0
35	452338 423913	AA960951 NM_016436	Hs.29147	hypothetical protein FLJ11015	2.3	4.1
	411737	AW160339	Hs.71791	hepatocellular carcinoma-associated anti	2.3	3.4
	412276	BE262621	Hs.73798	hypothetical protein	2.2	20
	456974	M12529	Hs.169401	macrophage migration inhibitory factor (apolipoprotein E	2.2	2.4
40	416033	NM_012201		Golgi apparatus protein 1	2.2	2.6
40	406739	AI568709	Hs.182426	ribosomal protein S2	2.2 2.2	10.4
	448848	AU077149	Hs.21704	transcription factor 12 (HTF4, helix-too	22	115.3 4.2
	437371	AK000868	Hs.6570	hypothetical protein FLI 10006	22	3.6
	451413 408665	AA448974	Hs.26387	PC3-96 protein	2.2	6.2
45	437548	T88845 Al701596	Hs.112200	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.2	3.2
	452053	A1750575	Hs.121592 Hs.173933	ESTS	22	3.0
	428303	AW974476	Hs.183601	nuclear factor I/A regulator of G-protein signalling 16	2.2	3.3
	441376	H94227	Hs.6592	ESTs, Weakly similar to salivary profine	2.2	3.4
£0	413399	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.2 2.2	2.5
50	448913	AA194422	Hs.22584	myosin VI	2.2	2.1 2.4
	439053	BE244588	Ha.6456	chaperonin containing TCP1, subunit 2 (b	2.2	3.1
	428065 425846	A1634048	Hs.157313	ESTS	2.2	3.5
	426404	AA102174 AA377607	Hs.159629	myosin IXB	2.2	7.1
55	423464	NM_016240	Hs.273138	ESTs CSR1 ambie	2.2	3.3
	436135	D85390	Hs.5057	CSR1 protein carboxypeptidase D	2.2	2.1
	450478	AL045285	Hs.246849	ESTs, Moderately similar to ALUB_HUMAN A	2.2	9.1
	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	2.2	2.5
60	433530	BE349534	Hs.281789	ESTS	2.2 2.2	2.8 2.1
UU	436297	A1084582	Hs.5105	hypothetical protein FLJ 10569	22	2.4
	433058 435924	H86865	Hs.280668	Homo saplens chromosome 19, cosmid R3218	2.2	2,3
	417125	AW029203 AW181998	Hs.191952	ESTS	2.2	3,2
	449338	H73444	Hs.81248 Hs.394	CUG triplet repeat, RNA-binding protein adrenomedullin	2.2	2.3
65	446065	AA085191	Hs.6949	ESTs, Weakly similar to T2D3_HUMAN TRANS	22	18.3
	410668	BE379794	Hs.65403	hypothetical protein	2.2	3.1
	424992	AW290893	Hs.96918	Homo sapiens cDNA: FLJ21561 fls, clone C	2.2	2.5
	437801	AA613866	Hs.5848	Homo seplens mRNA; cDNA DXFZp584L222 (fr	2.2 2.2	10.8 2. 5
70	412491	W31589	Hs.73957	RABSA, member RAS oncogene family	2.2	24
70	446392	AF142419	Hs.15020	homolog of mouse quaking QKI (IQH domain	2.2	3.4
	450503	R35917	Hs.25042	Homo saplens mRNA full length insert cDN	22	2.8
	432476 424251	T94344 AA677466	He 1/2000	gb:ye31h10.s1 Stretagene lung (937210) H	2.2	2.6
	456619	AV547917	Hs.143696 Hs.107153	coactivator-associated arginine methyltr	2.2	5.0
75	433411	A1658666	Hs.49994	inhibitor of growth family, member 1-lik ESTs	2.2	2.6
	424714	Al114630	Hs.208334	Homo sapiens cDNA: FLJ21874 fis, clone H	2.2	2.1
	416326	AF186780	Hs.79219	RalGDS-like gene; KIAA0959 orotein	22	2.7
	407698	A1697340	Hs.76549	ATPase, Na+/K+ transporting, sloha 1 pol	2.2 2.2	22
80	445939	BE018658	Hs.141003	Homo saplens cDNA: FLI21691 fis. clone C.	22	6.5 4.4
50	414765	X07854	Hs.77269	guanine nucleotide binding orotein (G or	22	8.2
	407138 453865	T64896 AA626250	Hs.287420	Homo sapiens cONA FLJ11533 fts. clone HF	2.2	2.8
	433608	AW340005	Hs.181165	eukeryotic translation elongation factor	2.2	2.3
			Hs.164485	ESTs	2.2	2.1

	447646	BE619752	Hs.66053	ESTs, Wealty similar to S22126 finger pr	2.2	4.1
	433139	AB029826	Hs.47649	3-methylcrotonyl-CoA carboxylase biotin-	2.2	11.7
	413433 421535	NM_003199 AB002359		transcription factor 4	2.2	2.2
5	428591	BE313029	Hs.105478 Hs.185807	phosphoribosylformylglycinamidine syntha	2.2	2.2
•	417248	AA329449	Hs.247302	Homo saptens clone 24758 mRNA sequence	2.2	4.8
	403966	74-023413	15.247502	bvisted gastrutation	2.2	2.5
	437112	AA744692	Hs.166539	ESTs	2.2	5.2
	414799	AI752416	Hs.77326	Insulin-like growth factor binding prote	2.2 2.2	3.0
10	431049	AA846576	Hs.103267	hypothetical protein FLJ 22548 similar to	22	4.9 4.4
	422100	AI096988	Hs.111554	ADP-ribosylation factor-like 7	2.2	2.5
	426543	AV650198	Hs.170311	heterogeneous nuclear ribonucleoprotein	2.2	2.4
	423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fis, clone C	2.2	4.2
16	443804	AL135352	Hs.255883	ESTs	2.2	2.2
15	435080	AI831760	Hs.155111	ESTs	2.2	2.5
	452808	AF244135	Hs.30670	hepatocellular carcinoma-associated anti	2.2	7.1
	433934	AW273261	Hs.216292	ESTs	2.2	2.1
	432004	BE018302	Hs.2894	placental growth factor, vascular endoth	22	4.4
20	452518 409600	AA280722	Hs.24758	ESTs	2.2	3.0
20	448965	AJ011679 AF092134	Hs.55099	Homo sapiens mRNA; cDNA DKFZp586D2123 (f	2.2	2.3
	444954	AW247076	Hs.22679 Hs.12163	CGI-24 protein	2.2	4.0
	458894	AW292171	Hs.23978	eukaryolic translation initiation factor scaffold attachment factor B	22	5.3
	402269	***********	11323370	SCENED SUBCERIBINE ISSUED	2.2	2.5
25	423798	AF047033	Hs.301617	Homo saplens mRNA full length insert cDN	2.2 2.2	2.2 4.0
	413836	W92003	Hs.70614	ESTs	2.2	3.6
	432231	AA339977	Hs.274127	CLST 11240 protein	21	2.1
	412204	Al125507	Hs.130829	ESTs	21	3.0
20	438807	AA848011	Hs.124570	ESTs, Wealdy similar to reverse transcri	21	2.2
30	404170				2.1	41.6
	434858	AW979012	Hs.134462	ESTs	21	2.2
	426982	AA149707	Hs.173091	ubiquitin-like 3	21	2.1
	421939	BE169531	Hs.109727	TAK1-binding protein 2; KIAA0733 protein	2.1	26.5
35	442432	BE093589	Hs.38178	Homo sapiens cDNA: FLJ23468 fis, clone H	2.1	3.7
7,7	424950 418123	AA602917	Hs.156974	ESTs	2.1	19.9
	440467	AA669830 AK001519	Hs.83530	hypothetical protein	2.1	4.6
	437092	AA744292	Hs.7194 Hs.181244	CGI-74 protein	2.1	5.3
	421579	NM_002975		major histocompetibility complex, class stem cell growth factor, lymphocyte secr	2.1	3.0
40	428953	AA306810	Hs.194676	DKFZP434C013 protein	21	3.3
	457313	AF047002	Hs.241520	transcriptional coactivator	2.1 2.1	5.0
	420570	AV453665	Hs.290870	ESTs, Weakly similar to S23650 retroviru	2.1	3.5
	446918	AL135125	Hs.13913	KIAA1577 protein	2.1	2.1 2.3
4 ~	427567	N24238	Hs.179662	nucleosome assembly protein 1-like 1	21	2.8
45	448383	AL117440	Hs.301967	Homo sapiens mRNA; cDNA DKFZp434M196 (fr	21	4.0
	428482	AI290352	Hs.184592	KIAA0344 gene product	2.1	2.8
	456559	Al336273	Hs.102548	glucocorticoid receptor DNA binding fact	2.1	2.3
	442819	BE622721	Hs.301766	ESTs, Weakly similar to hypothetical pro	2.1	27.1
50	428808	AA436007	Hs.188780	ESTs	2.1	5.0
20	414893	AA215295	Hs.77578	ubiquilin specific protease 9, X chromos	21	15.9
	447023 402250	AA358784	Hs.17109	Integral membrane protein 2A	2.1	3.0
	429952	AV655272 AF080158	Hs.20252 Hs.226573	novel Ras family protein	21	4.2
	420006	H14429	Hs.94300	inhibitor of kappa light polypeplide gen	21	7.9
55	407316	AA031663	Hs.28802	serologically defined colon cancer antig centaurin-alpha 2 protein	2.1	5.6
	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	2.1	4.4
	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.1 2.1	103.2 29.9
	430488	D19589	Hs.4220	ESTs, Moderately similar to tetracycline	21	2.1
60	428580	U69199	Hs.90259	ESTs, Wealty similar to alpha 1 (H.sapie	21	2.5
60	448501	AA332316	Hs.4273	hypothetical protein FLJ 13159	2.1	2.0
	422552	N39729	Hs.118243	deoxyribonuclease II, lysosomal	21	2.9
	419476	AW953030	Hs.59425	Homo sapiens cDNA: FLJ23323 fis, clone H	2.1	3.1
	408681	AW953853	Hs.292833	ESTs	2.1	3.9
65	417353 422070	AA375752	Hs.76362	general transcription factor IIA, 2 (12k	2.1	4.1
Ų,	442711	AF149785 AF151073	Hs.111128	pitultary tumor-transforming 1 Interacti	21	4.9
	450139	AK001838	Hs.8645 Hs.296323	hypothetical protein Homo sapiens cDNA FLJ10976 fis, clone PL	2.1	2.2
	452897	BE066058	Hs.269233	ESTs	2.1	7.4
	409147	AI889208	Hs.17283	hypothetical protein FLJ 10890	21	4.2
70	433028	AJ199144	Hs.283737	AD-017 protein	21	4.5
	407831	BE613377	Hs.15580	Homo sapiens cONA: FLJ22276 fis, clone H	21 21	2.6 8.5
	417871	AA521368	Hs.24252	ESTs	21	2.9
	428754	A1521102	Hs.301374	ESTs, Moderately similar to ALU5_HUMAN A	21	5.3
75	430127	AA219498	Hs.233952	proteasome (prosome, macropain) subunit,	21	4.3
75	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	2.1	8.5
	414242	AA749230	Hs.22666	ESTs	21	2.8
	433323	AA805132	Hs.30701	ESTs	2.1	5.0
	439022	AA356599	Hs.173904	ESTs	2.1	6.4
80	443357 449103	AW016773 T24968	Hs.75615	apolipoprotain C-II	2.1	20
-00	427512	AB018322	Hs.23038	HSPC071 protein	2.1	2.7
	426728	NM_007118	Hs.179607 Hs.171957	KIAA0779 protein	21	2.0
	440112	AA099014	Hs.231029	triple functional domain (PTPRF interact	21	29
		r=1033014	110-43 (02)	ESTs	2.1	23

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	446920	BE397649	Hs.31257	Homo saptens cDNA FLJ13634 fis, clone PL	21	4.8
	428459	D44850	Hs.184411	gene with multiple splice variants near	2.1	2.9
	432842 438829	AW674093 AA826926	Hs.279525 Hs.204214	hypothetical protein PRO2605	21	23
5	411442	N25956	Hs.101810	ESTs Homo sapiens cDNA FL114232 fis, clone NT	21	2.7
	409423	AI969783	Hs.43071	ESTs, Weakly similar to AF151900 1 CGI-1	21 21	2.2
	456804	Al421645	Hs.139851	caveolin 2	21	2.2 15.2
	434536	H14488	Hs.3903	Cdc42 effector protein 4; binder of Rho	21	2.8
10	447126	AW150632	Hs.62954	ferritin, heavy polypeptide 1	21	25.0
10	442328 444488	Al952430 AW192879	Hs.265237	ESTS	2.1	2.1
	438874	H02780	Hs.184798	ESTs, Weakly similar to PET2_HUMAN OLIGO gb:y 41a11.r1 Soares placente Nb2HP Homo	2.1	2.9
	412805	AW954569	Hs.296287	ESTs	21 21	10.6
1 ~	446334	U52427	Hs.14839	polymerase (RNA) II (DNA directed) polyp	21	4.6 2.3
15	427201	AB037860	Hs.173933	nuclear factor I/A	21	5.1
	436997	AA741151	Hs.137323	ESTs	21	3.0
	426369 453613	AF134157 F06838	Hs.169487	Kreister (mouse) maf-related leucine zip	2.1	23
	413276	Z24725	Hs.14763 Hs.75260	ESTs	- 21	2.4
20	422050	AA302741	Hs.25786	milogen inducible 2 ESTs	21	5.5
	424797	AA822394	Hs.153177	ribosomal protein S28	21 21	4.0
	437365	AW965771	Hs.91065	hypothetical protein DKFZp761B2423	21	2.1 3.0
	412482	AJ499930	Ks.181043	KIAA0788 protein	21	27
25	418662 404030	AI801098	Hs.151500	ESTs	21	2.1
23	437802	Al475995	Hs.122910	CCT-	21	2.1
	441130	Al160734	Hs.283429	ESTs SMC (mouse) homolog, X chromosome	21	3.8
	416084	L16991	Hs.79006	deoxythymidylate kinase (thymidylate kin	21 21	3.5
20	409944	BE297925	Hs.57687	four and a half LIM domains 3	21	7.4 6.3
30	425421	L11669	Hs.157145	tetracycline transporter-like protein	21	7.1
	428399	NM_006276		splicing factor, arginine/serine-rich 7	2.1	2.7
	421313 445229	NM_014923 BE276013		KIAA0970 protein	21	26
	401001	DE210013	Hs.172364	Homo saplens mRNA for FLJ00086 protein,	21	4.7
35	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	21 21	14.7
	438855	AW946276	Hs.6441	lissue inhibitor of metalloproteinase 2	. 21	7.2 4.9
	433369	Z49254	Hs.3254	mitochondrial ribosomal protein L23	21	25.0
	433228	F28212	Hs.284247	KIAA1491 protein	2.1	5.1
40	445392 433891	AA057478 AA613792	Hs.23272	ESTs	20	2.3
••	432572	A1660840	Hs.191202	gb:no97h03.s1 NCI_CGAP_Pr2 Homo saplens ESTs, Weakly similar to ALUE_HUMAN IIII	. 20	2.5
	448474	AI792014	Hs.13809	EST8	2.0	2.9
	427045	H86504	Hs.173328	protein phosphatase 2, regulatory subuni	2.0 2.0	12.1 2.9
45	444916	AB028958	Hs.12144	KIAA1033 protein	20	4.2
43	439177	AW820275	Hs.76611	ESTs	2.0	3.3
	423533 430057	NM_014339		interleukin 17 receptor	2.0	5.0
	424429	AW450303 U63830	Hs.2534 Hs.146847	bone morphogenetic protein receptor, typ	2.0	23
	428385	AF112213	Hs.184062	TRAF family member-associated NFKB activ putative Rab5-interacting protein	20	12.7
50	458946	AA009716	Hs.42311	ESTs	2.0 2.0	4.6 16.4
	444816	Z48633	Hs.283742	H.saplens mRNA for retrotransposon	20	4.9
	426829	AI761241	Hs.301719	ESTs	20	2.4
	433819 421985	AW965275	Hs.284288	hqp0256 protein	2.0	4.4
55	439895	AK001779 AB037773	Hs.110445 Hs.6762	CGI-97 protein hypothetical protein FLJ10595	2.0	3.6
	449188	AW072939	Hs.23200	myotubularin related protein 1	20	2.2
	404820			my out out an related protein (2.0 2.0	2.2 2.7
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	2.0	25
60	422163	AF027208	Hs.297332	Homo sapiens cDNA: FLJ21471 fls, clone C	20	3.7
00	431172 415200	Al125639 Al040328	Hs.250666	halry (Drosophila)-homotog	2.0	10.2
	458176	AU40328 Al961519	Hs.301912 Hs.140309	Homo sepiens cDNA: FLJ22920 fis, clone K	2.0	2.1
	407895	R44203	Hs.265540	ESTs, Weakly similar to KIAA0681 protein HSPC042 protein	20	5.0
	449816	AI701457	Hs.38694	ESTs	2.0 2.0	4.6
65	422976	AU076657	Hs.1600	sec61 homolog	2.0	2.0 5.7
	430220	BE378277	Hs.152230	ESTs	20	11.7
	435446	AA682305	Hs.133268	ESTs	2.0	4.2
	431031 425233	AA830335 Z17861	Hs.105273	ESTs	2.0	14.1
70	426458	D83032	Hs.155218 Hs.169984	E1B-SSkDa-associated protein 5 nucléar protein	20	5.6
	421965	AA301100	13.103304	gb:EST14128 Testis tumor Homo septens cD	20	5.9
	427128	AW301984	Hs.173685	Homo sapiens cDNA FLJ12619 fis, clone NT	2.0 2.0	2.1
	449722	BE280074	Hs.23960	cyclin B1	20	6.3 2.1
75	450816	BE271927	Hs.87385	ESTs	20	24
, ,	453507 422801	AF083217	Hs.33085	WD repeat domain 3	20	13.1
	422801 418178	AF125672 AA043951	Hs.287994	nuclear receptor co-repressor 2	2.0	3.5
	417819	AI253112	Hs.83715 Hs.133540	Sjogren syndrome antigen B (autoantigen ESTs	20	3.9
00	414787	AL049332	Hs.77311	BTG family, member 3	20	4.0
80	447032	AK000310	Hs.17138	hypothetical protein FLJ20303	2.0 2.0	4.0
	431742	NM_016652	Hs.268281	CGI-201 protein	2.0	7.0 2.5
	448431	BE613061	Hs.300697	ESTs, Weakly similar to CA13_HUMAN COLLA	2.0	6.5
	456444	AA884517	Hs.31856	ESTs, Wealthy similar to KIAA1453 protein	2.0	2.5

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	419178 446437	NM_006284		TATA box binding protein (TBP)-associate		2.0	6.0
	449910	AW014360 Al074585	Hs.202119	ESTs, Weakly similar to A46010 X-linked		2.0	22
	435963	AF271212	Hs.58440 Hs.87627	ESTs		2.0	2.1
5	421283	AJ760018	Hs.205071	disrupter of sitencing 10 ESTs		2.0	2.1
	414482	657498	Hs.76252	endothelin receptor type A		20	26
	450960	AB013897	Hs.25722	Homo saplens mRNA for HKR1, partial cds		2.0	24
	438544	Al126162	Hs.129037	ESTs		2.0 2.0	2.1
10	458343	AJ004775	Hs.205091	ESTs, Wealdy similar to WW domain bindin		20	2.1 6.5
10	412574	BE410731	Hs.74050	folloular lymphoma variant translocatio		2.0	12,4
	458079	AI796870	Hs.54277	ESTs .		2.0	3.8
	450582 409936	Al339732	Hs.13144	HSPC160 protein		2.0	2.8
	426865	AK001691 D63476	Hs.57655	hypothetical protein FLJ10829		20	3.1
15	448430	AA346837	Hs.172813 Hs.15075	PAK-interacting exchange factor beta		20	3.3
		7427007	113.13013	hypothetical protein DKFZp434E2216		20	2.0
	Table 4B:						
	Pkey:	Uniqu	e Eos probes	et identifier number			
20	CAT numb		cluster number				
20	Accessions	Genb	ank accession	numbers			
	Pkey	CAT Number	Annanian				
	447197	2176805_1	Accession	86167 Al366546			
	407192	2200202_1	AA602964	AA609200			
25	429007	327976_1		BF958169 AW904500 AL119015 D80642			
	429163	1238297_1	AW974271	AA592975 AA447312 AA884766			
	439579	24302_1		W73990 W79232			
	432060 416913	1235850_1	AA525021	AW971364 AA570759			
30	426413	924458_1 372468_1	AW934714	AW749864 AW749902 BE162498 BE161005 B	E162499 BE161006 AA	190449 AW5	13485 BE162500 BE161007
	433586	32908_1	**********	AA377823 BG219617 BG195685 BG616269 AI AW517087 AA601054 T85512	022688		
	448451	7632_32	AW000978	R39898 AW015994 Al598202 BFB21479 Al521	700		
	442495	928718_1	AJ184717	W518883 AF121173	/05		
35	439566	23928_1		W72711 W77884			
33	407939	600387_1		AW196215 W05608			
	453740 433854	812139_1		BG291384 T88779			
	413020	899720_1 1485885_1	BG0/5161	H59558 Al699484 AA610649 Al937812			
4.0	458050	61684_1	AK057874	R98738 Z42904 AW901381 AW901380 AV730240 T50211 AA82	M750		
40	440769	21430_5	BG419454	BF924037 R13764 AW793200 BE561793 BG69	28755 AA834708		•
	428832	1137856_1	B1008687 /	VA481353 AA436432 BI008686 AA578229 AA48	10295 BE2/UU//		
	414473	35761_3	BG392868	BE302693			
	422343	786037_1	AW961833	AA309282 AA551780 AI628633 AA551995 AW	378461		
45	431319 422221	122030_1	BG435498	BG924768 AV718638 AA873350 TR2428 TR243	ALIGEATE ARECOAL	2	
15	413399	319_18 1511159_1	DG310333	BE020/14 BF905312 AA305649 Z40822 N76R3	13		
	432476	1237465_1	AW973360	BE091874 BE091871 AA548913 T94344 AA834800 AA857492			
	438874	52147_1	AF075017	R66779 R22463 H02780			
<i>5</i> 0	433891	647290_1	AW182329	AA613792 T05304 AW858385			
50	421965	1883_13	BC022394	AI742351 BE676249 AI742341 AW57277R AISS	8256 A1538553 RJR370	NE A 4301100	AA620903 Al142397 AW082310 Al147387 BF509145
			AW968207	AA468415 AU185163 AW450843 A1668752 AV	/137191	00 70001100	AMUS2310 A1147387 BF509145
	TABLE 4C						
	Pkey:		o number eee				
55	Ret.	Seou	e nomber con	esponding to an Eos probeset	M		
		SEQUE	nce of human	The 7 digil numbers in this column are Genbank chromosome 22° Dunham, et al. (1999) Nature	identiner (GI) numbers.	Dunham, et	al." refers to the publication entitled "The DNA
	Strand:	Indica	les DNA stran	d from which exons were predicted	102.405-430.		
	Nt_position	: Indica	tes nucleotide	positions of predicted exons.			
60	Pkey	Ref					1
	400859	9757499	Strend Minus	Nt_position			
	405238	7249119	Minus	91888-92018,98131-98294,99474-99570 51728-51836			
	400992	8096828	Ptus	140390-140822			
65	400860	9757499	Minus	151830-152104,152649-152744			
Ç	402524 404210	9798518	Minus	20529-21098			
	402604	5006248 9909420	Plus	169926-170121			
	402855	9662953	Plus Minus	20393-20767			
	404029	7671252	Plus	59763-59909 108716-111112			
70	402605	9909420	Minus	47680-47973			
	404049	3688074	Minus	75765-78155			
	403549	8081591	Minus	137150-137362			
	404048	3888074	Minus	54421-56808			
75	404171 405649	9930793 4926908	Plus	173667-173783,176876-177055			
	405268	4156151	Minus Minus	50032-50132,50524-50764 24404-24521			
	405204	7230116	Phus	126569-126754			
	405517	9454624	Plus	114757-114877			
80	405203	7230116	Plus	125295-125463			
OU	405687	6249668	Minus	54787-54891,55844-55917			
	403988 402269	8568881 3128156	Plus	158193-158277,160116-160290			
	404170	9930793	Minus Ptus	1168-1324,5492-5611,23445-23851 168836-169248			
			, 103	100000-100240			

	404030	7671252	Plus	149362-151749			
	401001	7229886	Minus	113631-113762			
_	404820	4678240	Ptus	20475-21085			
5	=======================================						
	TABLE 5A Pkey:	: ABOUT 43 GI	ENES UPREGI	JLATED IN GLIOBLASTOMA THAT ENCODE PREI It Identifier number	DICTED MEMBRANE PROTE	ins	
	ExAcon:	Exen		number, Genbank accession number			
10	UnigeneID	: Unig:	ene number				
10	Unigene Ti R1:		ene gene title of brain tumor	to body atlas			
	R2:			to normal brain			
	Pkey	ExAcon	UnigenetD	Unigene title	R1	R2	
15	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	72.0	11.3	
	447072 451099	D61594 R52795	Hs.17279	tyrosylprotein autiotransferase 1	54.2	7.1	
	415910	U20350	Hs.25954 Hs.78913	Interleukin 13 receptor, elpha 2 chemokine (C-X3-C) receptor 1	22.0 21.2	7.6 3.0	
20	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	18.6	18.6	
20	417355 419721	D13168 NM_001650	Hs.82002	endothelin receptor type B	16.4	16.4	
	452355	N54926	Hs.288650 Hs.29202	aquaporin 4 G protein-coupled receptor 34	16.2 13.9	4.4 13.9	
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2 ·	11.9	2.9	
25	419723 414825	AL120193 X06370	Hs.92614 Hs.77432	Homo saplens growth differentiation fact	7.4	3.5	
	443898	AW804296	Hs.9950	epidermal growth factor receptor (avian Sec61 gamma	6.9 4.8	6.4 7.2	
	422033	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	4.3	6.1	
	414821 431556	M63835 AF016028	Hs.77424 · Hs.260039	Fc fragment of IgG, high affinity Ia, re sarcospan (Kras oncogene-associated gene	4.2	34.8	
30	435869	AF255910	Hs.54650	vascular endothelial junction-associated	4.0 3.7	3.8 4.2	•
	440516 428141	S42303	Hs.161	cadherin 2, type 1, N-cadherin (neuronal	3.5	5.1	
	428484	D50402 AF104032	Hs.182611 Hs.184601	solute carrier family 11 (proton-coupled solute carrier family 7 (cationic amino	3.5	2.4	
25	431053	\$40369	Hs.249141	Glutamate receptor subunit	3.4 · 3.3	2.8 2.4	
35	445070 430890	NM_000677	Hs.258	adenosine A3 receptor	3.2	7.6	
	423422	X54232 AC005175	Hs.2699 Hs.128425	glypican 1 NY-REN-24 antigen	3.2 3.2	4.3 4.0	
	413367	NM_006517	Hs.75317	solute carrier family 15 (monocarboxylic	3.1	2.6	
40	447471 427150	AF039843 BE616183	Hs.18676 Hs.173737	sprouty (Drosophila) homolog 2	3.0	4.1	
	422676	D28481	Hs.1570	ras-related C3 botulinum toxin substrate histamine receptor H1	3.0 . 3.0	4.1 2.1	
	430293	AJ416988	Hs.238272	inositol 1,4,5-triphosphate receptor, ty	3.0	6.3	
	453498 428281	AA442103 AA194554	Hs.33084 Hs.183434	solute carrier family 2 (facilitated glu ATPase, H+ transporting, lysosomal (vacu	28	7.4	
45	417446	AL118671	Hs.82163	monoamine oxidase 6	2.7 2.4	3.2 4.4	
	412676	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con	2.4	2.2	
	440225 450447	BE295782 AF212223	Hs.159 Hs.25010	turnor necrosis factor receptor superfami hypothetical protein P15-2	24	76.7	
50	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.3 2.3	2.3 4.1	
50	452036 447217	NM_003966	Hs.27621	sema domain, seven thrombospondin repeat	2.3	24	
	447023	BE465754 AA356764	Hs.17778 Hs.17109	neuropilin 2 Integral membrane protein 2A	2.3 2.1	3.0 3.0	
	422070	AF149785	Hs.111126	pituitary tumor-transforming 1 interacti	2.1	4.9	
55	456804 430057	AI421645 AW450303	Hs.139851	caveolin 2	2.1	15.2	
	422163	AF027208	Hs.2534 Hs.297332	bone morphogenetic protein receptor, typ Homo saptens cDNA: FLJ21471 fis, clone C	20 20	23 37	
	414482	S57498	Hs.76252	endothelin receptor type A	2.0	2.4	
60	TABLE 6/	A: ABOUT 397 (SENES DOWN	REGULATED IN GLIOBLASTOMA			
	Pkey: ExAccn:	Unic	lue Eos probes	et identifier number			
	Unigeneli	exe D: Unk	mpiar Accessio Iene number	n number, Genbank accession number			
65	Unigene 1	litte: Uniç	ene gene lille				
05	R1: R2:			in to body atlas			
			O OI HOITHGE DE	in to brain tumor .			
	Pkey 439340	Ex Accn AB032436	UnigenelD		R1	R2	
70	424846	AU077324	Hs.6535 Hs.1832	brain-specific Na-dependent inorganic ph neuropeolide Y	4.47 4.49	77.82	
	428874	W32133	Hs.194366	transthyretin (prealbumin, amyloidosis t	7.06	55.32 45.64	
	416838 401412	D54745 c14p3_2958	Hs.80247	cholecystokinin	9.45	44.59	
	451835	T63643	Hs.209715	exon ESTs, Weakly similar to ALU7_HUMAN ALU S	3.20 3.21	32.56 28.93	
75	412768	AW996044	Hs.26239	ESTs	3.16	26.53 28.12	
	415448 411305	T68645 BE241596	Hs.952	solute carrier family 10 (sodium/bile ac	3.27	27.04	
	438054	AA776626	Hs.69547 Hs.62183	myelin basic protein ESTs	13.80 3.59	25.92 25.06	
80	410837	BE145698		gb:ILO-HT0205-231199-145-a07 HT0205 Homo	3.05	24.43	
50	425121 458763	Al797511 AJ271351	Hs.154679 Hs.128180		6.92	23.67	
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	3.29 8.03	23.32 22.56	
	451892	AI821302	Hs.167834	ESTs	4.12	21.82	
				12			

	404000	DE4000				
	424922 411666	BE386547	Hs.217112		4.41	21.28
	432247	AF106564 AA531287	Hs.71346	neurotilament 3 (150kD medium)	5.27	21.20
	436812	AW298067	Hs.105805		3.25	21.14
5	422234	AF11981B	Hs.113287	gb:Ui-H-BWD-zip-g-09-0-ULs1 NCI_CGAP_Su	3.02	21.12
	435708	Al362949	Hs.75169	discs, large (Drosophila) homolog-essoci ESTs	3.38	20.50
	423135	N67655	Hs.26411	ESTs	8.79	20.45
	440600	A1807691	Hs.126351		6.82	20.28
10	405230	cNp1_7656		excn	3.58	20.09
10	456915	NS5540	Hs.78026	ESTs, Weakly similar to similar to ankyr	3.31	19.95
	425130	AA448208	Hs.99163	ESTs	3.14 3.53	19.40
	416812	H91010	Hs.44940	EST ₈	3.54	19.20 19.08
	454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	3.78	19.04
15	457463 454589	AW877031	Hs.272321	Homo saplens cDNA FLJ12571 ffs, clone NT	3.13	18.91
1.5	418104	AW809599	Ll. 477400	gb:MR4-ST0124-241199-028-e12 ST0124 Homo	4.10	18.60
	416357	T05726 T82050	Hs.177130	ESTs	3.17	18.41
	414683	S78298	Hs.268907 Hs.76888	ESTs	3.11	18.13
	447694	AJ420083	Hs.170303	internexin neuronal intermediate filamen ESTs	5.55	18.13
20	427627	R87582	Hs.179915		3.56	17.79
	428010	AA806554	Hs.185375	guanine nucleolide binding protein (G pr ESTs	4.63	17.65
	417159	R01761		gb:ye81f10.s1 Soares fetal liver spleen	3.03	17.40
	438788	AA766908	Hs.259047	ESTs	3.23	17.38
26	459349	AW749381		gb:QV3-BT0381-170100-060-c02 BT0381 Homo	3.16	17.21
25	450214	BE439763	Hs.227571	regulator of G-protein signaling 4	3.26 3.86	17.10
	438068	AI927209	Hs.283089	HMT1 (hnRNP methyltransferase, S. cerevi	3.54	17.04 16.48
	437268	AI754847	Hs.227571	regulator of G-protein signalling 4	5.63	16.32
	435315 424240	AA700240	Hs.165402	ESTs	4.06	16.12
30	412446	AB023185 Al768015	Hs.143535	calcium/calmodulin-dependent protein kin	4.69	15.92
	449714	AB033015	Hs.92127 Hs.23941	ESTs	6.44	15.75
	435832	AA425688	Hs.41641	KIAA1189 protein	4.59	15.43
	437397	AA349847	Hs.4221	Bruno (Drosophila) -like 4, RNA binding hypothetical protein DKFZp761H039	4.63	14.97
~ ~	435502	L13266	Hs.105	glutamate receptor, tonotropic, N-methyl	5.93	14.81
35	414187	BE312141		gb:601145962F1 NIH_MGC_19 Homo sapiens c	3.29	14.61
	417868	AJ078534	Hs.122592	ESTs	3.37	14.46
	428536	AJ143139	Hs.2288	visinin-like 1	7.57 5.16	14.22
	402125	c18p3_155		exon	3.10	13.98
40	440503	NM_006539	Hs.7235	calcium channel, voltage-dependent, gamm	3.49	13.94 13.92
70	419090	T85201	Hs.188468	ESIS	3.25	13.79
	437665 457113	AA765417	Hs.292053	ESTs	3.07	13.79
	424933	A1734016 AW999974	Hs.270508	ESTs	3.50	13.69
	443489	AI073512	Hs.5181 Hs.133916	proliferation-associated 2G4, 38kD ESTs	3.59	13.48
45	404289	c6p3_5821	16.155510	exou E218	3.24	13.20
	406534	ph2_4616		exon	3.99	13.12
	423280	AA324037		gb:EST26901 Cerebellum II Homo saplens c	3.89	13.10
	455421	AW937661	Hs.288324	Homo saplans cDNA FLJ13283 ffs, clone OV	3.38	13.03
50	433725	AF063559	Hs.283919	Homo sapiens clone HQ0117 PRO0117 mRNA.	3.04 3.71	12.93
20	416660	R98905	Hs.35992	ESTs	3.92	12.85 12.74
	407593	AW044083	Hs.237008	ESTs	3.85	12.67
	451734	NM_006176	Hs.26944	neurogranin (protein kinase C substrate,	7.41	12.59
	410366 405348	AI267589	Hs.25214	hypothetical protein	7.89	12.50
55	442338	cNp3_13716 Al761976	No 455000	exon	3.45	12.42
	424458	M29273	Hs.156080 Hs.1780	ESTs	3.69	12.35
	431400	AA504607	TIS. 1700	myelin associated glycoprotein	4.72	12.31
	417754	R13027	Hs.268703	gb:aa63a02.s1 NCI_CGAP_GCB1 Homo saplens ESTs	3.42	12.29
~	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	3.35	12.18
60	431339	AA506294	Hs.257268	ESTs	6.15	12.11
	452265	BE501516	Hs.114772	ESTs	3.50	11.97
	419297	AA446040	Hs.98640	Homo sapiens cDNA: FLJ21069 fis, clone C	3.82 3.16	11.96
	424991	AA775471	Hs.241467	ESIS	3.03	11.86
65	431988	AC002302	Hs.77202	protein kinase C, beta 1	3.78	11.64 11.62
05	450987 440607	AA017202	Hs.32794	EST8	3.28	11.61
	454566	AA894559	Hs.192097	ESTs	3.11	11.60
	442000	AW807605 H38671	Hs.8071	gb:MR4-ST0098-120100-001-b06 ST0098 Homo	3.26	11.54
	437948	AA772920	ris.00/1	KIAA0735 gane product; synaptic vesicle	3.44	11.51
70	401081	c11p3_921		gb:se73c09.s1 Strategene schizo brein 81	3.16	11.45
	438919	AW979114		gb:EST391224 MAGE resequences, MAGP Homo	3.18	11.35
	454578	AW809178		gb:MR4-ST0118-261099-012-c07 ST0118 Homo	4.16	11.35
	422279	H69644	Hs.114231	C-type lectin-like receptor-2	3.02	11.27
75	453101	AW952776	Hs.94943	ESTs	3.35	11.13
75	455836	BE145795		gb:MR0-HT0208-101299-103-a12 HT0208 Homo	3.21	11.07
	413324	V00571	Hs.75294	corticotropin releasing hormone	3.61	10.83
	412268	N59006	Hs.26133	ESTs	3.72 3.80	10.71
	436887	AW953157	Hs.193235	ESTs	3.60 7.24	10.60 10.56
80	454968 418162	AW849046		gb:JL3-CT0214-150300-085-H06 CT0214 Homo	3.05	10.55
-55	425537	T11958	Lla 4 FORGA	gb:AB0ZR Heart Homo sepiens cDNA clone A	3.07	10.53
	438230	AB007913 Al248723	Hs.158291	KIAA0444 protein	3.07	10.48
	431169	AW971240	Hs.17711	ESTS	3.09	10.45
				gb:EST383329 MAGE resequences, MAGL Homo	3.02	10.43

	447750	NILL 042002	Us tones		4.5	
	447359 457187	NM_012093 AA443927	Hs.18268 Hs.144360	adenylate kinase 5	5.91	10.40
	407539	X91103	15.144000	gb:H.sapiens mRNA for Hr44 protein.	3.30	10.39
	452855	R17746	Hs.84469	ESTs	3.02	10.35
5	440352	A1692322	Hs.65373	ESTs ·	3.02 3.03	10.26
	456116	728528	Hs.172004	Œn .	3.11	10.20 10.17
	458172	BE007237		gb:PM0-BN0139-050500-003-g09 BN0139 Homo	3.32	10.14
	445881	Al263029	Hs.210689	ESTs	3.04	10.11
10	454059	NM_003154	Hs.37048	statherin	3.27	9.97
10	402624	c1p1_2660		excon	3.05	9.94
	441539	AA937200	Hs.192939	EST ₈	3.27	9.82
	412172	N76794		gb:yv45g07.r1 Soares fetal liver spleen	3.03	9.78
	427942	AA417858		gb:zvQ1d05_r1 NCI_CGAP_GCB1 Homo sapiens	4.09	9.73
15	436887	BE041837	Hs.120316	ESTs	3.25	9.73
13	454688	AW814472		gb:MR3-ST0203-010200-109-b06 ST0203 Homo	3.41	9.73
	446122	Al362790	Hs.181801	ESTs	3.40	9.71
	420480	AL137381	Hs.98173	hypothetical protein	3.03	9.56
	433447	U29195	Hs.3281	neuronal pentraxin II	3.72	9.54
20	407178 415614	AA195651	Hs.104106	ESTs	3.89	9.47
20	450518	F12926	Hs.165998 Hs.270893	DKFZP564M2423 protein	3.06	9.45
	455675	BE245175 BE065984	ris.2/0033	ESTS	3.99	9.39
	456459	AA253074	Hs.146261	gb:RC3-BT0319-120200-014-e06 BT0319 Homo ESTs	3.46	9.32
	423420	AL571364	Hs.128382		4.08	9.30
25	455844	BE064521	115-120002	Homo saplens mRNA; cDNA DKFZp76111224 (f gb:RC4-BT0311-250200-014-d02 BT0311 Homo	5.18	9.23
	419800	AA282392	Hs.191525	ESTs	3.02 3,28	9.20
	430964	Y10929	Hs.248167	zinc finger protein 186 (Kruppel type)	3.26 3.04	9.16
	409716	AL117454	Hs.56027	Homo sapiens mRNA; cDNA DKFZp586J1717 (f	3.02	9.00
	412962	AW839578	Hs.18160	Homo sapiens cDNA FLJ11550 fis, clone HE	3.33	9.00 8.99
30	445040	AW444934	Hs.195929	ESTs, Wealthy similar to pre-serum emylol	3.50	8.96
	451496	AW503407		gb:UI-HF-BNO-akw-d-11-0-UI_r1 NIH_MGC_50	3.17	8.94
	424617	AA344151		gb:EST50059 Gall bladder I Homo sapiens	3.25	8.91
	441914	AA971496	Hs.128465	ESTs	3.42	8.88
26	405320	cNp3_12168		exon	3.30	8.84
35	449179	AI633785	Hs.196561	ESTs	3.43	8.84
	400335	Y13187	Hs.248066	Homo sapiens dmd gene, intron 11	3.13	8.78
	454962	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	4.16	8.74
	407803	AW081681	Hs.269064	ESTs	3.09	8.73
40	455260	AW878317		gb:MR3-OT0007-260300-206-e09 OT0007 Homo	3.78	8.70
40	431096	AA324358	Hs.249227	Homo sapiens DNA, cosmid clones TN62 and	4.01	8.67
	424481	R19453	Hs.1787	proteolipid protein (Pelizaeus-Merzbache	8.12	8.63
	407616	AW054849	Hs.246831	ESTs, Weakly similar to CIKG_HUMAN VOLTA	3.08	8.53
	434589 439239	AF147363 Al031540	U- 000004	gb:Homo saplens full length insert cDNA	3.26	8.51
45	410926	AW810708	Hs.235331	ESTS	5.78	8.48
	430004	U27768	Hs.227571	gb:MR2-ST0129-051099-007-g07 ST0129 Homo	3.34	8.47
	409623	AW4491B5	113.22/07	regulator of G-protein signalling 4 gb:Ul-H-Bi3-akg-e-05-0-Ul.s1 NCI_CGAP_Su	4.26	8.45
	420156	AW449258	Hs.6187	ESTs	3.32	8.43
	411555	AF113537	Hs.70669	HMP19 protein	3.40 5.85	8.38 8.34
50	408509	AA497035	Hs.110502	ESTs	3.17	8.34
	442368	AI698577	Hs.2024B1	ESTs	3.02	8.33
	457870	AA732217	Hs.294054	EST8	3.04	8.32
	437254	AAB31258		gb:oc73f04.s1 NCI_CGAP_GC81 Homo septens	3.35	8.24
55	415508	R39236		gb:yc91d03.s1 Soares Infant brain 1NIB H	3.07	8.22
55	409483	U49379	Hs.54506	diacylglycerol kinase, epsilon (64kD)	3.31	8.20
	435229	AA676558	Hs.269515	ESTs, Moderately similar to ALUB_HUMAN!	3.21	8.19
	458120	W21358	Hs.54523	ESTs, Wealdy similar to cytochrome P-450	3.22	8.17
	444613	H29627	Hs.79092	ESTs	3.78	8.16
60	41.7050 425607	N39540 U09860	Hs.108029	ESTs .	4.06	8.14
••	413263	BE075131	Hs.158333	protesse, serine, 7 (enterokinase)	3.68	8.06
	424549	AI873205	Hs.183114	gb:PM1-BT0585-110200-003-g03-BT0585 Homo Homo sapiens cDNA FLJ14238 fis, clone NT	3.40	8.04
	452689	F33868	Hs.284176	transferrin	3.27	8.03
	405476	cNp3_19940	110,204170	exou	3.03	8.01
65	403932	c5p1_533		exon	3.28 3.58	8.00 7.99
	407095	AF011757	Hs.105937	RAGE binding protein	3.32	7.96
	415967	H11124		gb:ym14h07.s1 Soares Infant brain 1NIB H	3.10	7.96
	417555	H65368		gb:yr67c10.r1 Soares fetal liver spleen	3.05	7.95
70	448985	AA324885	Hs.22777	carbonic anhydrase XI	5.30	7.79
70	428689	NM_014351	Hs.189810	sulfotransferase-related protein	3.87	7.74
	424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	4.68	7.74
	441099	AW339393	Hs.126573	ESTs	3.08	7.74
	448589	AF017090	Hs.21554	KIAA1107 protein	3.10	7.73
75	408112	ph0_24243		exon	3.22	7.70
13	458439	AV647220	Hs.282889	ESTs, Weakly similar to strong similarit	3.22	7.69
	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	3.15	7.68
	412090 413547	AW955826	Hs.12398	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.01	7.67
	447772	8E147440 Al924558	He 404300	gb:RC1-HT0229-080100-015-09 HT0229 Homo	3.01	7.66
80	411132	AW819191	Hs.161399	EST8	3.04	7.63
	425490	NM_002248	Hs.158173	gb:CM1-ST0283-071299-061-d08 ST0283 Homo potassium Intermediate/small conductance	3.72	7.61
	454568	BE141434		gb:MR0-HT0079-051099-002-d01 HT0079 Homo	3.15	7.60
	439099	AB037800	Hs.6462	KIAA1379 protein	3.16	7.59 7.57
					3.40	7.57

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	415669 428175	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	5.71	7.57
	413162	A1810774 BE068115	Hs.98376	ESTs gb:CM1-BT0368-051299-060-g07 BT0368 Homo	3.04	7.55
_	451361	AA053854	Hs.235390	Homo sapiens mRNA; cDNA DKFZp7618101 (fr	3.43 3.11	7.54 7.53
5	442527	AF150289	Hs.205436	ESTs	3.31	7.53
	450407	NM_000810	Hs.24989	gamma-aminobutyric acid (GABA) A recepto	5.24	7.53
	456966 441799	AJ589569 AW292276	Hs.190082 Hs.127872	ESTs	3.13	7.47
	424185	AA279752	Hs.142570	Homo sapiens clone 24529 mRNA sequence	3.38 3.16	7.41 7.40
10	429783	AA811987	Hs.125779	ESTs	3.13	7.38
	429268	AA205386	Hs.198481	RAR-related orphan receptor B	3.48	7.38
	400708 402598	c11p1_1292 BE314624	Hs.3128	exon polymerase (RNA) II (DNA directed) polyp	3.33	7.35
	455377	AW905347	115.5120	gb:QV2-NN1073-220400-159-108 NN1073 Homo	3.04 3.03	7.33 7.33
15	435070	AI821270	Hs.116930	ESTs	3.03	7.33
	405427	cNp3_17682		exon	3.03	7.25
	455149 402818	AW861879 c1p3_2531		gb:CM0-CT0341-260100-160-h12 CT0341 Homo exon	3.56	7.24
	422890	Z43784	Hs.78713	solute carrier family 25 (mitochondrial	3.13 3.40	7.21 7.15
20	422297	AW961290	Hs.155615	ESTs	3.44	7.10
	412688	AW984068		gb:RC0-HN0006-160300-011-e06 HN0006 Homo	3.91	7.09
	436383 412290	BE065178 BE069037		gb:RC1-8T0314-020200-012-h01 8T0314 Homo	3.09	7.09
	415488	H12214	Hs.13284	gb:QV3-BT0379-161299-040-e12 BT0379 Homo ESTs	3.04 4.22	7.08 7.07
25	407728	AW071502	Hs.175931	ESTs	3.05	7.06
	448548	R13209	Hs.21413	solute carrier family 12, (potassium-chi	5.93	7.05
	417275 418425	X63578 A1871247	Hs.81849 Hs.6262	parvalbumin ESTs	4.08	7.04
	440558	AA889574	Hs.177511	ESTs	4.10 3.28	7.04 7.04
30	411427	AW846080		gb:MR3-CT0176-081099-002-b09 CT0176 Homo	3.11	7.03
	422272	AI452421	Hs.77965	Clk-associating RS-cyclophilin	3.39	7.03
	410816 418375	AW806175 NM_003081	Hs.84389	gb:MR1-UM0108-130400-003-a06 UM0108 Homo	3.30	7.02
	421627	Al138551	Hs.97318	synaptosomal-associated protein, 25kD ESTs	9.93 3.10	7.01 7.01
35	447258	BE047911		gb:tz44a05.y1 NCI_CGAP_Bm52 Homo sapien	3.09	6.99
	455547	AW994078		gb:RC3-BN0036-090200-011-h02 BN0036 Homo	3.35	6.98
	432209 404541	AW971278 c8p1_6409		gb:EST383367 MAGE resequences, MAGL Homo exon	3.49	6.92
	451539	AA059467	Hs.218933	ESTs	4.62 3.01	6.89 6.88
40	429954	AI918130	Hs.21374	ESTs	3.82	6.87
	411138	AW819500		gb:RC5-ST0293-180100-012-C07 ST0293 Homo	3.08	6.87
	447464 454713	AW444957 AW815111	Hs.201897	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.33	6.85
	415734	NM_014747	Hs.78748	gb:QV4-ST0212-091199-023-c09 ST0212 Homo KIAA0237 gene product	3.16 5.00	6.84 6.84
45	429667	AA456275	Hs.44841	ESTs	3.09	6.80
	403008	c21p3_2374		exon	3.04	6.78
	446079 441869	T56522 NM_003947	Hs.154030 Hs.8004	ESTs	3.11	6.75
	437804	AA828257	Hs.124324	huntingtin-associated protein interactin ESTs	4.49 3.42	6.75 6.73
50	436454	AA757615	Hs.291509	ESTs .	3.01	6.72
	416334	H53139	Hs.36271	ESTs	3.12	6.70
	455965 445085	BE167014 AJ569295	Hs.179285	gb:CM2-HT0502-140200-088-d08 HT0502 Homo ESTs	3.05	6.68
	445611	AW418497	Hs.145583	ESTS	3.19 3.61	6.68 6.68
55	437762	T78028	Hs.154679	synaptotagmin 1	7.21	6.68
	416268	H49111		gb:yo21c07.r1 Soares adult brain N2b5HB5	3.02	6.67
	449768 443100	Al668690 Al033188	Hs.54773	ESTs	3.25	6.64
	408070	AW148852		gbtow94e08.s1 Soares_fetat_liver_spleen_ gbtxf05d05.x1 NCI_CGAP_Bm35 Homo sapien	3.07 3.12	6.64 6.60
60	451602	AW008846	Hs.60857	ESTa	3.05	6.59
	441447	AA934077	Hs.126980	ESTs	4.06	6.59
	445078 434501	AI869975 AF14387B	Hs.4775 Hs.194152	junctophilin 3	4.25	6.59
	415980	R49020	Hs.24974	Homo saplens clone IMAGE:115304 mRNA seq ESTs	3.25 3.34	6.58 6.58
65	403395	c3p1_11541		exon	3.59	6.57
	403051	c2p1_10450		exon	3.06	6.58
	419232 425984	A1382037 AW836277	Hs.87421 Hs.165636	ESTs	3.28	6.56
	403717	c4p1_3133	rts.100000	hypothetical protein DXFZp761C07121 exon	6.50 3.52	6.56 6.53
70	452178	AW043576	Hs.171929	ESTs	3.38	6.53
	455758	R15709	Hs.284231	Novel human gene mapping to chomosome 22	4.42	6.52
	433858	N69243	Hs.192974	Homo sapiens cDNA FLJ12735 fis, clone NT	3.58	6.52
	425440 419412	AA357518 AW161058	Hs.90297	gb:EST66256 LNCAP cells I Homo sapiens c synuclein, beta	3.15	6.49
75	423678	AW963357	Hs.7847	ESTs	5.60 3.47	6.47 6.47
	416625	R97839	Hs.35758	ESTa	3.10	6.46
	451854	T92536	Hs.194096		3.28	6.46
	405732 434619	AA487229 H43183	Hs.2064 Hs.32810	vimentin Cora	3.71	6.44
80	413797	BE167274	Hs.5996	ESTs ESTs	3.05	6.44
	438612	AW977980	Hs.292129		3.23 3.39	6.44 6.42
	412317	AW991979		gb:RC1-BN0014-210100-012-f05 BN0014 Homo	3.46	6.42
	422159	N76767	Hs.153408	ESTs	3.03	6.41

	429290	AF203032	Hs.198760	neurofilament, heavy polypepiide (200kD)	3.48	6.35
	427334	R44789	Hs.119486	ESTs, Weakly similar to transmembrane re	3.93	6.35
	453839 429096	AL138417 AB011106	Hs.196012	gb:OKFZp43481729_r1 434 (synonym: htes3)	3.06	6.34
5	444609	AW571659	Hs.278081	KIAA0534 protein ESTs	3.12 3.30	6.33 6.33
•	419515	581944	Hs.90791	gamma-aminobutyric acid (GABA) A recepto	3.11	6.33
	418900	BE207357	Hs.301709	ESTs	3.14	6.30
	437979	AA774318	Hs.121708	ESTs	3.25	6.29
10	410359 415990	R38624 R76929	Hs.106313 Hs.29533	ESTs ESTs	4.74	6.28
10	419392	W28573	113.23033	gb:51f10 Human retina cONA randomly prim	3.39 3.00	6.28 6.28
	424312	AB013452	Hs.144931	ATPase, aminophospholipid transporter (A	3.06	6.26
	444762	Al733700	Hs.143883	ESTs	3.09	6.25
15	447785	AL041765 AA884555	Hs.161423	ESTS	3.05	6.22
13	418199 440582	AA993337	Hs.86603 Hs.129082	ESTs ESTs	3.55 3.73	6.22 6.21
	457766	AL119470	Hs.145631	ESTs	3.69	6.21
	426814	AF036943	Hs.172619	KIAA1106 protein	4.71	6.21
20	412018	BE148152	11	gb:RC4-HT0231-041199-012-b04 HT0231 Homo	3.36	6.21
20	414699 420127	AI815523 AA360399	Hs.76930 Hs.44811	synuclein, alpha (non A4 component of am ESTs	3.68 3.54	6.19
	418833	AW974899	Hs.292776	ESTs	3.08	6.18 6.18
	441265	AA927180	Hs.153261	ESTs	3.21	6.17
25	413408	R51793	Hs.21745	ESTs	3.56	6.15
23	434512 422253	AW139932 W81526	Hs.188941 Hs.118329	ESTs	3.56	6.15
	439950	AW937417	Hs.293561	ESTs	5.04 3.24	6.10 6.10
	417210	N99228	Hs.49162	ESTs	3.54	6.10
30	414306	BE27219B	Hs.283869	Human DNA sequence from clone RP5-1013A2	3.35	6.10
30	411265 412734	AW834695 AW993498		gb:RC0-LT0001-261199-031-D05 LT0001 Hamo gb:RC2-BN0033-170300-019-b08 BN0033 Hemo	3.07	6.10
	425172	AA447729	Hs.12714	ESTs	3.36 5.40	6.09 6.06
	451759	W23161	Hs.32886	ESTs	3.21	6.02
35	432154	AI701523	Hs.112577	EST8	3.50	6.02
55	401313 448951	c13p1_435 Al350575	Hs.156730	exon ESTs	3.92 3.20	5.96 5.95
	440917	AA909651	Hs.160025	ESTs	3.06	5.94
	405961	ph0_14521		exon	3.12	5.91
40	428737 417292	AA984728	Hs.192760	kinesin family member 5A	3.05	5.90
40	448681	N69197 AL109781	Hs.191361 Hs.21754	ESTs Homo saplens mRNA full tength insert cDN	3.62 3.52	5.89 5.88
	452524	AW136499	Hs.29796	Homo sapiens mRNA; cDNA DKFZp434D1319 (f	3.07	5.88
	426575	M74826	Hs.170808	glutamate decarboxytase 2 (pancreatic is	4.08	5.87
45	423641 420755	AL137256 Al699437	Hs.130489 Hs.165268	Homo saplans mRNA; cDNA DKFZp761K0912 (f ESTs	3.28 3.17	5.87 5.86
	448116	AW352276	Hs.170700	ESTs	3.28	5.86
	412694	AW984373		gb:PM3-HN0011-200300-001-f01 HN0011 Homo	3.00	5.83
	437612 411522	AA827715 AW850286	Hs.105153	Homo sapiena cDNA FLJ14230 fis, clone NT	3.09	5.82
50	456910	BE185921	Hs.98073	gb:IL3-CT0219-161199-031-H11 CT0219 Homo ESTs	3.26 3.20	5.81 5.80
	439915	AJ521791	Hs.252358		3.55	5.80
	404403	c8p1_1094		exon	3.23	5.80
	405332 411167	cNp3_13017 AW820204		exan gb:QV2-ST0298-190100-029-c11 ST0298 Homo	3.51 3.04	5.78 5.78
55	416139	H21109	Hs.172853		3.63	5.77
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.65	5.77
	415247 446037	F02431 AI076806	Hs.6581 Hs.282965	ESTs ESTs	3.08	5.75
	450478	AW451709	Hs.271200		3.42 3.80	5.75 5.72
60	446588	AV659343	Hs.282954		3.29	5.72
	413118	BE065939	11- 00545	gb:RC3-BT0319-100100-012-c11 BT0319 Homo	3.03	5.72
	416946 454751	NM_012324 AW819132	Hs.80545	mitogen-activated protein kinase 8 Inter gb:RC3-ST0281-240400-015-c10 ST0281 Homo	3.91 3.06	5.72 5.72
	457194	H20669	Hs.35406	ESTs, Highly similar to unnamed protein	3.54	5.71
65	438601	AAB11713	Hs.163222	ESTs	3.26	5.71
	439032 408940	AA829487 M58583	Hs.274412 Hs.662		3.10	5.67
	437700	AA766060	Hs.122848	cerebellin 1 precursor ESTs	3.32 3.23	5.67 5.66
70	416061	R45518	Hs.25119	ESTs	3.85	5.65
70	452861	BE177663		gb:RC1-HT0598-020300-011-h11 HT0598 Homo	3.04	5.64
	430330 435312	AA476583 AJ243396	Hs.132981 Hs.4865		3.51	5.63
	400710	c11p1_1297		voltage-gated sodium channel beta-3 subu exon	5.67 3.04	5.62 5.61
75	457130	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	3.31	5.60
75	434513	AF143888	Hs.18213	Homo saplens clone IMAGE:121736 mRNA seq	3.93	5.60
	434277 440854	X77748 AW444900	Hs.3786 Hs.246715	glutamate receptor, metabotropic 3 i ESTs	3.67	5.58
	457088	AA412591	Hs.204685		3.30 3.37	5.58 5.57
80	431883	AA731404	Hs.105510) ESTS	3.67	5.56
80	400758	AA158742 AW904039	Hs.225084		3.43	5.55
	455374 440750	AW105131	Hs.245405	gb:CM3-NN1040-200400-156-d03 NN1040 Homo 5 ESTs	3.36 3.10	5.52 5.50
	451865	H43737	Hs.33186	ESTs, Weakly similar to unknown protein	3.38	5.50

PCT/US02/29560

	453100	AW805871	Hs.224788	ESTs		3.30	5.49
	433940	H05129	Hs.7459	cyclic AMP-regulated phosphoprotein, 21		3.24	5.49
	454935 435447	AW846075 AJ872932	: No 440440	gb:MR3-CT0176-081099-002-b02 CT0176 Home	•	3.26	5.48
5	402953	c20p3_3451	Hs.142442	HP1-BP74		3.89	5.47
_	456233	AA203339		exch		3.28	5.47
	407718	AW070784	Hs.243243	gb:zx56a01z1 Soares_fetal_liver_spleen_ EST		3.02	5.47
	417429	AI950629	Hs-286237	Homo saplens cDNA FLJ11841 fis, clone HE		3.30	5.45
	446408	AI797169	Hs.208486	ESTs		3.31	5.38
10	441792	AW873635	Hs.143962	ESTs		3.07 3.19	5.37
	450681	AW952160	Hs.32916	ESTs		3.70	5.35 5.35
	433932	AW954599	Hs.169330	neuronal protein		8.78	5.33
	427002	AA524093	Hs.23158	ESTs		4.00	5.32
15	428741	AA461386		gb:zx70h06.r1 Soares_total_fetus_Nb2HF8_		3.10	5.32
13	446383	T05816	Hs.92511	EST		3.39	5.30
	442988	Al026130	Hs.131683	ESTs		3.07	5.29
	426713 421294	AI655299	Hs.130055	ESTs		3.33	5.29
	406452	AA713488 ph2_21981	Hs.180291	ESTs		3.44	5.28
20	423508	AW604297	Hs.129711	exon		3.20	5.28
_ •	442114	BE217975	Hs.157021	hepatitis A virus cellular receptor 1 ESTs		3.26	5.27
	432508	AJ808915	Hs.190201	ESTs		3.32	5.26
	425604	U94320	Hs.158330	neuropeptide Y receptor Y5		3.46 3.26	5.26
0.0	417925	R26789	Hs_23995	ESTs		3.08	5.23
25	444448	H66317	Hs.143660	ESTs		3.81	5.23 5.22
	413024	AF038268	Hs.75149	SH3-domain GRB2-like 2		3.71	5.22
	437911	AA848010	Hs.124250	ESTB		3.11	5.18
	435406	F26698	Hs.4884	calcium/calmodulin-dependent protein kin		4.95	5.17
30	407131 435776	R98679	I hacanan	gb:yr31c03.s1 Soares fetal (Iver spleen		3.30	5.16 .
-	455532	AI537182 AW984828	Hs.263988	ESTs		3.14	5.13
	457352	AA489099		gb:RC1-HN0015-120400-021-h11 HN0015 Hom		3.14	5.13
	428670	AA431682	Hs.134832	gb:aa56h09.s1 NCI_CGAP_GCB1 Homo saplen ESTs	3	3.48	5.12
	445962	AJ268410	Hs.201386	ESTs		3.17	5.12
35	418153	R13696	Hs.112830	ESTs		3.14	5.12
	440565	AW103823	Hs.131586	ESTs		3.16 3.08	5.10
	431446	AW294929	Hs.255369	Homo saplens cDNA FLJ10265 fis, clone HE		3.42	5.10 5.09
	456036	BE536554	Hs.75839	zinc finger protein 6 (CMPX1)		3.21	5.09
40	420883	AJ735488	Hs.111436	ESTs		3.17	5.08
40	455528	AW984757		gb:RC1-HN0015-040400-011-g10 HN0015 Hom	0	3.35	5.08
	408442	R59608	Hs.21435	ESTs		3.10	5.07
	446093 403489	Al346849	Hs.145896	ESTs		3.30	5.06
	405278	c3p1_2255 cNp3_1070		exon		3.43	5.05
45	412804	H18857	Hs.22547	exon		3.05	5.03
	458407	W90022	Hs.186809	ESTS		3.63	5.03
	407387	AA130773	16.100003	ESTs, Highly similar to LECT2 precursor gb:zo13d01.r1 Stratagene colon (937204)		3.52	5.03
	439108	AW163034	Hs.6467	synaptogyrin 3		3.51	5.02
~ ^	445335	AI220339	Hs.166775	ESTs		5.63 3.21	5.01
50 .	435404	AI240661	Hs.124995	ESTs		3.99	5.01 5.00
						3.33	5.W
	TABLE 68						
	Pkey:			et identifier number			
55	CAT numb Accession		cluster numb				
J J	ACCOSSION	. Gent	ank accession	numbers			
	Pkey	CAT Number	Accounts				
	410837	282574_1		MARGE ACO OFFICE AT DEPOS AND ALLEGO AS ALLEGO			
	436812	659779_1	AW978773	AW866469 BF898475 BF898476 AW866540 AW8 AW298067 AA810101 AW194180 AA731645 AJ69	66614 BE145698 AV	886575	
60	454171	1049240_1	AW854832	AW854798 AW854857 AW854816 AW854834 AW	UD/3		
	454589	28039_6	BG674750 E	3F374578 AW810080 AW810106 AWR10084 DC3	03401/ 7/766 AMMONDOM DE	33 439 4 DEG	74590 BF374594 AW809699 BF374588 AWB10437
		_	AW810161 /	AW809562 AW810151	14132 WAA003051 DL	3/4/34 8F3	4590 BF374594 AW809699 BF374588 AW810437
	417159	2075888_1	R01760 N49	7787 R01761			
CE	459349	1027822_1	AW749381 I				
65	414187	315279_1	BE259777 B	E312141 BF942980			
	423280	881045_1		H86636 AA324037			
	431400	1233918_1	AW969094 /	AA504607 AA504705			
	454566	164604_1	AW807605 /	AW807690 AW807677 AW807752 AW807673 AW	807900 AW807955 A	W807679 A	N807615 AW807917 AW807849 AW807832 AW807821
70							
, •							
	437948	330397_1		AW807952 AW807918 AW807670 AW807760 AW 059870 D61151 AI591331 BF960996	807508 AW	W807683 A	W807839 AW807601 AW807822 AW807898
	438919	1242818_1	AW979114	AA828060 AA837606 AA829203			
75	454578	1670_3	BE150647 A	W971143 AWR09224 AWR09221 RE753820 AWR	00000 AIADOO430 **	U000450 AT	MARARE 111000100
	455836	1518824_1	9E 143600 E	1E 14332 DE 1430/3 DE 1458/1 MF1454(I) HE146	707 054 85705		8U9195 AW809175
	454968	1085677_1	AW848279	AW849039 AW847956 AW847957 AW849046 AW	7.4.502 VANDAGUSA V	VARIA DOSS	
	418162	2189291_1	111756 120	135 119729 111958 111815 R45874	e recover nerocate A	************	
80	431169	1235760_1	AW971240	AA493723 AA493843			
90	458172	363900_1	BE007237 E	BE546311 AA984819 BI256810 W19919 BE00726	3 8G000322 BF3270	11 AA89019	3 BE007496
	412172	709034_1	4404120 WM	109/333 N99221			
	427942 454588	465847_1 1066481_1	BE543851 A	A417856 AV756446 BG\$05084 BI460307 BI4609	93 BG613293		
	707000	.~~~1	BF3/5123 A	W814472 AW814474 AW813343 AW816161 AW8	313380 AW813300		

	455675	1490763_1	DEGESOOA O	PERSONS DEPOSED IN PROCESS
	455644	1489581_1		ED66085 BE085942 BE065956
	451496	85420_1		E064441 BE064426 BE064285 BE064286
	424617	895912_1		F327988 AW503407 AA018131 AA344151 AA344472
5	454962	323094_1		
_	455260	231032_1	DE161DOE A	AW854083 BF962818 AW847791 BI035483 AW847645 BF961514 BF963484 BF952264 BF963521
	434589	14876_1		W876317 BE161759 BF870032 BF869588 47219 T47218
	410926	1084369_1		47213 147210 AW810808 AW810771 AW810924
	409623	830636_1		BE220971 AW449185
10	437254	1239876_1		AA831258 AA765857 AA747712 AJ784019
	415508	1874742_1		822 R39738
	413263	1497122_1		E075131 BE075130 D60395 BF688035
	415957	1899490_1	H49130 H11	1230 BF363165 H49061 H11124
	417555	1978200_1		N.697143 H65368
15	413547	1520005_1		SE147563 BE147708 BE147440
	411132	1070974_1	AW819177	AW819242 AW819191 AW819175 AW819252 AW819244 AW819265 AW819269 AW819190 AW819268 AW819183 AW819246 AW819194
			AW819249	AW819188 AW819180 AW819189 BE158470 AW819251 BE152602 AW819263
	454568	1061859_1	AW807909	AW807824 AW807826 AW807903 AW807766 AW807750 AW807911 BE141434 AW807611 AW807837 AW807899 BF374481
~~	413162	1492355_1	BE058104 E	3E058096 BE058198 BE068115 RE068102 RE068154 RE068103
20	455377	154707_1	BF947516 A	W905291 BF947512 BF952606 BF952706 BF952525 BF952524 BF952619 BF947500 BF952608 BF952523 BF952532 BF952344
			BF746516 E	3F947614 BF746511 BF952358 AW905400 AW905300 BF947617 AW905349 BF952531 AW905403 BF952528 BE081655 8F746513
			AW905286	BF952868 BF947513 BF947510 BF947618 BF947619 AW905347
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	411427	1083097_1		AW846074 AW846118 AW846130
	410816	1060611_1	AW806175	AW806176 AW806170 AW806156
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	454713	1071173_1		AW819503 AW819481 AW819459 BF375618
	455965	1067889_1 1555935_1		AW815094 AW815218
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	443100	416959_1		
	408070	632273_1	AW148852	AW804074 BE089437 BE089439 BE089378 BE089438 BE004795 W02375 Al033188 BF332422 BF332418 BE178660 BG994152
	425440	1228191_1		AA357518 AA360531
	412317	1164038_1		AW991981 AW991983 AW936856 AW991977 AW991971 AW936852
40		3209657_1	AL138417 /	
	419392	215562_2	W28573 W	
	412018	147109_1	BE148133	BE148132 BF736564 BE148152 BE148159 BF893700
	411265	1074383_1		AW834717 AW834714
15	412734	1245451_1	AW993498	AW993484 AW993490 BF512974
45		1243393_1	AW984388	AW984392 AW984379 AW984351 AW984381 AW984377 AW984366 AW984348 AW984391 AW984373 AW984372 AW984353 AW984362
	411522	1089092_1	BE143505	BF374194 BF374190 AW850286
	411167	1071740_1	AW820323	AW820314 AW820321
	413118 454751	1490760_1 1070838_1	BE0650/9	BE065939 BE065956
50	452861	319757_1	AVV019132	AW819122 AW819018 AW819135 AW819126 AW819024 AW819012 AW819141 AW994738 AJ923735 BF948431 BF948329
-	455374	1161013_1		AW904030 AW904039 AW904031 AW904032 AW904046
	454935	1083098_1	AWR48075	AW846103 BF333976 AW846077 AW846122 AW846129 AW846095 AW846078 BF333979 BF333978 AW846092
	456233	2635744_1	AA203339	A996160 A929005
	428741	1384399_1		AAA33841 AAA33845
55	455532	1243692_1		AW984787 AW984806 AW984817 AW984826 AW984822 AW984773 AW984786 AW984803 AW984796
	457352	1233795_1	AW968968	AA489099 N72933 AA489184
	455528	1243660_1		AW984757 AW984797 AW984745
	407387	4907_1	AF085983	H72550 H72951 AA130773
60	-in-	_		
UU		-		
	Pkey:	Uni	dae unweet co	presponding to an Eos probeset
	Ref:	Sec	quence source.	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. Dunham, et al. refers to the publication entitled The DNA
	Strand:	seq	DRINGS OF HOME	si chromosome 22" Dunnam, et al. (1999) Nature 40:2489-495.
65	, ouanu: Ni_posifi	indi	CEIES UNA SU	and from which exons were predicted.
	· · Christia	u. Bra	Laios Hucieouc	ta positions of predicted exons.
	Pkey	Ref	Strand	Nt_position
	401412	7940103	Minus	43347-45776
	406230	7249032	Minus	97493-97682
70	402125	4033680	Plus	172732-172868
	404289	2769644	Plus	15049-15286,30267-30457
	406534	7711477	Plus	40463-40586,41191-41336,41856-41986,4300
	405348	2914717	Minus	43310-43462
75	401081	3478647	Plus	105163-105306
75		7885063	Minus	31308-31439
•	405320	3478667	Minus	118511-118926,119175-119331
	405476	2121229	Plus	69890-70883
	403932	7454203	Minus	8142-8753
80	406112	9133145 7249204	Plus	6183-62028
	405427	7243204	Plus Minus	118115-119445
	402816	6723302	Minus	6509-6729 : 25104-25291
	404541	8318559	Plus	103456-103664

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6070398
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                    403395
                                         9438353
                                                                                                144947-145075
                                                                     Minus
                    403061
                                         8954192
7259747
                                                                                                142875-143008
                    403717
                                                                     Minus
                                                                                               79166-79758
   5
                    401313
                                         9212516
                                                                      Minus
                                                                                                190842-191090
                    405961
                                         8190197
                                                                                                45132-45254
                                                                      Plus
                    404403
                                         7272157
                                                                                               72053-72238
                                                                     Minus
                    405332
                                         3169141
                                                                                                70483-71207
                    400710
                                         7249204
                                                                     Phis
                                                                                                158753-157120
10
                    402953
406452
                                         9408724
9588380
                                                                      Minus
                                                                      Minus
                                                                                               76322-76427
                    403489
                                          7331314
                                                                      Minus
                                                                                                38897-39212
                    405278
                                         6139075
                                                                     Minus
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15
                    TABLE 7A: EXTENDED GLIOBLASTOMA SEQUENCES: This table includes sequence information for 21 DNA and protein sequences
                    Gene name: Protein tyrosine phosphatase, receptor-type, Z polypeptide 1
                    Unigene number:
                                                                  Hs.78867
20
                    Probeset Accession #: M93426
Nucleic Acid Accession #: NM_002851
                    Coding sequence: 148-7092
                                                    11
                                                                                    21
                                                                                                                                                    41
                                                                                                                                                                                    51
25
                    CACACATACG CACGCACGAT CTCACTTCGA TCTATACACT GGAGGATTAA AACAAACAAA
                                                                                                                                                                                                                             60
                   CAAAAAAAA ATTTCCTTCG CTCCCCCCC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA
CGGCAGGGG CCGCAGACCG TCTGGAAATG CGAATCCTAA AGCGTTTCCT CGCTTGCATT
CAGCTCCTCT GTGTTTGCCG CCTGGATTCG GCTAATGGAT ACTACAGACA ACAGAGAAAA
CTTGTTGAAG AGATTGGCT GTCCTATACA GGAGCACTGA ATCAAAAAAA TTGGGGAAAG
                                                                                                                                                                                                                          120
                                                                                                                                                                                                                          180
                                                                                                                                                                                                                          240
                                                                                                                                                                                                                          300
30
                   AMATATCCAA CATGTAATAG CCCAAAACAA TCTCCTATCA ATATTGATGA AGATCTTACA
CAAGTAAATG TGAATCTTAA GAAACTTAAA TTTCAGGGTT GGGATAAAAC ATCATTGGAA
AACACATTCA TTCATAACAC TGGGAAAACA GTGGAAATTA ATCTCACTAA TGACTACCGT
GTCAGCGGAG
GAGTTTCAGA AATGGTGTTT AAAGCAAGCA AGATAACTTT TCACTGGGGA
                                                                                                                                                                                                                          420
                                                                                                                                                                                                                          480
                                                                                                                                                                                                                          540
                    AAATGCAATA TOTCATCTGA TGGATCAGAG CATAGTTTAG AAGGACAAAA ATTTCCACTT
GAGATGCAAA TCTACTGCTT TGATGCGGAC CGATTTTCAA GTTTTGAGGA AGCAGTCAAA
                                                                                                                                                                                                                          600
35
                                                                                                                                                                                                                          660
                    GGAAAAGGGA AGTTAAGAGC TTTATCCATT TTGTTTGAGG TTGGGACAGA AGAAAATTTG
GATTTCAAAG CGATTATTGA TGGAGTCGAA AGTGTTAGTC GTTTTGGGAA GCAGGCTGCT
                                                                                                                                                                                                                          720
                   GATTICARAG CGATTATTGA TGGAGTCGAA AGTGTTAGTC GTTTTGGGAA GCAGGCTGCT
TTAGATCCAT TCATACTGTT GAACCTTCTG CCAAACTCAA CTGACAAGTA TTACATTTAC
AATGGCTCAT TGACATCTCC TCCCTGCACA GACACAGTTG ACTGGATTGT TTITAAAGAT
ACAGTTAGCA TCATCCTGAAAG CCAGTTGGCT GTTTTTTGTG AAGTTCTTAC AATGCAACAA
TCTGGTTATG TCATCCTGAT GGACTACTTA CAAAACAAT TTCGAGAGCA ACAGTACAAG
TCTCTCTAGAC AGGTGTTTC CTCATACACT GGAAAGAAT ATACCAGCCT TCTTGTTACA
TGGGAAAGAC CCAGAAAATGT TCAGGCTGAC CCAGAGAATT ATACCAGCCT TCTTGTTACA
TGGGAAAGAC CTCGAGTCGT TTATGATACC ATGATTGAGA AGTTTGCACT TTTGTACCAG
CAGTTGGTT GGAGGACCA AACCAACCAT CAATTTCAACACT TTTGTACCAG
CAGTTGGTT GGAGGACCA AACCAACCAT CAATTTCAACACTCCTTT
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40
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                   1200
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                    ANCTIGICOS GACCICCAGA ATCCITARAT ACAGITICIA TACAGGATA TOAGGAGGAGA AGITTATIGA CCAGITICAA GCITGATACI GAGCIGAAG ATCCITACAG CICCAGICCC GCAACITCIG CATCICCAT CATCICCAGA AACATATCC AAGGGTATA ATTITCCTCC GAAAAACCCAG AACCATAACA ATATGATGC CITATACCAG AATCTCCTAG AAATCCTCC
                                                                                                                                                                                                                       1860
                                                                                                                                                                                                                       1920
                                                                                                                                                                                                                       2040
                    GAAGATTCAA CITCATCAGA TACAGAGAA TCACTAAAGG ATCCTTCTAT GGAGGGAAAT
GTGTGGTTTC CTAGCTCTAC AGACATAACA GCACAGCCCG ATGTTGGATC AGGCACAAGA
AGCTTTCTCC AGACTAATTA CACTGAGATA CGTGTTGATG AATCTGAGAA GACAACCAAG
TCCTTTTCTC CAGGCCCAGT GATGTCACAG GGTCCCTCAG TTACAGATCT GGAAATGCCA
                                                                                                                                                                                                                        2100
  60
                                                                                                                                                                                                                       2160
                                                                                                                                                                                                                       2220
                                                                                                                                                                                                                       2280
                    CATTATTCTA CCTTTGCCTA CTTCCCAACT GAGGTAACAC CTCATGCTT TACCCCATCC TCCAGACAAC AGGATTTGGT CTCCACGGTC AACTGGTAT ACTCGCAGAC AACACAACC GTATACAATG GTGAGGTACC TCTTCAACCT TCCTACAGTA GTGAAGTCTT TCCTCTAGTC ACCCCTTTGT TGCTTGAACA TCAGATCCTC AACACTACCC CTGCTGCTTC AAGTAGTGAT
                                                                                                                                                                                                                        2340
                                                                                                                                                                                                                       2400
  65
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                    TOGGCOTTOC ATGGTCACCC TETRATICC AGCGTCGATC CAGCTGGTTC AGGTAGTGGT TCTCCTCATC ATGGTCATCCA ATGGTCACCC TTTCCTCATC ATGGTCACCC TTTCCTCATC TTTCCTCATC TTCCTCATC TAGTGAATT TTTCCCCATC TCCATACAGT TTCTCAAATC CTTCCACAAG TTACTTCAGC TACCGAGAGT GATAATGGTC CTTCCTCACA GTGGTTGGG GTGATTTGCT ATTAGAGCCC AGCCTTGCTC AGTATTCTGA TGTCCTCTCA ACTACTCATG CTGCTTCAGA GACGCTGGAA TTTCTCAAGT ATACAGCCC AGCCTTGGTA AATCTCGTGT TCTTTATAAA ACGCTTATTT TTTCTCAAGT TGAACCACCC
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  70
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                    TITGGTAGTG AATCTGGTGT TCTTTATAAA ACGCTTATGT TTTCTCAAGT TGAACCACCC AGCAGTGATG CCATGATGCA TGCACGTTCT TCAGGGCCTG AACCTTCTTA TGCCTTGTCT GATAATGAGG GCTCCCAACA CATCTTCACT GTTTCTTACA GTTCTGCAAT ACCTGTGCAT GATTCTGTGG GTGTAACTTA TCAGGGTTCC TTATTTAGCG GCCCTAGCCA TATACCAATA CCTAAGTCTT COTTAATAAC CCCAACTGCA TCATTACTGC AGCCTCATCA TGCCCTCTCT GGTGATGGGG AATGGTCTGG AGCCTCTTCT GATAAGTGTAT TTCTTTTACC TGACACAGAT GGGCTGACTG GTGCTTTTG GTGAACTTTC ATTACCACCA TCTGTGTTTTG GTGAACTGC AAATTCCTTC TTCAACAGA AGGGTCTACC CTCTGTAGAACTGC AAATTCCTTC TTCAATGAG ATGGTTTAC CTTCTGTAAAG CACAGTCATG CCCAACAGAT TAGAGTAGTTG AAATTAATTTA AAATTAATTTG AAATTAAGTTG AAATTAACTTT ATTACAACTA CCCCAACAGAT TAGAGTATTAC CTTCTGTATCC CTCCAACAGTT AGAGTATATG AAATTAAGTTG AAATTAAGTTG AATGGGTCTT TACAAGGAAC CTCTGTTTCC
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                     ACTGRACTIC ARATTCCTTC TTTCAATGAG ATGGTTTACC CITCTGAAAG CACAGTCATG
CCCAACATGT ATGATAATGT AAATAAGTTG AATCCGTCTT TACAAGAAAC CTCTGTTTCC
ATTTCTAGCA CCAAGGGCAT GTTTCCAGGG TCCCTTGCTC ATACCCACCAC TAAGGTTTTT
GATCATGAGA TTAGTCAAGT TCCAGAAAAT AACTTTTCAG TTCAACCTAC ACATACTGTC
TCTCAAGCAT CTGGTGACAC TTCGCTTAAA CCTGTGCTTA GTGCAAACTC AGAGCCAGCA
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	ACCTCAGCTT	CTTTTAGTAC	TGAAATGTTA TGAAGTATTG	CTACAACCTT	CTCAGCTCTT	ATTTTATGAG	3660 3720
	GACACCTTGC	TTAAAACTGT	TCTTCCAGCT	GTGCCCAGTG	ATCCAATATT	GGTTGAAACC	3780
5	CCCAAAGTTG	ATAAAATTAG	TTCTACAATG	TTGCATCTCA	TTGTATCAAA	TTCTGCTTCA	3840
3	agtgaaaaca	TGCTGCACTC	TACATCTGTA	CCAGTTTTTG	ATGTGTCGCC	TACTTCTCAT	3900
	GTTTTTTA	DARGERADAG	TTCCCACCAA	ATTICCTATG	CAAGTGAGAA	ATATGAACCA	
	TTGTTCCAAA	CGGCCAATTT	GGAGATTAAC	CAGGCCCATC	CCCCABABGG	AAGGCATGTA	4020
••	TTTGCTACAC	CTGTTTTATC	AATTGATGAA	CCATTAAATA	CACTAATAAA	TAAGCTTATA	4140
10	CATTCCGATG	AAATTTTAAC	CTCCACCAAA	AGTTCTGTTA	CTGGTAAGGT	ATTTGCTGGT	4200
	ATTCCAACAG	TTGCTTCTGA	TACATTTGTA	TCTACTGATC	ATTCTGTTCC	TATAGGAAAT	4260
	TTCCTCTTTC	CTTCTAAGG	AACTTCTCCC	CACAGAGATG	GTTCTGTAAC	CTCAACAAAG TGATGCCGGT	4320
	TTAGTGGGTG	GTGGTGAAGA	TGGTGACACT	GATGATGATG	GTGATGATGA	TGATGACAGA	4380 4440
15	GATAGTGATG	GCTTATCCAT	TCATAAGTGT	ATGTCATGCT	CATCCTATAG	AGAATCACAG	4500
	Gaaaaggtaa	TGAATGATTC	AGACACCCAC	GAAAACAGTC	TTATGGATCA	GAATAATCCA	4560
	ATCTCATACT	CACTATCTGA	GAATTCTGAA CAGAAGTCCT	GAAGATAATA	GAGTCACAAG		4620
	CAAAAGCACA	ATGATGGAAA	AGAGGAAAAT	GACATTCAGA	CTTGGTAGTGC	TCTGCTTCCT	4680 4740
20	CTCAGCCCTG	AATCTAAAGC	ATGGGCAGTT	CTGACAAGTG	ATGAAGAAAG	TGGATCAGGG	4800
	CAAGGTACCT	CAGATAGCCT	TAATGAGAAT	GAGACTTCCA	CAGATTTCAG	TTTTGCAGAC	4860
	ACTAATGAAA	AAGATGCTGA	TGGGATCCTG	GCAGCAGGTG	ACTCAGAAAT	AACTCCTGGA	4920
						CCACGTTTCA GGGGTTGGAA	4980
25	TCCGAGAAGA	AGGCAGTTAT	ACCCCTTGTG	ATCGTGTCAG	CCCTGACTTT		5040 5100
	GTGGTTCTTG	TGGGTATTCT	CATCTACTGG	AGGAAATGCT	TCCAGACTGC	ACACTTTTAC	5160
	TTAGAGGAÇA	GTACATCCCC	TAGAGTTATA	TCCACACCTC	CAACACCTAT	CTTTCCAATT	5220
	TCAGATGATG	TCGGAGCAAT	TCCAATAAAG	CACTTTCCAA	AGCATGTTGC	AGATTTACAT	
30	AGCTGTACTG	TTGACTTAGG	AGAATTTGAG	GACACTGAAAG	AGTTTTACCA	CAACAAGCAC	5340
	AAGAATCGAT	ACATAAATAT	CGTTGCCTAT	GATCATAGCA	GGGTTAAGCT	AGCACAGCTT	5460
	GCTGAAAAGG	ATGGCAAACT	GACTGATTAT	ATCAATGCCA	ATTATGTTGA	TGGCTACAAC	5520
	AGACCAAAAG	CTTATATTGC	TGCCCAAGGC	CCACTGAAAT	CCACAGCTGA	AGATITCTGG	5580
35	GGAAGGAGAA	GGGAACATAA AATCTCATCA	TGIGGAAGTT	ATTGTCATGA	TAACAAACCT	CGTGGAGAAA CGGGAACTTT	5640
	CTGGTCACTC	AGAAGAGTGT	GCAAGTGCTT	GCCTATTATA	CTGTGAGGAA	TTTTACTCTA	5700 5260
	AGAAACACAA	AAATAAAAA	GGGCTCCCAG	AAAGGAAGAC	CCAGTGGACG	TGTGGTCACA	5820
	CAGTATCACT	ACACGCAGTG	GCCTGACATG	GGAGTACCAG	AGTACTCCCT	GCCAGTGCTG	5880
40	ACCITIGIGA	GAAAGGCAGC	CTATGCCAAG	CGCCATGCAG	TGGGGCCTGT	TGTCGTCCAC	5940
	ATTCAACACG	AAGGAACTGT	CARCATATTT	GGCTTCTTAA	AACACAGTAT	GTTGCAGCAG TTCACAAAGA	6000
	AATTATTTGG	TACAAACTGA	GGAGCAATAT	GTCTTCATTC	ATGATACACT	GGTTGAGGCC	6120
	ATACTTAGTA	. Aagaaactga	GGTGCTGGAC	AGTCATATTC	ATGCCTATGT	TAATGCACTC	6180
45	CTCATTCCTG	GACCAGCAGG	CAAAACAAAG	CTAGAGAAAC	AATTCCAGCT	CCTGAGCCAG	6240
73	CAAATATAC	CTATCATCC	TOTOGRADO	GCCCTAAAGC	AATGCAACAG	GGAAAAGAAT CCTGAGTGGA	6300
	GAAGGCACAG	ACTACATCAA	TGCCTCCTAT	ATCATGGGCT	ATTACCAGAG	CAATGAATTC	6420
	ATCATTACCC	: AGCACCCTCT	CCTTCATACC	ATCAAGGATT	TCTGGAGGAT	GATATGGGAC	6480
50	CATAATGCCC	: AACTGGTGGT	TATGATTCCT	GATGGCCAAA	ACATGGCAGA	AGATGAATTT	6540
50	GTTTACTGGC	CAAATAAAGA	TGAGCCTATA	AATTGTGAGA	GCTTTAAGGT	CACTCTTATG CTTTATCTTA	6600
	GAAGCTACAC	AGGATGATTA	TGTACTTGAA	GTGAGGCACT	TTCAGTGTCC	TARATGGCCA	6720
	AATCCAGATA	GCCCCATTAG	TAAAACTTTT	GAACTTATAA	GTGTTATAAA	AGAAGAAGCT	67B0
55	GCCAATAGGG	ATGGGCCTAT	GATTGTTCAT	GATGAGCATG	GAGGAGTGAC	GGCAGGAACT	6840
23	CACCTACCC	TGACAACCCT	TATGCACCAA	CTAGAAAAAG	AAAATTCCGT	GGATGTTTAC	
	CAGTTTCTCT	TADTDAAAAA 1	CCTCAGCCTT	CCAGGAGICI	COCACONAGA	TGAGCAGTAT GAATCCATCC	6960 7020
	ACCTCTCTG	ACAGTAATGG	TGCAGCATTG	CCTGATGGAA	ATATAGCTGA	GAGCTTAGAG	7020
60	TCTTTAGTT	T AACACAGAAA	GGGGTGGGGG	GACTCACATO	TGAGCATTGT	TTTCCTCTTC	7140
OO	CTAAAATTAC	GCAGGAAAAT	CAGTCTAGTI	CTGTTATCTG	TTGATTTCCC	ATCACCTGAC	
	TTTGCAAGITI	- AIGACAIAGG	CTTATTATCA	TTGAATTTATA	TCATTAACAA	TGTGTGCCTT	7260
						ATTTCAATTT	7320 7380
65	ATAGAGGTT	GGAATTCCAA	ACTACAGAAA	ATGTTTGTTT	TTAGTGTCAR	ATTTTTAGCT	7440
03	GTATTTGTAG	CAATTATCAC	GTTTGCTAGA	AATATAACTI	TTAATACAGI	AGCCTGTAAA	7500
	TARARCACTO	TTCCATATGA	TATTCAACAI	TTTACAACTO	CAGTATTCAC	CTAAAGTAGA ATTTATATTT	7560
	ATAATTGTA	ATTTTTATA	TTTACTACTO	AGTCAAGTTT	TOTAGACCA	TGTAATTGTT	7620 7680
70	TAGTTTAATY	2 ACGTAGTTC	\ TTAGCTGGT(TTACTCTACC	: AGTTTTCTGA	CATTGTATTG	7740
70	TGTTACCTA	A GTCATTAACI	TTGTTTCAGG	ATGTAATTT	AACTTTTGTO	GAAAATAGAA	7800
	ATACCTTCA	TTTGAAAGA	GTTTTTATG	GAATAACAC	TTACCAAAC	TTGTTCAAAT	7860
	GGITTTTAN	A AAAAAAAA	GAAAAATAA	TATAAATAT	GCCATTAAA	AAAAAAAA	7920
~-			• ••				
75	Protein s	equence 1					
	Gene name	Protein	yrosine pho	osphatase, 1	receptor-typ	e, 2 polype	ptide 1
	Protein A	umber: Hs. ccession #:	78867 ND 002943				
	Signal se	quence: 1-	NP_002842				
80	Pfam doma	in: carb ar	hydrase (3)	3-300]			
	Transmemb	rane domain	s: 1639-160	51			
	Cellular	Localization	o: plasma m 21	membrane 31	43	51	
	ī	î	î.	i	41 	51 	
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						139	

	MRILKRFLAC	IQLLCVCRLD	WANGYYROOR	KLVEEIGNSY	TGALNOKNWG	KKYPTCNEPK	60
	A35 THITDEDA	TOWNVERKE	KPTKWDKTEL	PATE I LIMITATE	TRANSPORT OF THE PARTY OF THE P	TM10000000000	120
_	EVVOVITIEUM	GNUNMSSUGS	KHSLETAKPP	LEMOTVOORS	DDDDDDDDAM	******	180
5	TOTADMTALK	LDFKAIIDGV DTVSISESQL	AVECEVITMO	USKING MUA	T ANDIDO CAAU	*********	240
							300
	upt ningion	TOTAL PUNITUD	NMSYVLATVA	TOMOTORY	COAT TIME		360 420
	DIGIOSTIVE	REFORDITEE	ALVNPORDSA	TWO TRICKEDO	T OTHER TANKS		480
10	GSKTVLREDH	GKGDVPNTSL MNLSGTAESL	NSTSQPVTKL	ATEXDISLTS	OLALEPAHL	VEGTEASLND	540
	PUIDAGITES	SENPETITYD	VLIPESARNA	REDSTORGED	DOT MADOWEN	ATT BUTTO COMMO	600
	TWALLAGOR	PALIMINITE	INVDESERT	Kabayuno	OCHOCKETON TRA	**************************************	660 720
	TOATEDWEIL	BERGOULVST	VXVVVVCCYTTC		TICH CORRESPONDE		780
15	TEL LI LI LANGO DO	DSALHATPVP BDKVPLHASL	PSVDVSPRSI	LESSYTMADE.	DRECLERCED	7 170127 1702100	840
	VITTER SUVER	PSSDAMMHAR	SSGPEPSVAL.	STATESCAUTO	MICHARATOR	TTT: CT 14T 10T 10T 10T	900
	COLOGEOUS	IPKSSLITPT	AHLIOPTHAL.	REMARKS	COORDI I DOM	-	960 1020
	& A D A W D L T I I	ISVEGDONKA	LSKSETTYCN	RTELATORDA	DWW DODOWN	14700 4	1080
20	mwardet51	OIDDIMMIP	USLAHITTKU	FRUETCAMOS	MATE CANADADA	110010000	1140
	AVPSDPILVE	ASSDPASSEM TPKVDKISST	MI.HI.TVONON	ETBASFSTEV	LLQPSFQASD	VDTLLKTVLP	1200
	TAGINODNID	PVLLKSESSH	OVVPRLYRNO	ELECTRANT DT	ATM & TEN IN COMMEN	*****	1260
	OR THE PERSON	THOUSTLITET	KEEVTGKVFA	GIPTUACHTD	VOTINUOUSIA	ATOMINA WINDOWS	1320 1380
25	EHICOGO A TOT	MILITARIA I B	ELSHSARNDA	CIT.VICECTORING IN	ALCOHOLD TO THE PERSON NAMED IN	700000 0 mm	1440
	PGKSPSANGI.	CEXVMNDSDT	HENSLMDONN	PISYSLSENS	EEDNRVTSVS	SDSQTGMDRS	1500
						SDSQTGMDRS GQGTSDSLNE SEABASNSSH	1560
	POWIGHTON	ESEKKAVIDI.	VIVSALTETC	TARMARCTE TV	UDW/CDAMAND		1620 1680
30	TOTALLTER	ISDDAMILI	KHEPKHUADI.	RIGGREEF	DET VERTVARIE	^^~	1740
30	MUDDINGRUM	HKNKYINIVA	YIDHSSVIKT.AC	T. N D'UTVOUT MA	VYLIE LANGE CO.		1800
	LAYYTVRNFT	LRNTKIKKGS	OKCESSORAN	TOVEVETOWER	PADGSEEYON	PLVTQKSVQV LTFVRKAAYA	1860
	MARMAGRAAA	MCSAGVGRIG	TAIAIDNMIU	OTOURGRANT	PORT WITHOU	D1000	1920 1980
35							2040
<i></i>							2100
	EERLIIODPI	LEATODDYVI.	POGONMAEDE	PVYWPNRDEP	INCESPKVTL	MAEEHKCLSN AANROGPMIV	2160
	TING A TWG	TE CATLLITANT	OFFICENSADA	YOVAKMINIM	PECTRATKER	YQFLYKVILS	
40	LVSTRQEENP	Steldengaa	LPDGNIABSL	ESLV		EGITANIGATES	2280
70	DNA SEQUENC	777 0					
	Gene name:						
			TEATE HILLER		•		
			otein sulfot 10903	ransferase	1		
15	Unigene num Probeset Ad	mber: Hs.11	10903 D61594		1		
45	Unigene num Probeset Ad Nucleic Aci	mber: Hs.11 cession #: id Accession	10903 D61594 1 #: NM 003		1		
45	Unigene num Probeset Ad Nucleic Aci	mber: Hs.11 cession #: ld Accession Lence: 82-1	10903 D61594 1 #: NM_003	3596			
45	Unigene num Probeset Ac Nucleic Aci Coding sequ 1	mber: Rs.11 cession #: id Accession ience: 82-1 11	10903 D61594 1 #: XM_003 1194 21	31	41	51 1	
	Unigene num Probeset Ac Nucleic Aci Coding sequ 1 GTAGACTGTC	mber: Hs.11 cession #: ld Accession lence: 82-1 11 	10903 D61594 1 #: NM_003 1194 21	3596 31 	41	1	60
45 50	Unigene num Probeset Ac Nucleic Aci Coding sequ 1 GTAGACTGTC TAACAAGATA	mber: Hs.11 cession #: id Accession lence: 82-1 11 CATGGCCTGA ACCACATCAA	10903 D61594 1 #: NM_003 1194 21 ACATITICCG GATEGITICAL	31 AAAATCATTT	41 TGAGCAAAAT	ATCTGTTTAA	60 120
	Unigene num Probeset Ac Nucleic Aci Coding sequ 1 GTAGACTGTC TAACAAGATTA CTGGTGATTA	mber: Hs.11 Cession #: Id Accession Lence: 82-3 11 CATGGCCTGA ACCACATCAA AACGTAGCCA	L0903 D61594 1 #: NM_003 L194 21 ACATTTCCG GATGGTTGCA	31 AAAATCATTT AAGCTGAAGC CTGGGCCAGC	41 TGAGCAAAAT AGAACTTACT ATGCCATGGA	ATCTGTTTAA ATTGGCATGT ATGCCATCAC	120 180
	Unigene num Probeset Ad Nucleic Ad Coding sequi 1 GTAGACTGTC TAACAAGATA CTGGTGATTA CTGGTAGAGG GGCCTGGACC	nber: Hs.11 cession #: dd Accession lence: 82-1 11 CATGGCCTGA ACCACATCAA GTTCTGTGAC AACGTAGCCA ATCAAAGCCAA	L0903 D61594 1 #: NM_003 L194 21 } ACATTITCCG GATGGTTGGA TGTGTTTTAC GCCAGTCAAA	31 AAAATCATTT AAGCTGAAGC CTGGGCCAGC TTGGAGAGCAGC	41 TGAGCAAAAT AGAACITACT ATGCCATGGA CAAGGACCAC	ATCTGTTTAA ATTGGCATGT ATGCCATCAC TGTGAGAACT	120 180 240
50	Unigene num Probeset Ad Nucleic Adi Coding sequi 1 GTAGACTGTC TAACAAGATA CTGGTGATTA CGGATAGAGG GATTGGGGTGG	nber: Hs.11 Cession #: Id Accession tence: 82-3 11 CATGGCCTGA ACCACATCAA GTTCTGTGAC AACGTAGCCA TCAAAGCCAA	L0903 D61594 1#: NM_003 1194 21 ACATITICES GATGGTTGGA TGTGTTTAC GCCAGTCAAA CCAAAACCTTT	31 AAAATCATTT AAGCTGAAGC CTGGGCCAGC TTGGAGAGCA GCCTATCACA	41 TGAGCAAAAT AGAACTTACT ATGCCATGGA CAAGGACCAC AAGATATGCC	ATCTGTTTAA ATTGGCATGT ATGCCATCAC TGTGAGAACT TTTAATATTT	120 180
	Unigene num Probeset Act Nucleic Act Coding sequi 1 GTAGACTGTC TAACAAGATA CTGGTGATTA CTGGTGATTA GGCTTGGAGGT GGCTTGGAGGT GACATTCGGTGTT	mber: He.11 cession #: dd Accession lence: 82-1 11 CATGGCCTGA ACCACATCAA GTTCTGTGAC AACGTAGCCA TCAAAGCCAA TGCCTCGAG GTTGAGGAGGA	10903 D61594 H: NM_003 1194 21 ACATITICCS GATGGTTGGA TGTGTTTTAC GCCAGTCAAA CCAGCAA AACCAGGGTC	31 AAAATCATTT AAGCTGAAGC CTGGGCCAGC CTGGAGAGCA GCCTATCACA GCCTATCACA GCCTATCACA	41 TGAGCAAAAT AGAACTTACT ATGCCATGGA ATGCCACCAC AAGATATGCC CCATGCTGGA	ATCTGTTTAA ATTGGCATGT ATGCCATCAC TGTGAGAACT TTTAATATTT CGCACATCCT	120 180 240 300
50	Unigene nur Probeset Ac Nucleic Ac Coding sequ 1 GTAGACTGTC TAACAAGATA CTGGTGATTA CGGATAGAGG GGCCTGGACC ATTGGGGTG GACATTCGCT TGGTCACCGT TGGTCACCGT CTGGATTCTGCT	mber: Re.11 cession #: dd Accession lence: 82-1 11 CATGGCCTGA ACCACATCAA GTTCTGTGAC AACGTAGCCAA TGCATGGGGG GTGGAGAGGA CAAGTAAAGC CAAGTAAAGCAA CCATGGAGAGC	L0903 D61594 1 #: NM_00: 1194 21 ACATITICCG GATGGTTGGA TGGGTCAAA CCAAAACCTTT TGGAACCACA AACCAGGGTC GAAGATCCGC GAAGATCCGC CATATITICTA	31 AAAATCATTT AAGCTGAAGC CTGGGCCAGC TTGGAGAGCA GCCTATCACA CTCATGAGGG ATTCCCCGAA CTGGATGAGG	41 	ATCTGTTTAA ATTGGCATGT ATGCCATCAC TGTGAGAACT TTTAATATTT CGCACATCCT GAAGCAGATG TGATGAAGTG	120 180 240 300 360 420 480
50	Unigene nur Probeset Aci Nucleic Aci Coding sequ 1 	mber: He.11 cession #: id Accession lence: 82-1 11 CATGGCCTGA ACCACATCAA GTTCTGTGGC AACGTAGCCA TCAAAGCCA TGCAGGGGAGGGA CAAGTAAAGA CCATGCAAG CCAATGCAAG CTAATGAAGC	LO903 D61594 1 #: NM_003 1194 21 1 ACATITICCG GATGGTTGGA TGTGTTTTAC GCCAGTCAAA CAAAACCTTT TGGAACCACA AACCAGGGTC GAAGATCCGC CTTCTTACTAC	31 AAAATCATTT AAGCTGAAGC CTGGGCCAGC TTGGAGAGCA GCCTATCACA CTCATGAGGG ATTCCCCGAA CTGGATGAGG GAAATTATCG	41 TGAGCARAAT AGBACTTACT ATGCCATGGA CAAGGACCAC CCATGCTGGA TCCTGGCCTTAC CTGGTGTTAC TTAAGCATGG	ATCIGITTAA ATTIGGCATGT ATGICATCAC TGIGAGAACT TITAATATTT CGCACATCIT GAAGCAGATG TGATGAAGTG GGAGCCAGCC	120 180 240 300 360 420 480 540
5 0 ·	Unigene nur Probeset & Nucleic Aci Coding sequ 1 GTAGACTGTC TAACAGATA CTGGTGATTA CGGATAGAGG GGCCTGGACC ATTGGRGGTG GACATTCGC TGGTCACGGT CTGGTCACGGT CTGGTTATTAT TTCCCCAATG	mber: He.11 cession #: d Accession ence: 82-1 l CATGGCCTGA ACCACATCAA GTTCTGTGAC AACGTAGCCAA TGCCTCGGAG GTGGAGAGGGA CAAGTAAAGCA CCATGCAAGC CAAGTAAAGCA CCATGCAAGC CTAGCAAGC CTAGCAAGC CCATGCAAGC CCATGCAACC CCATG	LO903 D61594 1 #: NM_003 1194 21 ACATTITICES GARGGTTGGA TGTGTTTTAC GCCAGTCAAA CCAAACCTTT TGGAACCACA AACCAGGGTC GAAGATCCGC CTTCTTACTA TCCTTTTGCCA CCTTCTTACTA	31 AAATCATTT AAGCTGAAGC CTGGGCCAGC TTGGAGAGCA CTCATGAGGG ATTCCCGAA ATTCCCGAA CTGATGAGG GAAATCATT	41 TGAGCARAAT AGRACITACT ATGCCATGGA CAAGGACCAC AAGATATGCC CCATGCTGGA TCCTGGCCCT CTGGTGTTAC TAAAGEATGG TAAACTTACCT	ATCIGITTAA ATTGGCATGT ATGCCATCAC TGTGAGAACT TTTAATATTT CGCACATCCT GAAGCAGATG TGATGAAGTG GGAGCCAGCC TTCTAGGTTA	120 180 240 300 360 420 480 540
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5 0 ·	Unigene nur Probeset & Nucleic Aci Coding sequ 1 GTAGACTGTC TAACAGATA CTGGTGATTA CGGATAGAGG GACATTGGC ATTGGRGGTG TCGGTCACCATG ATTTCTCGAA AAGTGGAATC TCGCATGTTG TCGCATGTTGG TCAAGTTCC TAAAGTTCC AAAGTGGGATC AAAGTGGGATC AAAGTGGGATC AAAGTTGGG TTAAAGTTCC AAAGTTGGG GTCAATGTGG GTCAATGTGG GTCAATGTGG GTCAATGTGG GTCAATGTGG GTCAATGTGG	mber: He.11 cession #: dAccession ence: 82-1 l CATGGCCTGA ACCACATCAA GTTCTGTGAC AACGTAGCCAA TCACAGCCAA TCACAGCCAA CCAAGCCAA CCAAGCCAA TCACTAGCAAG CCAAGTAAAGA CCAAGTAAAGA CCAAGTAAAAGA CCAAGTAAAAGA TCACAGATTACTAT GTGCTATGA TCCAGATTCC GAGTGTCCTATC	LO903 D61594 1 #: NM_003 1194 21 ACATITICCG GATGGTTGGA TGTGTTTTAC GCCAGTCAAA CCAGACCACA AACCAGGGTC GAAGATCCGC CTTCTTACTA TCCTTTTGCA CCTGATCGGT AGCTGGATTT GACCATGTAT ACACTGTTACTA ACACTGTTACTA ACACTGTTACTA ACACTTGTC ATGGAACCAC ATGAAAACTTGTC ATGAAACTTGTC ATAGAACTACAC GTCAAAAGTTT	31 AAAATCATTT AAGCTGAAGC CTGGGCCAGC TTGGAGAGCA GCCTATCACA CTCATGAGGG ATTCCCCGAA ATTCCCCGAA CTGGATTAC CTGAAATCTT CAGATTGCC GATCTGAACA AACCAGTGTA TTACATCCTG TCAGTATTGC GAGGAGTTTGC GAGGAGTTTGC GAGGAGTTTGC GAGGAGTTTGC GAGGAGTTTGC	41 J TGAGCARAAT AGRACTTACT AGRACTTACT ATGCCATGGA CAAGGACCAC AGATATGCC CTGGTGTTAC TTAAGCATCAC GGCATCAGT GACCATCAGT ACCATGGAGTTGA ACCGTGGAGAC ACCATGAGAG ACCATGAGAG ACCATGAGAG ACCATGAAGA CAAAACCAAGT	ATCIGITTAA ATGCATGT ATGCATCAC TGTGAGAACT TTTAATATT CGCACATCCT GAAGCAGATG TGATGAAGTG GGAGCCAGCC TTCTAGGTTA ACATTCAATG CTGTTTGACA TTATAAAAAG GAGAACACT GATGATTCGG AATCAAGCCA	120 180 240 300 360 420 480 540 600 660 720 780 840
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50 55 60	Unigene nur Probeset & Nucleic Aci Coding sequ 1 GTAGACTGTC TAACAGATA CTGGTGATTA CGGATAGAGG GGCCTGGACC ATTGGTGTC TGGTCACCGT TCGGTTTTATTAT TTCCCCAATG ATTTCTCGAA AAGTGGAATC TTCACAGTT TTCACCAGT TTCACCAGT TTCACCAGT AAGTGGAGT TTAAAGTTCC AAAGCTGGGG GTCAATGTAG ATTCACGGAT ATTCACGAA ATTCACGAA ATTCACGAA AAGTGGAAT TTCAACTAC ATTCACAGTAA ATTCACACTAC TTCAACTAC	mber: He.11 cession #: dd Accession lence: 82-1 1 CATGGCTGA ACCACATCAA GTTCTGTGAC AACGTAGCCAA TCAAAGCCAA TCACAGGAGGA CAAGTAAAGA CCAAGTAAAGA CCAAGTTACTAT GTGCTATGA TCACGATTCC GAGTGTCTTT TCACGATTCC TGAGCTCTTT TAGCTCTTAT AACCTGATCC TTGCTCCTTAT AACCTGATCC TTGCTCCTTAT AACCTGATCC TTGCTCCTTAT AACCTGATCC TTGCTCCTTT TCCTCCTTAT AACCTGATCC TTGCTCCTTCT TCCTGCTTTCT TCCTCTGTTCT TCCTGCTTCT TCCTCTGTTCT TCCTCTGTTCT TCCTCTTTT TCCTCTTCT TCTCTCTTCT TCTCTCTTCT	LO903 D61594 1 #: NM_003 1194 21 ACATITICCG GATGGTTGGA TGGGTCAAA CCAGTCAAA ACCAGGGTC GAAGATCCGC CCTGATCGCC CCTGATCGCC CCTGATCGTC ACCAGTGTT ACCAGGTTT ACACTGTT ACACTGTC ATGAAACTT ACACTGTC AAAATACT ACACTGCCAAAG CCAAAATTATT AAAAATAATA	31 AAAATCATTT AAGCTGAAGC CTGGGCCAGC TTGGAGAGCA GCCTATCACA CTCATGAGGG ATTCCCCGAA ATTCCCCGAA ATTCCCCGAA ATTCCCCGAAATCTC CAGAATCTC CAGAAGATCCTC TCAGTATTGC GAGAGATACC GAGAGATAC CTTGGAATCTC GAGAGATAC CTTGGATATTG GAAAACACTCC CACAGGATCC	41 J TGAGCARAAT AGRACTTACT AGRACTTACT AGRACTAGCA CAAGGACCAC AGGATATGCC CTGGTGTTAC CTGGTGTTAC GGCATCAGT TGAGCATCAGT ACCTTAGGGA ACCGTGGACAGT ACCATGAGAC ACCATGAGAC ACCATGAGAC ACCATGAGAC ACCATGAGGA CAGAGCTTA	ATCTGTTTAA ATTTGGCATGT ATGCCATCAC TGTGAGAACT TTTTAATATTT GGCACATCGT GAAGCAGATG TGATGAAGTG GGAGCCAGCC TTCTAGGTTA ACATTCAATG CTGTTTTGACA TTATAAAAAG GAGGAACACTC GAATCAACCCA TTTACAAGCA CTACACCCACCT TAAGGGAAAA	120 180 240 300 360 420 540 660 720 780 840 900 960 1020
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                                                                                                                   1140
                                                                                                                   1260
10
                                                                                                                   1380
15
           Protein sequence 4
Gene name: chemokine (C-X3-C) receptor 1
           Unigene number: Hs.78913
           Protein Accession #: NP_001328
           Signal sequence: 1-44
Pfam domain: 7tm_1 [48-293]
20
           Cellular Localization: plasma membrane
1 11 21 31
          MOOPPESVTE MFEYDDLABA CYIGDIVVFG TVFLSIFYSV IFAIGLVGNL LVVFALTNSK KPKSVTDIYL LNLALSDLLF VATLPFWTHY LINEKGLENA MCKPTTAFFF IGFFGSIFFI TVISIDRYLA IVLANASMEN RTVGHGVTIS LGVWAAAILV AAPOPMPTKQ KENECLGDYP EVLQSIWPU RNVETNFLGF LLPLLIMSYC YFRIIQTLFS CXNHKKAKAI KLILLVVIVF FLFWTFYNVM IFLETLKLYD FFFSCDMKO LRLALSVYET VAPSHCCLMP LIYAFAGEKF RRYLYHLYGK CLAVLCGRSV HVDFSSSESQ RSRHGSVLSS NFTYHTSDGD ALLLL
25
                                                                                                                     180
                                                                                                                     300
30
           DNA sequence 5
           Gene name: cannabinoid receptor 1 (brain)
           Cens hame: Cannession 1: 12986
Nucleic Acid Accession 1: NM_001840
35
           Coding sequence: 92-1510
         11
                                             21
40
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45
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70
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                                                                                                                   1920
                                                                                                                   2040
           ARATARACCT TARTATTTCT TCCCARARAR ARARA
75
           Protein sequence 5
           Gene name: cannabinoid receptor 1 (brain)
Unigene number: Ms.75110
Protein Accession #: NP_001831
80
          Signal sequence: none found

Fignal sequence: none found

Pfam domain: 7tm_1 [133-397]

Transmembrane domains: 121-143, 156-178, 195-217, 237-259, 276-298, 344-366, 378-400

Cellular Localization: plasma membrane

1 11 21 31 41 51
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	1	1		1			
	MKSILDGLAD	TTFRTITTOL	LYVGSNDIOY	EDIKGDMASK	IGYPPOKEPI.	TOPPOSTED	60
	KMTAGDNPQL	VPADQVNITE	PYNKSLSSPK	ENEENIQUE	NPMDIECPMV	LNPSOOLAIA	120
5	VLSLTLGTFT	VLENLLVLCV	ILHSRSLRCR	PSYHFIGSLA	VADLLGSVIP	VYSPIDPHVP	180
3	HRKDSRNVFL	PKLGGVTASF	TASVGSLFLT	AIDRYISIHR	PLAYKRIVTR	PKAVVAFCLM	240
	AHSHAVRMIO	RGTOKSIIIH	TSEDGKVOVT	IDETYLMFWI RPDOARNOIR	GVTSVLLLFI 1.AKTI.VI.TI.V	VLIICHGPLL	300 360
	AIHVYDVPGK	MIKLIKTUPA	FCSMLCLLNS	TVNPIIYALR	SKOLRHAFRS	MPPSCEGTAO	420
10	PLDNSMGDSD	CLHKHANNAA	SVHRAAESCI	KSTVKIAKVT	MSVSTDTSAE	AL	
10	TWO comments						
	DNA sequences	endothelin	recentor t	·vne B			
		mber: Hs.82		.,pc b			
15		cession #:					
13	Nucleic Act	d Accession	#: NM_000	115			
	1	lence: 238- 11	21	31	41	51	
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20	GAGACATTCC	GGTGGGGGAC	TCTGGCCAGC	CCGAGCAACG	TGGATCCTGA	GAGCACTCCC	60
20	AGGTAGGCAT	TTGCCCCGGT	GGGACGCCTT	GCCAGAGCAG	TGTGTGGCAG	GCCCCCGTGG	120
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	CAGCCGCCTC	CAAGTCTGTG	CSGACGCGCC	CTGGTTGCGC	TGGTTCTTGC	CTGCGGCCTG	240 300
25	TCGCGGATCT	GGGGAGAGGA	GAGAGGCTTC	CCGCCTGACA	GGGCCACTCC	GCTTTTGCAA	360
25	ACCGCAGAGA	TAATGACGCC	ACCCACTAAG	ACCTTATGGC	CCAAGGGTTC	CAACGCCAGT	420
	CCACGCACCA	TCTCCCCTCC	CCCGTGCCAA	GGACCCATCG	ACAGGACGGC	AGGATCTCCG GACTTTCAAA	480 540
	TACATCAACA	CGGTTGTGTC	CTGCCTTGTG	TTCGTGCTGG	GGATCATCGG	GAACTCCACA	600
30	CTTCTGAGAA	TTATCTACAA	GAACAAGTGC	ATGCGAAACG	GTCCCAATAT	CTTGATCGCC	660
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	AAAGCCTCCG	TGGGAATCAC	TGTGCTGAGCT	CTATGTGCTC	TGAGTATTCA	CAGATACAG	780 840
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35	ATTGTTTTGA	TTTGGGTGGT	CTCTGTGGTT	CTGGCTGTCC	CTGAAGCCAT	AGGTTTTGAT	960
33	ATAATTACGA	TOGACTACAA	AGGAAGTTAT	CTGCGAATCT	GCTTGCTTCA	TCCCGTTCAG CAGTTTCTAT	1020
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	AAAADAAAA	GTGGCATGCA	GATTGCTTTA	AATGATCACC	TAAAGCAGAG	ACGGGAAGTG	1200
40	GCCAAAACCG	TCTTTTGCCT	GGTCCTTGTC	TTTGCCCTCT	GCTGGCTTCC	CCTTCACCTC	1260
40	AGCAGGATTC	TGAAGCTCAC	TCTTTATAAT	CAGAATGATC	CCAATAGATG	TGAACTTTTG TTCCTGCATT	1320
	AACCCAATTG	CTCTGTATTT	GGTGAGCAAA	AGATTCAAAA	ACTGCTTTAA	GTCATGCTTA	1380 1440
	TGCTGCTGGT	GCCAGTCATT	TGAAGAAAAA	CAGTCCTTGG	AGGAAAAGCA	GTCGTGCTTA	1500
45	AAGTTCAAAG	CTAATGATCA	CGGATATGAC	AACTTCCGTT	CCAGTAATAA	ATACAGCTCA	1560
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	TAAAATATTA	AGTGTAATTA	TITTAACACT	CACAGCTACA	TATGACATTT	TATGAGCTGT	1680 1740
	TTACGGCATG	GAAAGAAAAT	CAGTGGGAAT	TARGARAGOC	TYTTYTTAA	እ ርር እርተተክክተ	1800
50	TTTTTACAGT	TAGCACTTCA	ACATAGCTCT	TAACAACTTC	CAGGATATTC	ACACAACACT TTTATTTTTA	1860
50	AATCAATGGG	ACTCTGATAT	AAAGGAAGAA	TANGTCACTG	TAAAAAGAGA	CTTTTAAATG	1920 1980
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	CAACATGTCA	CARACARGEA	GCATGTAACA	GACTGGCACA	TOTOCCAGOT	GAATTTAAAA	2220 2280
	TATAATACTT	AADAAAATT	AATTATTACA	TCCTTTACAT	TCAGTTAAGA	TCARACCTCA	2340
	CAAAGAGAAA	TAGAATGITT	GAAAGGCTAT	CCCAAAAGAC	TTTTTTGAAT	CTGTCATTCA	2400
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	GCCAGTGACC	TCATAATAAA	GACTOTGAAC	TGCCTGGTGC	AGTGTCCACA	TGACAAAGGG	2640
	GCAGGTAGCA	CCCTCTCTCA	CCCATGCTGT	GOTTAAAATG	GTTTCTAGCA	TATGTATAAT	2700
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	AGCTTTGTGC	GTTCCTGCCT	AATTTTTATA	TCTTCTAAGC	AAAGTGCCTT	AGGATAGCTT	2940
	GGGATGAGAT	GTGTGTGAAA	GTATGTACAA	GAGAAAACGG	AAGAGAGAG	AAATGAGGTG	3000
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	GAGTGACTTT	' CGAAATAAAT	TGGGCCCAAG	AGCTTTAACI	CGGTCTTAAA	ATATGCCCAA	3180
	ATTTTTACTI	GITTITCIT	TTAATAGGCT	GGGCCACATO	TTGGAAATAA	GCTAGTAATG	3240
	GAARGARAG	TCAATATTGA	ATGTGATGGT	ACAGTAAACC	AAAACCCAAC	AATGTGGCCA	3300
75	ACAAACTTGT	TCTTTAATTT	CATCCCAATC	ACTITICA	ALICIATITA AGGCCTGTT	TAAATCACCC	3360 3420
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	TTCTTTACAT	CTCAAAACC	AAGATAGAA	AAGGTGCTAT	COTTCAACT	CANADCATOR	2780
	TTCCTAGTAT	TAAGGACTTI	AATATAGCAI	CAGACAAAA	TATIVITYAN	A THEOLOGY A CHARLES	2040
	CAGCTCAAA	LAATTTATAA A	AGATTTTAAC	CTATTTTCTC	CCTTATTATY	TEATTOTTANT	3900
	JIGGAIGIA:	. SIICHAUAC	CITITAGTAT	. IUMIAGCITA	LATATGGCC	AAGGAATACA	3960

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                                          Protein sequence 6
Gene name: endothelin receptor type B
Unigene number: Rs.82002
Protein Accession #: NP_000106
     10
                                          Signal sequence: 1-27
Pfam domain: 7tm_1 [118-386]
                                          Transmembrane domains: 100-122, 138-160, 173-195, 221-243, 277-299, 325-347, 358-380
Cellular Localization: plasma membrane
1 11 21 31 41 51
     15
                                       MOPPPSLCGR ALVALVLACG LSRINGEERG FPPDRATPLL OTABIMTPPT KTLMPKGSNA SLARSLAPAE VPKGDRTAGS PPRTISPPPC QGPLEIKETP KYINTVVSCL VFVLGIIGNS TLLRIIYKMK ORROGNILI ASLALGDLLH IVIDIPINVY KLLAEEMPPG AEMCKLVPPI QKASVGITVL SLCALSIDRY RAVASWSRIK GIGVPKNTAV BIVLLWVUSV VLAVPEAIGP DIITMOYKGS YLRICLLHPV QKTAPHQFYK TAKDMULPSP YFCLPLAITA PFYTLMTCEM LRXKSGMQIA LMDHLKORRE VAKTVPCLVL VPALCWLPLH LSRILKLTLY MONDENRCEL LSFLLVLDIG GIMBASINSC INPIALYLVS KRPKNCPKSC LCCWCQSFEE KQSLBEKQSC
     20
                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                                                                                                                                                              300
    25
                                          LKPKANDHGY DNFRSSNKYS SS
                                          DNA sequence 7
                                        DAM sequence 7
Gene name: G protein-coupled receptor 34
Unigene number: Hs.29202
Probeset Accession #: N54926
Nucleic Acid Accession #: AF039686
Coding sequence: 79-1224
    30
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TGATCTCCAC AGAAGACAAT GAGAAGCGC TITTATAACCA ACATTAGCGA CAACCGCCA
AGCTGGCCTT ACTCCTCCCA CAGAATCGGC TITTATAACCA ATCATACGGA CCAACCGCCA
ACGTGTTAA CCACATCCTA CTCTGTTATT TCATCGTGG GACTGGTTGG GAACACTAACCA
ACGTGTTAA CCACATCCTA CTCTGTTATT TTCATCGTGG GACTGGTTGG GAACACTAACCT
AACGTAGCCA TTGCAGACCT CCTACTCATC TAAAGAAAATT CCATTCCAAAT TTATCTACTT
AATAACCAAA ACAAGTGGAC ACTAGGTGG ATTCTGGCCCC CTTTCCGAAT CATTTAACCAA
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  55
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                                    Protein sequence 7
Gene name: G protein-coupled receptor 34
Unigene number: Hs.29202
Protein Accession #: AAD50531
Signal sequence: none found
Pfam domain: 7tm_1 [71-327]
Transmembrane domains: 90-112, 126-148, 171-193, 217-239, 263-285
Cellular Localization: plasma membrane
1 11 31 41 51
| | | | | | | |
  60
 65
                                   MRSHTITMTT TSVSSMPYSS HEMREITNHS DOPPONESAT PNVTTCPMDE KLLSTVLTTS
YSVIFIVOUV GRILALYVEL GIHRKRNSIQ IYLLAVAIAD LLLIPCLEPR IMYHINONKW
TLGVILCKVV GTLFYMMYI SIILLGFISL DRYIKINSSI QORKAITTKO SIYVCCIVWM
VALGGFLTMI LITLKKGGHN STMCFHYRDK HNAKGEAIFN PILVVMFMLI PLLIILSYIK
IGKNILRISK RESKPENSGK YATTARNSFI VLIIFTICFV PYHARRFIYI SSOLMVSSCY
WKEIVHKTNE IMLVLSSFNS CLIPVMYFLM SSNIRKIMCQ LLFRRFQGEP SRSESTSEPK
PCYSLEDTSV AVKIQSSSKS T
 70
                                                                                                                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                                                                                                                            240
 75
                                     DNA SEQUENCE 8
                                     Gene name: exostoses (multiple)-like 2
Unigene number: Hs.61152
Nucleic Acid Accession #: NM 001439
80
                                     Coding sequence: 288-1280
                                                                                              11
                                                                                                                                              21
                                                                                                                                                                                                                                                                                                                                      51
                                     CACTITIGOGG GCGGCACTIT TICCAGGITG THANTCCAGC TAATGGAGAA GGATAGATGC
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		A ATGAGCAAAC GAGACGCCCC TTCCGTTTTA 12	
	TGATAACTAA GCTGCAGGGA AATAAATC	GG CTGGCCCTAC TGCAATCTAC TGCACTCGAG 18	
		TT TAATAGTGAC AAGTGAGCCT GCTTCTGTCA 24	
5		A AATTAAACTT CAACACAATG AGGTGTTGCC 30	
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	AACAGACAGC AAACAGGATG AGAAATCG	AC TOCAGGTOTT TOCTGAACTG GAAACCAATG 72	0
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		TG CTTTGATAGA TGATACTCAA AACTGTGATG 102	
		GC ATATTGGCAA GACTTCAGGG ATATTTGTGA 108	
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		TT ATTGTATAAA TAAGCTTGTT AATATCTATG 120	
20	ATACCATCC CTTANCATO TCCANCAT		-
	ACTRONADO NARATATAN RACTARA		
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		GC AGTGCTTCTA GGATATAAAA TTCACATTAC 144	
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40		AT TCTTAAGGTT GCCTACTCTC TGTTATGTGA 24	00
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		AGT ATATGTGTCT TAATGCAGTC AGATTGTAAA 27	
45	AAACAAAAC AAAGAAACTA AGAATCT		60
			20
	ACTITIGCCA TCC		
	Protein sequence 8		
50	Gene name: exostoses (multip	le)-like 2	
	Unigene number: Hs.61152	,	
	Protein Accession #: NP_0014	30	
	Signal sequence: 1-38	••	
	Transmembrane domains: none	found	
55	Cellular Localization: plasm		
	1 11 21	31 41 51	
	Macana a managana a ma		
	PROCEST IN ORDER OF THE PROPERTY OF THE PROPER	VLL LVAGALTALL PSVKEDKMLM LRREIKSQGK	60
60	SIRDSFILIM GIINKIDLLL KLLNHYQ	AVP NLHKVIVVWN NIGEKAPDEL WNSLGPHPIP 1	.20
00	ATTEMOTION ON COMMITTEE OF THE LITTLE OF THE	MVD DDTLISTPDL VFAFSVWQQP PDQIVGFVPR 1	.80
			40
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	VNIYDSMPLR YSNIMISQFG FPYANYK	RKI	
65			
UJ	DNA SEQUENCE 9		
		th differentiation factor 1 (GDF1)	
	Unigene number: Hs.92614		
	Probeset Accession #: AL1201		
70	Nucleic Acid Accession #: NM	_021267	
70	Coding sequence: 73-1125		
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	TGCACGGACT GCGGCTGGGG GCTGGCG	CGT CGCGGCCTGG CTGAGCACGC GCACCTGGCG 2	240
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	GCCACTGCGC GCCTCTTTCG GCCCCTG	GCG AAGCGGTGCT GCCTCCAGCC CAGAGATGCC 3	360
00	GCCAAGATGC CCGAGAGCGC TTGGAAG	TIT CICITCIACC TGGGCAGCTG GAGCTACAGT	120
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	CGGTACCACA ATGTGGGCAT CCTTGTG		720

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	GAGAAGCCAC	TGAGGAACGG	CCTGGTGAAG	CACAACCCC	TOTOLANOCOC	TCGGCCCCGC	
	CCCCCTCCAC	CCCCCCCC	000027000	COCCOCI	TCTGAACCCC	TGGCCGCCCC	1140
	GCC1 CCCCC	COUNCECNE	CCCGAATACC	CCGGCCACGC	Teccercer	TGGCCGCCCC	1200
10	TCCACCCCCT	CCAACTCTGC	TCCTCTAGGG	CCGCCGCCAC	CTCCCCTGGG	ACCCCGCCCC	1260
10	CTCATCCTGC	CTCCATTTCC	CCCCACCC	COCCACCA CC	CONCERNO	~~~~~~~	1320
	GGCCCCGCCC	TCAGCCCACT	GGTCCCGGGC	CGCCGCGGAC	CALASSAS CAL	CTCTCCCCCC	1380
	CGCCTGGGAG	GAAGATGCCA	COCCOCACA	AACCTCCCCCC	000000000000000000000000000000000000000	CTCCTCCTCC	
	TOCTOCOCOT	CONCERNOON	**************************************	AV001CCC10	COGCONCERC	CICCICCICC	1440
	TCCTGGCCCT	GCIGCIGCCC	rusciscuce	TGACCCGCGC	CCCCGTGCCC	CCAGGCCCAG	1500
15	CCGCCGCCCT	GCTCCAGGCT	CTAGGACTGC	GCGATGAGCC	CCAGGGTGCC	CCCAGGCTCC	1560
13	GGCCGGTTCC	CCCGGTCATG	TGGCGCCTGT	TTCGACCCC	CCACCCCACA	CACACOM	1620
	CIGGCTCGCG	GCGGACGTCC	CCAGGGGTCA	CCCTGCAACC	GTYCH CANA	CACCACCTOC	1680
	GGGTCGCCGG	AAACATCGTG	CGCCACATCC	CCCACCCCC	TOCOCCOCACC	CGGGCCTCGG	
	AGCCTGTCTC	GGCCGCGGGGG	CATHICCCATC	ACTOCACACT	COTCOTO	CTGTCGGCTG	1740
	TEGAACCCCC	TONCOCOCO	2000000000	WOLDOWCKOT.	COICIICANC	GCGCGGCGG	1800
20	CCCACCCCC	2010000000	70000000	GCC1GCMGC1	GCGTTTCGCG	GCGGCGGCGG	1860
20	CGGCAGCCCC	GGAGGGCGC	TGGGAGCTGA	GOGTGGCGCA	AGCGGGCCAG	GCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	1920
	CGGACCCCCG	GCCGGTGCTG	CTCCCCCAGT	TOTOTOTO	CONCRETE	CCDOROCO	1980
	CGGAGCTGCT	GGGCGCCCCT	TGGGCTCGCA	ACCCCTCATG	GCCGCGCAGC	CTCCGCCCTCG	2040
	CGCTGGCGCT	ACGCCCCCGG	GCCCCTGCCG	CALASTAS CASTAS	CCTGGCCCGAG	CONTROPONDO D	
	TGCTGGTGAC	CCTCGACCCG	CCCCACAGGCC	*CCCCCCCCC	CCTOOCCGNG	CGCGACGCCG	2100
25	AACCCCCCCCCC	accessores	0000000000	ACCCCCIOGC		CUCUACUCCU	2160
	MCCCCG1G11	3335535555	CCCGGGGGG	CLIGICGCGC	GCGGCGGCTG	TACGTGAGCT	2220
	TCCGCGAGGT	GGGCTGGCAC	CGCTGGGTCA	TCGCGCCGCG	CGGCTTCCTG	GCCAACTACT	2280
	GCCAGGGTCA	GTGCGCGCTG	CCCGTCGCGC	TOTOGGGGGTC	CCCCCCCCCCC	CCCCCCCCC	2340
	ACCACGCTGT	GCTGCGCGCG	CTCATGCACG	CCCCCCCCCC	GGGAGCCGCC	GACCOCCOCC	2400
	GCTGCGTGCC	CGCGCGCCTG	TOGCCCATCT	CCCTCCTCTT	CTTTCACAAC	AGCGACAACG	
30	TGGTGCTGCC	CCACTATGAG	GACATGGTGG	accross care	CITIONCANC	AGCGACAACG	2460
			avex100100	TOGACGAGIG	CGGCTGCCGC	TAACCCGGGG	
					•		
	Protein sec	mence 9					
	Gene name:	Homo sapie	ens growth o	lifferentiat	ion factor	1 (GDF1)	
	Unigene num	mber: Hs.92	2614			- (00.4)	
35		ession #:					
		ence: none					
	Transmembra			148-169, 18	34-206, 244	-266, 285-30	7
	Cellular Lo	calization:	plasma me	embrane			
40	1	11	21	31	41	51	
40		1	1	1	1	1	
	MAAAGPAAGP	TGPEPMPSVA	OT.VORCWESA	LAAABCCTOC	CUCT ADDOT A	i Ekahlappel	
							60
		TAI.DCAATAD	LEBBI APROCC		20211111111111		
	DULALGALGW	TALRSAATAR	LFRPLAKECC	LOPRDAAKMP	ESAWKPI.RVI.	GCWQVCAVI.I.	120
	FGTDYPFFHD	PPSVFYDWTP	LFRPLAKRCC GMAVPRDIAA	LOPRDAAKMP	ESAWKPLPYL HSTVATIVMD	GSWSYSAYLL	
15	LHHVVTLILI	PPSVPYDWTP VSSYAPRYHN	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD	LQPRDAAKMP AYLLQGSFYG ISDVOLEFTK	ESAWKPLFYL HSIYATLYMD LNIYPKSRGG	GSWSYSAYLL TWRKDSVVML SVHBLHALAA	120 180
45	LHHVVTLILI DLGCLSFGFS	PPSVPYDWTP VSSYAPRYHN WFWFRLYWPP	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATERC	LQPRDAAKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIPF	ESAWKPLFYL HSIYATLYMD LNIYFKSRGG YFFFNALLL	GSWSYSAYLL TWRKDSVVML SVHBLHALAA	120 180 240
45	LHHVVTLILI DLGCLSFGFS	PPSVPYDWTP VSSYAPRYHN WFWFRLYWPP	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATERC	LQPRDAAKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIPF	ESAWKPLFYL HSIYATLYMD LNIYFKSRGG YFFFNALLL	GSWSYSAYLL	120 180
45	LHHVVTLILI DLGCLSFGFS	PPSVPYDWTP VSSYAPRYHN WFWFRLYWPP	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD	LQPRDAAKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIPF	ESAWKPLFYL HSIYATLYMD LNIYFKSRGG YFFFNALLL	GSWSYSAYLL TWRKDSVVML SVHBLHALAA	120 180 240
45	LHHVVTLILI DLGCLSFGF8 YIVAFAAKVL	TALRSAATAR PPSVFYDWTP VSSYAPRYHN WFWFRLYWPP TGQVHELKDL	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATERC	LQPRDAAKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIPF	ESAWKPLFYL HSIYATLYMD LNIYFKSRGG YFFFNALLL	GSWSYSAYLL TWRKDSVVML SVHBLHALAA	120 180 240
45	LHHVVTLILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENO	TALRSAATAR PPSVFYDWTP VSSYAPRYHN WFWFRLYWFP TGQVHELKDL CE 10	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS	LQPRDAAKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL	ESAWKPLPYL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL	120 180 240 300
	LHHVVTLILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name:	TALRSAATAR PPSVFYDWTP VSSYAFRYHN WFWFRLYWPP TGQVHELKDL CE 10 epidermal	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATEHC REYDTAEAQS growth faci	LQPRDAAKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL	ESAWKPLPYL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL	120 180 240 300
45 50	LHHVVTLILI DLGCLSFGPS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur	TALRSAATAR PPSVFYDWTP VSSYAFRYHN WFWFRLYWPP TGQVHELKDL CE 10 epidermal mber: Hs.7	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS growth fact 7432	LQPRDAAKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL	ESAWKPLPYL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF	GSWSYSAYLL TWRKDSVVML SVHBLHALAA	120 180 240 300
	LHHVVTLILI DLGCLSFGPS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur	TALRSAATAR PPSVFYDWTP VSSYAFRYHN WFWFRLYWPP TGQVHELKDL CE 10 epidermal mber: Hs.7	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS growth fact 7432	LQPRDAAKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL	ESAWKPLPYL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL	120 180 240 300
	LHAVYTLILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nu Nucleic Ac:	TALRSAATAR PPSVFYDWTP VSSYAPRYHN WFWFRLYWPP TGQVHELRDL CE 10 epidermal nber: Hs.7'	LFRPLARRCC GMAVPRDIAR VGILVLPHHD LKVLYATSHC REYDTAEAQS growth fact 7432	LQPRDAAKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL	ESAWKPLPYL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL	120 180 240 300
	LHAVYTLILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nu Nucleic Ac:	TALRSAATAR PPSVPYDWTP VSSYAPRYHN WFWFRLYWPP TGQVHELRDL CE 10 epidermal nber: Hs.7' id Accession lence: 187-	LPRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS growth fact 7432 #: NM_00: -3819	APLIQGSFYG AYLLQGSFYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL COT recepto:	ESAWKPLFYL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKOKRF (avian er	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL THIODLASTIC	120 180 240 300
50	LHHVVTLILI DLGCLSFGPS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac: Coding sequ	TALRSAATAR PPSVPYDWTP VSSYAPRYHN WFWFRLYWPP TGQVHELRDL CE 10 epidermal nber: Hs.7' id Accession lence: 187-	LFRPLARRCC GMAVPRDIAR VGILVLPHHD LKVLYATSHC REYDTAEAQS growth fact 7432	LQPRDAAKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL	ESAWKPLPYL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL	120 180 240 300
50	LHAWVILLLI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nu Nucleic Ac: Coding sequence	TALRSAATAR PRSVFYDWTP VSSYAPRYHN WEWFRLYWPP TGQVHELKDL CE 10 epidermal mber: Hs.7' td Accession lence: 187: 11	LPRPLAKRCC GMAVPRDIAA VGILVLPIHD LKVLYATSHC REYDTAEAQS 970wth fact 7432 1 %: NM_00: -3819 21	LOPRDAAKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL COT recepto:	ESAWKPLFYL HSIYATLYMD LNIYFKSRGG YFFFNALLL RNGLVKDKRF (avian er	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL ythroblastic	120 180 240 300
	LHAWVILLLI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene num Nucleic Act Coding sequence 1	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWPP TGQVHELRDL EE 10 epidermal nber: Hs.7 id Accession tence: 187 11	LPRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS GROWTH fact 7432 1 %: NM_00: -3819 21 CGAGGTAGCC	LOPRDARKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL OF receptor 5228 31)	ESAWKPLFYIL HSIYATLYMD LNIYFKSRGG YFFFNALLLL RNGLVKDKRF (avian er;	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWPL ythroblastic	120 180 240 300
50	LHAVVILILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac: Coding sequence 1 GCCGCGCTGC AGGCCACCTC	TALRSAATAR PRSVFYDWTP VSSYAPRYHN WEWFRLYWPP TGQVHELRDL CE 10 epidermal nber: Hs.7' Id Accession Lence: 187' 11 GCCGGAGTCC GTCGGGGTCC	LPRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS growth fact 7432 1 #: NM_00: -3819 21 CGAGCTAGCC GCCCGAGTCC	LOPRDARKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL COT receptor 5228 31 CCGGCGCCCCGC	ESAWKPLFYL HSIYATLYMD LNIYFKSRGG YFPFNALLL RNGLVKDKRF (avian ex)	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWPL ythroblastic	120 180 240 300
50	LHAWVILLLI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac: Coding sequence Geoggetge AGGCCACCTC GCACGGCCCC	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WFWFRLYWFP TGQVHELRDL CE 10 epidermal nber: Hs.7' id Accession lence: 187- 11 GCCGGGAGTCC GTCGGCGTCC CTGACTCCGT	LPRPLAKRCC GNAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS growth fact 7432 #: NM_00: -381: CGAGCTAGCC GCCCGAGTCC CCCAGTATTGA	LOPRDARKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL TOT receptor 5228 31 CCGGCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ESAWKPLFYL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian er) 41 GCCCGCCCAG GCCAACGCCA	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWFL ythroblastic 51 ACCGGACGAC CAACACCGC	120 180 240 300 leukemia
50	HAWVILLLI DLGCLSFGFS YIVAPAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac; Coding sequence GCCGCGCTGC AGGCCACCTC GCACGGCCCC GCACGGCCCC	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWPP TGQVHELRDL EE 10 epidermal nber: Hs.7 id Accession ence: 187 11 GCCGGAGTCC GTCGGCGTCC CTGACTCCGT GACCTCCGG	LPRPLARRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS 9rowth fact 7432 1 %: NM_00: -3819 21 CCAGCTAGCC GCCCGAGTCC CCAGTATTGA	LOPRDARKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL OF receptor 5228 31 CCCGCCCCCCC CCCCCCCCCCCCCCCCCCCCCCCC	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YPPFNALLLL RNGLVKDKRF (avian er; 41 CGCCGCCCAG GCCAACGCCA GGCAACGCCA	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWPL ythroblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGA	120 180 240 300 leukemia 60 120 180
50 55	HAWVILILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac: Coding sequil GCCGCGCTGC AGGCCACCTC GCACGGCGCCC GCAGCGAGG	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWPP TGQVHELKDL CE 10 epidermal taber: Hs.7' Ld Accession tence: 187' 11 GCCGGAGTCC GTCGGGGTCC CTGACTCCGT GACCCTCCGG GTCGGGCTCT GTCGGGCTCT	LPRPLAKRCC GMAVPRDIAA VGILVLPHHD LKVLYATSHC REYDTAEAQS growth fact 7432 a #: NM_00: -3819 21 CGAGCTAGCC GCCCGAGTCC CCAGTATTGA GACCGCCGGG GGAGGAAAAG GGAGGAAAAG	LOPRDARKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL OF receptor 5228 31 CCGGCGCCGC CCGCCTCGCC TCGGGAGAGG GCAGCGTTGCC	ESAWKPLFYL HSIYATLYMD LNIYFKSRGG YFFFNALLL RNGLVKDKRF (avian ex) 41 CGCCGCCCAG GCCAACGCCA GCCAACGCCA CGGAGCGAGC	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWFL ythroblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGA GGCTGCGCTC	120 180 240 300 leukemia 60 120 180 240
50	HAWVILILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac: Coding sequil GCCGCGCTGC AGGCCACCTC GCACGGCGCCC GCAGCGAGG	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWPP TGQVHELKDL CE 10 epidermal taber: Hs.7' Ld Accession tence: 187' 11 GCCGGAGTCC GTCGGGGTCC CTGACTCCGT GACCCTCCGG GTCGGGCTCT GTCGGGCTCT	LPRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS growth fact 7432 a #: NM_00: -3819 21 CGAGCTAGCC GCCCGAGTCC CCAGTATTGA GACCGCCGGG GGAGGAAAAG GGAGGAAAAG	LOPRDARKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL OF receptor 5228 31 CCGGCGCCGC CCGCCTCGCC TCGGGAGAGG GCAGCGTTGCC	ESAWKPLFYL HSIYATLYMD LNIYFKSRGG YFFFNALLL RNGLVKDKRF (avian ex) 41 CGCCGCCCAG GCCAACGCCA GCCAACGCCA CGGAGCGAGC	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWFL ythroblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGA GGCTGCGCTC	120 180 240 300 leukemia 60 120 180 240 300
50 55	HAWVILLII DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac; Coding sequence GCCGCGCTGC AGGCCACCTC GCACGGCCCC GCACGGATGC TGCCCGGCGTGC AGGCCACTTGC AGGCCACTTGC AGGCCACTTGC AGGCATTGG	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WFWFRLYWFP TGQVHELRDL EE 10 epidermal nber: Hs.7' Id Accession GCCGGAGTCC GTCGGCGTCC CTGACTCCGT GACCTCCGG GTCGGGCTCT GCACTTTTGA	LPRPLAKRCC GNAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS GYOWTH fact 7432 #: NM_00: -3819 21 CGAGGTAGCC GCCCGAGTCC CCAGTATTGA GACGCCGGG GGAGGAATAGA GAGGAATATTT	LOPRDAKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL FOR receptor CCGGCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ESAWKPLFYIL HSIYATLYMD LNIYFKSRGG YFFFNALLLL RNGLVKDKRF (avian er) 41 CGCCGCCCAG GCCAACGCCA GGCAACGCCA TGGAGCTGGT AAGGCAACGAG	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWFL /throblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGAC TCTTCGGGGCTC TAACAAGCTC TAACAAGCTC	120 180 240 300 leukemia 60 120 180 240
50 55	HAWVILILI DLGCLSFGFS YIVAPAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac; Coding sequence 1 GCCGGGCTGC AGGCCACCTC GCACGGATGC TGCCCGGCGA AGGCATGC TGCCCGGCGA AGGCATGC TGCCCGGCGA	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWPP TGQVHELRDL EE 10 epidermal nber: Hs.7 id Accession ence: 187 11 GCCGGAGTCC GTCGGCGTCC CTGACTCCGT GACCTCTGG GTCGGGCTCT GCACTTTGA TTGGGAATTT	LPRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS 9rowth fact 7432 a #: NM_00: -3819 21 CCAGGCTAGCC GCCCGAGTCC CCAGTATTGA GACCGCCGGG GGAGGAAAAG AGATCATTTTA GGAAATTACC	LOPRDAKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL OF receptor 5228 31 CCGGCGCCCGC CCGCCTCGCC TCGGGAGAGC CCAGCCTCCC AAAGTTTGCC TCAGCCTCC TATGTCAGA	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YPPFNALLLL RNGLVKDKRF (avian er: 41 CGCCGCCCAG GCCAACGCCA GGCAACGCCA TGGCGCTGCT AAGGCACGAG AQAGGATGTT CGAATTATCA	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL ythroblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGA GGCTGCGCT TAACAAGCTC CAATAACTGT TCTTCTTCGTGTA	120 180 240 300 leukemia 60 120 180 240 300
50 55	DIAGCLEFGES YTVAFAARVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac: Coding sequil GCCGCGCTGC AGGCCACCTC GCAGGGCCCC GCAGGGCCCC GCAGGAGGATGG AGGCAGTTGG GAGGAGTGGT GCAGGGGCCC TGCCCGGGGA AGGCAGTTGG GAGGTGGTCG TGCCGGGGAGATTGG GAGGTGGTCG TTAAAGACCA TTAAAGACCA	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WFWFRLYWFP TGQVHELRDL CE 10 epidermal nber: Hs.7' 1d Accession Lence: 187- 11 GCOGGAGTCC GTCGGCGTCC CTGACTCCGG GTCGGCTTCCGG GTCGGCTTCTGA TTGGGAATTT TCCAGGAGTTTTCCAGGAGGTT TCCAGGAGGTT	LPRPLAKRCC GNAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS growth fact 7432 a #: NM_00: -3819 21 CGAGGTAGCC GCCCGAGTCC CCAGTATTGA GACGGCCGG GGAGGAAAAG AGATCATTTT GGAAATTACC GGCTGGTTAT	LOPRDAKMP AYLLOGSFYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL FOR recepto: 5228 31 CCGGCGCCGC CCGCCTCGC TCGGGAGAGC GCAGCGCTCC AAAGTTTGCC AAAGTTTGCC TATGGCAGTA	ESAWKPLFYL HSIYATLYMD LNIYFKSRGG YFFFNALLLL RNGLVKDKRF (avian er; (avian er; (GCCGCCCAG GCCAACGCCAG GCCAACGCCAG TGGCGCTGCT AAGGCACGAG AAGGCACGAG AAGGCACGAG AAGGCACGAG AAGGCACGAG AAGGCACGAG AAGATTATGA	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWPL ythroblastic 51 ACCGGACGAC CAACCACCAC GGCTGCGCT TAACAAGCTC CAATAACTGT TCTTTCCTTC	120 180 240 300 1eukemia 60 120 180 240 300 360
50 55	HAWVILLII DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac; Coding sequence GCCGCGCTGC AGGCCACTC GCACGGCCCC GCAGGGATGC TGCCGGGGGG TGCCCGGGGGG TGCCGGGGGGATGC TTAAAGACCA ATTCCTTTGG	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WFWFRLYWFP TGQVHELRDL EE 10 epidermal nber: Hs.7' Id Accession location GCCGGAGTCC GTCGGCGTCC GTCGGCGTCC GTCGGCGTCC GTCGGCTCT GACCTTCGG GTCTGGACTTTGA TTGGGAATTT TCCAGGAGGT TCCAGGAGGT TCCAGGAGGT TCCAGGAGGT TCCAGGAGGT TCCAGGAGGT TAAAACTGCA	LPRPLAKRCC GNAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS GYOWTH fact 7432 H: NM_OOS -3819 21 CGAGGTAGCC GCCCGAGTCC CCAGTATTGA GACGCCGGG GGAGGAAAAG AGATCATTTT GGAAATTACC GGCTGGTTATCA TATCATCATCATCATCATCATCATCATCATCATCATCATC	LOPRDAKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL OF receptor 5228 31 CCGGCGCCCC TCGGCGCCCCC TCGGGAGC GCAGCTCC AAAGTTTGCC CTCAGCCTCC TATGTGCAGA GTCATTGG	ESAWKPLFYIL HSIYATLYMD LNIYFKSRGG YFFFNALLLL RNGLVKDKRF (avian er) 41 CGCCGCCCAG GCCAACGCCA GGAGCGAGC TGGAGCTAGT AAGGCAACACA AGAGGATTATGA CCCTCAACAC	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWFL /throblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGAC GGCTGGGCTC TAACAAGCTC CAATAACTGT TCTTTCCTTC AGTGGACGAC	120 180 240 300 1e leukemia 60 120 180 240 300 360 420 480
50 55 60	HAWVILILI DLGCLSFGFS YIVAPAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac; Coding sequence GCCGCGCTGC AGGCCACTGC GCACGGATGC GCACGGATGC TGCCCGGGAA ACGCAGTTGG GAGGTGTGC TTAAAGACCA ATTCCTTTGG TTAGCAGTGT	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWPP TGQVHELRDL E 10 epidermal nber: Hs.7 id Accession ence: 187 11 GCCGGAGTCC GTCGGCGTCC CTGACTCCGG GTCGGCGTCC GACCTCTGG GACCTCTGG GACCTTTGA TTGGGAATTT TCCAGGAGGT AAAACCTGCA TATCTAACTA	LPRPLAKRCC GMAVPRDIAA VGILVLPHD LKVLYATSHC REYDTAEAQS 9 rowth fact 7432 1 %: NM_00: -3819 21 CAAGCTAGCC GCCGAGTCC CCAGTATTGA AGACGCCGGG GGAGGAAAAG AGATCATTAT GGCTGGTTAT GGCTGGTTAT GGAAATTACC GGCTGGTTAT GATCATCAGAA TGATGCAGAAT	AVALUGSFYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL OF receptor 5228 31 COGGOGCCGC CCGCCTCGCC TCGGGAGGCTCC AAAGTTTGCC AAAGTTTGCC TATGGCAGC GTCTCATGGGAAATATGT	ESAWKPLFYIL HSIYATLYMD LNIYFKSRGG YFFFNALLLL RNGLVKDKRF (avian er: 41 CGCCGCCCAG GCCAACGCCA GGCAGCGAGCAGCAGAGAGAG	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL ythroblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGA GGCTGGGCT TAACAAGCTC CAATAACTGT TCTTTCCTTC AGTGGAGCGA TCCTATGCC GCCCTATGCC	120 180 240 300 300 1eukemia 60 120 180 240 300 360 420 480 540
50 55	HAWVILILI DLGCLSFGFS YIVAPAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac; Coding sequence GCCGCGCTGC AGGCCACTGC GCACGGATGC GCACGGATGC TGCCCGGGAA ACGCAGTTGG GAGGTGTGC TTAAAGACCA ATTCCTTTGG TTAGCAGTGT	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWPP TGQVHELRDL E 10 epidermal nber: Hs.7 id Accession ence: 187 11 GCCGGAGTCC GTCGGCGTCC CTGACTCCGG GTCGGCGTCC GACCTCTGG GACCTCTGG GACCTTTGA TTGGGAATTT TCCAGGAGGT AAAACCTGCA TATCTAACTA	LPRPLAKRCC GMAVPRDIAA VGILVLPHD LKVLYATSHC REYDTAEAQS 9 rowth fact 7432 1 %: NM_00: -3819 21 CAAGCTAGCC GCCGAGTCC CCAGTATTGA AGACGCCGGG GGAGGAAAAG AGATCATTAT GGCTGGTTAT GGCTGGTTAT GGAAATTACC GGCTGGTTAT GATCATCAGAA TGATGCAGAAT	AVALUGSFYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL OF receptor 5228 31 COGGOGCCGC CCGCCTCGCC TCGGGAGGCTCC AAAGTTTGCC AAAGTTTGCC TATGGCAGC GTCTCATGGGAAATATGT	ESAWKPLFYIL HSIYATLYMD LNIYFKSRGG YFFFNALLLL RNGLVKDKRF (avian er: 41 CGCCGCCCAG GCCAACGCCA GGCAGCGAGCAGCAGAGAGAG	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL ythroblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGA GGCTGGGCT TAACAAGCTC CAATAACTGT TCTTTCCTTC AGTGGAGCGA TCCTATGCC GCCCTATGCC	120 180 240 300 1eukemia 60 120 180 240 300 360 420 480 540 600
50 55 60	DIAGCLEFGES YIVAFAARVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac: Coding sequil GCCGCGCTGC AGGCCACCTC GCACGGCGCCC GCAGGGACCTC GCACGGTGGC AGGCCACTC GCACGGTGGC TTGCCCGGGGA ATTCCTTTGG ATTCCTTTGC TTACAGGCT TAATTACAGG	TALRSAATAR PSYMPTOWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL CE 10 epidermal nber: Hs.7' Id Accession Lence: 187- II GCOGGAGTCC GTCGGGGTCC CTGACTCCGG GTCCGGGTCTC GACCTTCGG GTCGGGTTT TGCAGGAGTT TTCCAGGAGTT TTCCAGGAGTT TTCCAGGAGT AAAACCTGCA TATCTAACTA AAATCTGCA	LPRPLAKRCC GMAVPRDIAA VGILVLPHD LKVLYATSHC REYDTAEAQS growth faci 7432 gth: NM_00: -3819 21 CGAGGTAGCC GCCCGAGTACC CCAGTATTGA GACGGCCGG GGAGAAAAG AGATCATTTT GGAAATTACC GGCTGGTTAT GATCAACATT GATCAACAT TGGGCGCGT TGGCCGCGT	APROARMP AYLLOGSFYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL FOR recepto: 5228 31 CCGGCGCCGC CCGCCTCGC CCGCCTCGC GCAGGGCTCC ARAGTTTGCC TATGTGCAGA GTCCTCATTG GGAAATATGT AAAACCGGAC CCGCTCAGC	ESAWKPLFYTL HSIYATLYMD LNIYPKSRGG YPFFNALLLL RNGLVKDKRF (avian er; (accededage GCCAACGCCA GCCAACGCCA ACGAGGAG TGGCGCTGCT AAGGCACGAG ACGAGTTT GCAATTATGA ACTACGAAAA TGAAGGAGA TGAAGGAGAA TGAAGGAGAG TGAAGGAGAA TGAAGGAGAGA	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWPL 51 ACCGGACGAC CAACCACCAC GGCTGCGCT TCTTCGGGGA GGCTGCGCT TAACAAGCTC CAATAACTGT TCTTTCCTTC AGTGGACGAA TTCCTATGCC GCCCATGAGA	120 180 240 300 1e leukemia 60 120 180 240 300 360 420 480 540 600 660
50 55 60	HAWVILLII DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac; Coding sequence GCCCGGCTGC AGGCCACTC GCACGGCCCC GCACGGCCCC GCACGGCCCC GCACGGCCCC GCACGGCCCC GCACGGCCCC GCACGGCCC TTAGCAGTTCG TTAGCAGTCT AATTTACAGG TTAGCAGTCT AATTTACAGG TTAGCAGGCCA	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL TGQVHELRDL TGQVHELRDL TGQVHELRDL TGQVHELRDL TGQVHELRDL TGQVHELRDL TGQVHELRDL TGQVHELRDL TGQCTCC TGCCGTGGGTCC TGCCTCCGG TGCCTCCCGT TGCACTTCTGA TTGGGAATTT TCCAGGAGGT TTCCAGGAGGT TAAAACCTGCA TATCTAACTA AAATCCTGCA TCCAGGGGG TCCAGGGGG	LPRPLAKRCC GNAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS GYOWTH fact 7432 1 %: NM_00: -3819 21 CGAGCTAGCC GCCCGAGTCC CCAGTATTGA GACGCCGGG GGAGAAAAG AGATCATTTT GGAAATTACC GGCTGGTTAT GGTAATTACC GGCTGGTTAT TGATCATCAGA TGATGCACATT TGGCGCCGTG TGATGCACATT TGGCGCCGTG TGATGCACATT TGGCGCCCTGT TGATGCACATT TGGCGCCCTGT TGATGCACATT TGGCGCCCTGT TGATGCACATT TGGCGCCCTGT TGGCGCCCTGT TGATGCACATT TGGCGCCCTGT TGGCGCCCTGT TGATGCACATT TGGCGCCCTGT TGGCACATGT TGGCGCCCTGT TGGCACATGT TGGCGCCCTGT TGGCACATGT TGCACATGT TGGCACATGT TGCACATGT TGCACAT	APROARMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL OF recepto: 5228 31 CGGGGGCGGC CCGCTCGCC TCGGGAGGG GCAGGGTCCC AAAGTTTGCC CTCAGCCTCC TATGTGCAGA GTCCTCATTG GGAAATATG AAAACCGGAC CCGGTCAGCC CCGGGGGCGCC CCCATGG CGGGGTCAGC AAAGTTGCAATG AAACCGGAC AAAGTTGCAATG AAACCGGAC CGGTTCAGCC CGGTTCAGCC CGGTTCAGCA AAACCGGAC AAAGCAGTGAC AAACCGGAC AAACCGGAC AAACCGGAC AAACCGGAC AAACCGGAC AAACCGGAC AAACCGGAC AAACCGGAC AAACCGGAC AACCGGAC AACCGCAC AACCGCAC AACCGCAC AACCGCAC AACCGCAC AACCGCAC AACCCGAC AACCGCAC AACCGCAC AACCGCAC AACCGCAC AACCGCAC AACCGCAC AACCCAC AACCGCAC AACCGCAC AACCGCAC AACCCCAC AACCCCAC AACCCCAC AACCCAC AACCCCAC AACCCCCAC AACCCCAC AACCCCCAC AACCCCAC AACCCCCAC AACCCCCAC AACCCCCC	ESAWKPLFYIL HSIYATLYMD LNIYFKSRGG YFFFNALLLL RNGLVKDKRF (avian er) 41 CGCCGCCCAG GCCAACGCCA GCCAACGCCA TGGGGCTGCT AAGGCAACAC CGCAACAC CCTCAACAC ACTACGAAA TGAAGGAGCT ACAACCCTGC ACAACCCTGC ACAACCCTGC ACAACCCTGC ACAACCCTGC	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWFL /throblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGAC GACTACCACCGC TCTTCGGGGTT TAACAAGCTC TAACAAGCTC TAACAAGCTC CAATAACTGT TCTTTCGTTC AGTGGAGCGA TCCTATGGCAC CCTGTGCAAC	120 180 240 300 leukemia 60 120 180 240 300 420 480 540 600 660 720
50 55 60	INHVIVILILI DLGCLSFGFS YIVAPAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac: Coding sequence I GCCGCGCTGC GCACGGCCCC GCACGGATGC TGCCCGGCGA AGGCATTGG TGCCCGGCGA AGGCATTGG TTAAAGACCA ATTCCTTTGG TTAACAGG TTAACAGG TTAACAGG TTAACAGG TTAACAGG GTGGAGAGCC ATTTACAGG GTGGAGAGCC AATTTACAGG	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWPP TGQVHELRDL EE 10 epidermal nber: Hs.7 id Accession ence: 187 11 GCCGGAGTCC GTCGGGTCC GTCGGGTCC GACTCCGG GTCGGGCTCT GACTCCGG GTCGGGCTCT TCAGTCGGT TCCAGGAGTT TCCAGGAGTT TCCAGGAGTT TCCAGGAGTT AAAACCTGCA TATCTACTA AAATCCTGCA TCCAGTGGG	LPRPLAKRCC GMAVPRDIAA VGILVLPHD LKVLYATSHC REYDTAEAQS 9FOWTH fact 7432 1 %: NM_00: -3819 21 CAAGCTAGCC GCCGAGTCC CCAGTATTGA AGACGCCGGG GGAGGAAAAG AGATCATTATC GGAATTACC GGCTGGTTAT GGAATTACC GGATTACGAAT TGGCGCCGTG GGACCATACTCA GGACCATACTCA GGACCATACTCA TGGCGCCGTG GGACCATACTCA GCACCATACTCA GGACCATACTCA GGACCATACTCA TGGCGCCGTG GGACCATACTCA GCACCATACTCA GCACCATACTCA CAGCTGCTCA CACCTCACTCA CACCTCACTCA CACCTCACTCA	LOPRDARKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL OF receptor 5228 31 CCGGCGCCCCC CCGCCTCGCC TCGGGAGAGC GCAGCGCTCC GCAGCCTCC TCAGCTCC TATGTGCAGA AGCTATG GGAAATATGT AAAACCGGAC AGCGTTCAGCAC AGCAGTGACT AAGCTCATTG AAGCTATG AAGCTATGACA AGCAGTGACT AAGCTATGACACA AGCAGTGACT AAGCTTCAGCA AAGCTTCAGCAA AAGCTTCAGCAAACAA AAGCTTCAGCAAAAAAAAAA	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YPPFNALLLL RNGLVKDKRF (avian er; 41 CGCCGCCCAG GCCAACGCCA CGAAGCGAG CGAAGCGAG CGAAGCAGAG AGAAGAATATGA ACCATCAAAAA TGAAGAGGT TGCAACAC TTCTCAGCAA	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL 51 ACCGGACGAC CCAACCACCGC TCTTCGGGGA GGCTGGGCTC TAACAAGCTC CAATAACTGT TCTTTCCTTTC	120 180 240 300 1e leukemia 60 120 180 240 300 360 420 480 540 600 660
50 55 60	DIAGCLEFGES YTVAFAARVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac: Coding sequence 1 GCCGCGCTGC AGGCCACCTC GCACGGCGCCC GCAGGGACGC GCAGGGATGG AGGCAGTTGG GAGGGATGG ATTCCTTTGG TTAAAGACCA ATTCCTTTGG GTGGAGAGCA GACTTCCAGA GCTTCCAGA GTGGAGGAGCA GACTTCCAGA TGCTGGGGTG	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WFWFRLYWFP TGQVHELRDL E 10 epidermal nber: Hs.77 id Accession lence: 187 11 GCCGGAGTCC GTCGGGGTCC GTCGGGGTCC GTCGGGGTCT GACCTTCGG GTCGGGTCT GACTTTTGA TTGGGAATTT TCCAGGAGTT TTGGGAATTT TCCAGGAGT ATACTAACTA AAATCCGCA TCCAGTGGCG ACCACTGGCG ACCACCTGGCG ACCACCTGGG	LPRPLAKRCC GMAVPRDIAA VGILVLPHD LKVLYATSHC REYDTAEAQS growth fact 7432 gth: NM_009 -3819 21 CGAGCTAGCC GCCCGAGTCC CCAGTATTGA GACGCCCGGG GGAAATTACC GGCTGGTTAT GATCATCAGA TGATGCAAATT TGACCGCCGTG GGACATAGCA CGCTGCCAG GGACATAGCC CAGCTGCCAG AGACTGCCAG	LOPRDARKMP AYLLOGSPYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL TO recepto: 5228 31 CCGGCGCCGC CCGCCTCGCC TCGGGAGAGC GCAGCGCTCC AAAGTTTGCC TATGTGCAGA GTCCTCATG GGAAATATGT AAAACCGGAC CGGTTCAGCA AAGTTTGACC AAGTTTGACC AAGTTTGACC AAGTTTGACC AAGTTTGACC AAGTTTGACC AAGTTTGACC AAACTTGACC AAACTTGACC AAACTTGACC AAACTTGACC AAACTTGACC AAACTTGACCA AAACTGGACC AAACTTGACCA AAACTGGACC AAACTTGACCA AAACTTGACCA AAACTGGACC AAACTTGACCA AAACTGGACC AAAACTGGACC AAAACTGACC AAACTGACC AAAACTGACC AAAACTCACC AAAACTGACC AAAACTGACC AAAACTGACC AAAACTGACC AAAACTGACC AAAACTCACC AAAACTCACCACC AAAACTCAC	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian erg 41 CGCCGCCCAG GCCAACGCCA ACGAGCCAA CGCAACGAGC TGGCGCTGCT AAGGCACGAG ACAGGAGT TGAATTATGA CCCTCAACAA TGAAGGAGCT ACAACCTGC TTCTCAGCAA CAAGCTGTCC AAAGCTGTCC AAAGCTGTCC AAAGCTGTCTC	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWPL 51 ACCGGACGAC CACCACCAC CACCACCAC GGCTGCGCT TAACAAGCTC CAATAACTGT TCTTTCCTTC AGTGGAGGAC ACCACTGGCAC ACCACTGGCAC CATTAGCAC CCATTAGCAC CCTTTCCTTC AGTGGAGCAC CCTTTCCGTTC CAATACGAGCAC CCTTTCCGTTC CAATACGAGCAC CCTTTCCGTTC CAATAGCACC CCTTTCCGATTC CAATAGCACC CATGTCCGATTC CAATGGGAGC CATGTCCGATTC CAATGCGCACC CACCACCACC CCTCCCACCACCAC CCTCCCACCACCACC CCCCCACCACCACCAC CCCCCACCAC	120 180 240 300 leukemia 60 120 180 240 300 420 480 540 600 660 720
50 55 60 65	HAWVILLII DLGCLSFGPS YIVAPAAKVI DNA SEQUENC Gene name: Unigene nur Nucleic Ac; Coding sequence GCCGCGCTGC AGGCCAC GCACGGCCCC GCACGGCCCC GCACGGCTGC AGGCAGTTGG TGCCGGGGGA AGGCAGTTGG TGAGGAGTGC TTAAAGACCA ATTCCTTGG TTAGCAGTCT AATTTACAGG TTAGCAGTCT AATTTACAGG TTAGCAGTCT AATTTACAGG TTAGCAGTCT TTAGCAGTCT TTAGCAGTCT TTAGCAGTCT TTAGCAGTCT TTAGCAGTCT TTAGCAGTCT TTAGCAGTCT TGCTGCGGGG TGCTGCGGGGC TGCTGCGGGGC TGCTGCGGGGC	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WFWFRLYWFP TGQVHELRDL TEE 10 epidermal nber: Hs.7' Id Accession Ince: 187' IT GCCGGAGTCC GTCGGGGTCC CTGACTCCGT GACCTTCCGG GTCGGGCTCT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTT AAAACCTGCA TATCTAACTA AAATCCTGCA TATCTAACTA AAATCCTGCA TCCAGGAGGGC ACCACCTGGG CAGGAGAGGA ACCACCTGGG ACC	LPRPLAKRCC GNAVPRDIAA VGILVLPLHD LKVLYATEHC REYDTAEAQS GYOWTH fact 7432 1 %: NM_00: -3819 21 CGAGCTAGCC GCCCGAGTCC CCAGTATTGA GACGCCGGG GGAGAAAAG AGATCATCAGA TGATCATCAGA TGATCATCAGA TGATCATCAGA TGATCAGAAT TGGCGCCGTG GGACATAGTC CAGCTGCCAA GAACTGCCAG GAACTGCCAG GAACTGCCAC	LOPRDARKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL OF recepto: 5228 31 COGGCGCCCC TCGGCG CCCCTCGCC TCGGGAGGC CCAGCCTCC TCGGAGAGC CCAGCCTCC TATGTGCAGA GTCCTCATTG GGAAATATGT AAACCGGAC AGGTTCAGCA AGGTTCAGCA AGGTTCAGCA AAGTTGTGATC AAACTGACCA AAGTGTGATC AAACTGACCA AAGTGTGATC AAACTGACCA AAGTGACCACCA AAGTGACCACCACCACCACCACCACCACCACCACCACCACCACC	ESAWKPLFYIL HSIYATLYMD LNIYFKSRGG YFFFNALLLL RNGLVKDKRF (avian er) 41 CGCCGCCCAG GCCAACGCCA GCCAACGCCA TGGGGCTGCT AAGGCACGAG ACCACACAC ACTACAACA TGAAGGAGCT ACAACCTGC TCTCAGCAA ACAACCTGC TTCTCAGCAA ACAACCTGCC AAATCATCTG ACCAACCTGCC ACAACCTGCC AAATCATCTG	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWFL /throblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGAC GACTACTGGGAC TCATACAGCTC TAACAAGCTC TAACAAGCTC TCATTGGTC AGTGGAGCA CCTGTGCAAC CCTGTGCAAC CATGTGCAAC CATGTGCAAC CATGTGCAAC CATGTGCAAC CATGTGCAAC CATGTGCAAC CAATGGGAGC TCAATGGGAGC TGCCCAGCAG TCCCAGCAG TCCCAGCA	120 180 240 300 1eukemia 60 120 180 240 300 360 420 480 540 600 660 720 780
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50 55 60 65	INHVIVILILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac; Coding sequence Coding sequence GCCCGCGCTGC AGGCCACCTC GCACGGCCCC GCAGGGATGC TGCCCGGCGA AGGCAGTTGG GAGGTTGGTCC TAAAGACCC TAAAGACCC TAAAGACCA GACTTCCAGA GACTTCCAGA GACTTCCAGA GCTCCAGGGT TGCCCGGGCG GCCTCCACAG GCTCCACAG ACGTCCAGACAG ACGTCCAGACACAG ACGTCCAGACACACACACACACACACACACACACACACAC	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WFWFRLYWFP TGQVHELDL E 10 epidermal nber: Hs.77 id Accession Ecnce: 187 11 GCCGGAGTCC GTCGGGTCC GTCGGGGTCC GTCGGGGTCC GTCGGGGTCC GTCGGGGTCC TGACTCCGT GACCTTCGG GTCGGGGTCC TATCTAACTA AAATCCTGCA ACACCTGGG ACCACCTGGG GCCGCGGGGG GCCCCCGGGG GCCCCCGGGG GCCCCCGGG	LPRPLAKRCC GNAVPRDIAA VGILVLPHD LKVLYATEHC REYDTAEAQS growth fact 7432 gth: NM_009 -3819 21 CGAGCTAGCC GCCCGAGTCC CCCAGTATGA GACGCCGGG GGAAATTACC GGCTGGTTAT GATCATCAGA TGATGCAAAT TGGCGCCGTG GGACATAGTC CAGCTGCCAA GAACTGCCCC GAGCGACTGC CAGGTCCCC GGAGCGACTGC GAGCGACTGC GAGCGACTGC GAGCGACTGC GAGCGACTGC GAGCGACTGC GAGCGACTGC CCCACTGTTAT	LOPRDAKMP AYLLOGSPYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL COT recepto: 5228 31 CCGGCGCCGC CCGCCTCGCC TCCGGGAGAGC GCAGCGCTCC TATGTGCAGA GTCCTCATTG AAAACCGGAC AGGAGTTCACT AAGTTTGACC AAGTGAGCAC AAGTGAGCAC AAGTGAGCAC CCGGTTCAGCC CCGGTTCACC CCGGTTCACC CCGGTTCACC CCGGTTCACC CCGGTTCACC CCGGTTCACC CCGGTTCACC CCGGTTCACC CCGTTCACC CCCTTCACC CCCTTCACC CCCTTCACC CCGTTCACC CCCTTCACC CCCTTCACC CCCTTCACC CCCTTCACC CCCTTCACC CCCT	ESAWKPLFYL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian erg 41 CGCCGCCAG GCCAAGGCCA CGGAGCGAGC CGGAGCGAGC	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWFL 51 ACCGGACGAC CAACACCGC CAACACCGC TCTTCGGGGA GGCTGCGCTC TAACAAGGTT CATTAGCAC GCCATTAGGA CCTGTGCAAC CATGTGGAGC CATGTGAGAC CAGAGGAGCC CCCCCCCCCC	120 180 240 300 300 1eukemia 60 120 180 240 300 360 420 480 540 600 660 6720 780 840 900 960
50 55 60 65	INHVIVILILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac; Coding sequence Coding sequence GCCCGCGCTGC AGGCCACCTC GCACGGCCCC GCAGGGATGC TGCCCGGCGA AGGCAGTTGG GAGGTTGGTCC TAAAGACCC TAAAGACCC TAAAGACCA GACTTCCAGA GACTTCCAGA GACTTCCAGA GCTCCAGGGT TGCCCGGGCG GCCTCCACAG GCTCCACAG ACGTCCAGACAG ACGTCCAGACACAG ACGTCCAGACACACACACACACACACACACACACACACAC	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WFWFRLYWFP TGQVHELDL E 10 epidermal nber: Hs.77 id Accession Ecnce: 187 11 GCCGGAGTCC GTCGGGTCC GTCGGGGTCC GTCGGGGTCC GTCGGGGTCC GTCGGGGTCC TGACTCCGT GACCTTCGG GTCGGGGTCC TATCTAACTA AAATCCTGCA ACACCTGGG ACCACCTGGG GCCGCGGGGG GCCCCCGGGG GCCCCCGGGG GCCCCCGGG	LPRPLAKRCC GNAVPRDIAA VGILVLPHD LKVLYATEHC REYDTAEAQS growth fact 7432 gth: NM_009 -3819 21 CGAGCTAGCC GCCCGAGTCC CCCAGTATGA GACGCCGGG GGAAATTACC GGCTGGTTAT GATCATCAGA TGATGCAAAT TGGCGCCGTG GGACATAGTC CAGCTGCCAA GAACTGCCCC GAGCGACTGC CAGGTCCCC GGAGCGACTGC GAGCGACTGC GAGCGACTGC GAGCGACTGC GAGCGACTGC GAGCGACTGC GAGCGACTGC CCCACTGTTAT	LOPRDAAKMP AYLLOGSPYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL COT recepto: 5228 31 CCGGCGCCGC CCGCCTCGCC TCCGGGAGAGC GCAGCGCTCC TATGTGCAGA GTCCTCATTG AAAACCGGAC AGGAGTTCACT AAGTTTGACC AAGTGATGAC AAGTGATGACT AAGTGTGACC CCGGTTCACC CCGGTTCACC CCGGTTCACC CCGGTTCACC CCGGTTCACC CCGGTTCACC CCGGTTCACC CCGGTTCACC CCGGTTCACC CCGTTCACC CCCTCACC CCCTTCACC CCCTTCACC CCCTTCACC CCCTTCACC CCCCTTCACC CCCTTCACC CCCTTCACC CCCTTCACC CCC	ESAWKPLFYL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian erg 41 CGCCGCCAG GCCAAGGCCA CGGAGCGAGC CGGAGCGAGC	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWFL 51 ACCGGACGAC CAACACCGC CAACACCGC TCTTCGGGGA GGCTGCGCTC TAACAAGGTT CATTAGCAC GCCATTAGGA CCTGTGCAAC CATGTGGAGC CATGTGAGAC CAGAGGAGCC CCCCCCCCCC	120 180 240 300 300 1eukemia 60 120 180 240 300 360 420 480 540 600 660 6720 780 840 900 960
50 55 60 65	INHVIVILILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac; Coding sequence GCCGCGCTGC AGGCCACCTC GCACGGATGC GCACGGATGC TGCCCGGGGATGC TGCCCGGGGATGC TTAGCAGTCC TTAGCAGTCC TTAGCAGTCC AATTTCCTTGG TTAGCAGTCT AATTTACAGG GTGGAGAGCA GCTGCGGGTG GTGGAGGAGCA GACTTCCAGA TGCTGGGGTG GTGCTGGGGTG GTGCTGCGGGT GGCTGCACAG ACGTGCAACG GCTGCACAG	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL TE 10 epidermal nber: Hs.7: Ld Accession ence: 187: 11 GCCGGAGTCC GTCGGGGTCC CTGACTCCGT GACCTCCGG GTCGGCTTCT GCACTTTTMA TTGGGAATTT TCCAGGAGTT TCCAGGAGTT TCCAGGAGTT TATCTAACTA AAATCCTGCA TATCTAACTA AAATCCTGCA TATCTAACTA AAATCCTGCA CACCTGCG CAGGAGAGGA ACCACCTGCG GCCCCCGGGA ACACCTGCGT ACACCTGCG ACACCTGCG ACACCTGCG ACACCTGCG ACACCTGCGA ACACCTGCA ACACT	LPRPLAKRCC GNAVPRDIAA VGILVLPHD LKVLYATSHC REYDTAEAQS 9 ** NM_00: -3819 21 CGAGCTAGCC GCCCGAGTACC CCAGTATTGA GAGGCCGGG GGAGGAAAAG AGATCATCAGA TGATCATCAGA TGATGCAGCCGTTAT GGGACATAGCC GGCTGGTAT CGGACTAGCC GGCTGGTAT CGGACTAGCC GGACTAGCC GGACTAGCC GAGCTAGCC GAGCTAGCC GAGCTGCCAA CAGCTGCCCA CAGCTGCCCA CAGCTGCCCA CCACTCTTG CCACTCTTGGT CAGCTTATTG CAGCTTATTT CAGCTTATT CAGCTTATTT CAGCTTATT	LOPRDAAKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL OF recepto: 5228 31 COGGCGCCCC CCGCCTCCCC CCGCGGCGCCCC CCGCGGCGCCCC CCGGGGGCCCC CCGCCTCCC CTCAGCCTCC CTCAGCCTCC TATGTGCAGA GTCCTCATTG GGAAATATGT AAACCGGAC AGGTTCAGCA AGCAGTGACT AAGTGTGACC CCCTCTACAGC CTCTGCCC CTCTACACC CTCTTACACC CTCTTACACC CTCTTACACC CCCTCTACACC CCCTCTACACC CCCTCTACACC CCCTCTACACC CCCTCTACACC CCCTCTACACC CCCTCTACACC CCCTCTCCC CCCTCTCCC CCCTCTCCC CCCTCTCCC CCCTCTCCC CCCTCTCCC CTCTCCCC CTCTCCCC CTCTCCCC CTCTCCCC CTCTCCCC CTCTCCCC CCTCTCCCC CTCTCCCC CTCTCCCC CTCTCCCC CTCTCCCC CTCTCCCC CTCTCCCC CCTCTCCC CCCTCTCCC CCCTCTCCCC CCCTCTCCC CCCTCCCC CCCTCTCCC CCTCTCCC CCCTCTCCC CCTCTCCC CCCTCTCCC CCCTCTCC CCCTCTCCC CCCTCTCCC CCCTCTCC CCTCTCCC CCCTCTCC CCTCTCTCC CCCTCTCC CCCTCTCCTC	ESAWKPLFYIL HSIYATLYMD LNIYFKSRGG YFFFNALLLL RNGLVKDKRF (avian er) 41 GCGCCGCCCAG GCCAACGCCA GCCAACGCCA GCCAACGCCA AGGCACGAG AGGCAGGAG AGGCAGGAG AGGCAGGAG ACTACGAAA TCAACGCTGC AAATCATCTG GCCACACCA GCCACACCA GCCACACCA CCACCACGTA AGCCACGCA ACTACGAAA ATCATCTG GCCACACCA ACTACGCA ACTACCACGCA ACTACGCA ACTACCA ACTACGCA ACTACA ACTACGCA AC	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWFL S1 ACGGACGAC CAACCACCGC TCTTCGGGGAC TCATCGGGGCT TAACAAGCTC TAACAAGCTC TCATGGGAC ACTGGAGCA CCATGAGAGCC CCATGAGA CCTGTGCAAT CCATTGCGAT CAATGGGAGC TGCCCAGCAG GTGTGCTGC AGACGAGCC CCAGATGGAT CCATGGAAC CCAGATGGAT TCATGGAAC CCAGATGGAT TCATGGAAC CCAGATGGAT TCATGGAAC CCAGATGGAT TCAGAAGCC CCAGATGGAT	120 180 240 300 300 1eukemia 60 120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50 55 60 65	INHVIVILILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENG Gene name: Unigene nur Nucleic Ac: Coding sequence I I GCCGCGCTGC AGGCCACTC GCACGGCCCC GCACGGATGC TGCCCGGCAA AGGCATTGG TGCCCGGCAA TTCCTTTGG TTAAAGACCA ATTCCTTTGG TTAAGGCGT TTAAGGCGT TTAAGGCGT TTAAGGCGT TTAAGGCGT TTAAGGCAGTGGT AATTTACAGG TTGGTAGGCAG TGCTCCGGGT TGCTCAGGG TTATTTGGTGA	TALRSAATAR PSVPTDWTP VSSYAPRYHN WFWFRLYWFP TGQVHELRDL CE 10 epidermal nber: Hs.77 id Accession Lence: 187 il GCOGGAGTCC GTCGGGGTCC CTGACTCCGG GACCTCCGG GACCTCCGG GTCGGGGTCC CTGACTCCGT TCCAGGAGTT TCCAGGAGTT TCCAGGAGTT TCCAGGAGT AAAACCTGCA TATCTAACTA AAATCCTGCA ACCTGGG ACGACTGGG ACGCTGGGG ACGCCGGGA ACACCTGCC AGGGGAATAT AAATCCTGCA ACCCGGGA ACACCTGCC AGGGGAATACACGG ACACCTGCC AGGGCAATA	LPRPLAKRCC GMAVPRDIAA VGILVLPHD LRVLYATSHC REYDTAEAQS growth faci 7432 growth faci 7432 1 CARGCTAGCC GCCCGAGTCC CCAGTATTGA GACCGCGGG GGAGAAAG GGAGGAAAG GGAGGAATAGCC GCCGGTTAT GATCATCAGA TGATGCAGA TGATGCAGA GACTGCCAG GAACTGCCAG CAGTGCCAG CAGCTTTGGT CAGCTTTGGTT CAGCTTTGGTT CAGCTTTGGTT CAGCTTTGGTT CAGCTTTGGTT CTCGTGCGTC	LOPRDAAKMP AYLLOGSFYG 1SDVQLEFTK SLRTVPDIPF EOF recepto: 5228 31 CCGGCGCCCCC CCGCCTCCC AAAGTTTGCC AAAGTTTGCC GCAAATATGT AAAACCGAC AGCAGTCATG GGAAATATGT AAAACCGAC AGCAGTCACT CCGGTCACTCC CTGTCTCC CTGTCTCC CTGTCTCC CTGTCTCC CTGTCTCC CTCTACAACC GCCACCTGCC GCCACCTGCC CGGTCTCCC CTCTACAACC GCCACCTGCC CGGCCCCTCTC CGGCCCCTCTCCC CGCCCCCCC CCGCCCCCCC CCGCCCCCCC CCGCCCCCC	ESAWKPLFYL HSIYATLYMD LNIYFKSRGG YFFFNALLLL RNGLVKDKRF (avian er; (avian er; (GCCGCCCAG GCCAACGCCA ACGAGCAGC TGGCGCTGAG ACGAGCAGC ACGAGCAGC ACGAGCAGC ACTACGAACA ACTACGAACA ACTACGAACA ACTACGAACA ACTACGAACA CAAGCTGTCC TCTCAGCAA CAAACTATCTG GCCACAACCA GCAAATTCCG GCCACAGTA TGAAGAGTT TGAAGAGT TGAAGAG	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWPL 51 ACCGGACGAC CAACCACCOC TCTTCGGGGA GGCTGCGCTC TAACAAGCTC CAATAACTOT TCTTTCCTTC AGTGGAGCGA TCCTATGCC GCCCATGAGGA CCTGTGCAAC CATGGGAGC CATGTCGATG CAATAGGGAGC CATGTCGATG CAATAGGAGC CATGTCGATG CCAGGAGGAGGATGCAC CCAGGAGGATGCAT TCCCCGTAATT TCTCCCGTAATT TCTCCCGTAATT TCTCCCGTAATT	120 180 240 300 300 1eukemia 60 120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50 55 60 65 70	INHVIVILILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac; Coding sequence GCCGCGCTGC AGGCCACTC GCAGGGCCC GCAGGGATGC TGCCCGGGGG TGCCCGGGGGAGAGGC TAAAGACCA ATTCCTTGG TTAGCAGTC TAATTACCAGA TGCTGGGTG TGCTCCGGGC GGTGCACAGG GCTGCACAG GCTTCCGGGC GGTGCACAGG TGTTCTGGGAC TGTTTGGGAC TGTTTGTGAA	TALRSAATAR PSYVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL E 10 epidermal nber: Hs.77 Id Accession GCCGGAGTCC GTCGGGGTCC GTCGGGGTCC GTCGGGGTCC GTCGGGGTCC GTCAGCTCCGT GACCTTCGG GTCTCGGGTTCT GACTTTGA TTGGGATTTTGA TTGGGATTTTTA TCCAGGAGGT TATCTAACTA AAATCCTGCA TATCTAACTA AAATCCTGCA ACCACTGGG GCGCCCGGGA ACCACTGGG GCCCCCGGGA ACACTGCCC AGGGCAAATA CAGGTCACCA GGGCAAATA CAGGTCACCA	LPRPLAKRCC GNAVPRDIAA VGILVLPHD LKVLYATEHC REYDTAEAQS growth fact 7432 growth fact 7432 li #: NM_00: -3819 21 CGAGCTAGCC GCCCGAGTATGA GACGCCCGG GGAAATTACC GGCTGGTTAT GGAAATTACC GGCTGGTTAT TGATCATCAGA TGATCATCAGA TGATGCAATTT GGAAATTACC GGCTGGTAT GGACATAGCA CAAGTCCCC GAGCGCCCAG GAACTGCCCC CAGCTCCCC CAGCTCCCCC CAGCTCCCC CAGCTCCCCC CAGCTCCCCC CAGCTCCCCC CCCCCTTCGGT CCCCCTTTGGT CCCCTTCTGGT CCTCTTGGTC CTCTTGGTATAGAAG	LOPRDAKMP AYLLOGSPYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL TOT receptor 5228 31 CCGGCGCCCC CCGCCCCCCCC CCGCGCGCCCCC CCGCGCGCCCC TATGTGCAGA GCAGTCACT AAACCGGAC AGGATCACT AAACCGGAC AAACTGACC CCTCTACAACC CCTCTACAACC CCCTCTACAACC CCCCCCCC	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian erg 41 GCCCGCCCAG GCCAAGGCCA CGGAGCGAG CGAGCGAG	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWFL 51 ACCGGACGAC CAACACCGC CAACACCGC TCTTCGGGGA GGCTGCGCTC TAACAAGCTC CAATAACTGT TCTTTCCTTC AGTGGAGCAC CCTGTGCAAC CATGTGCAAC CATGTGCAC CATGTGCAC CATGTGCAC CATGTGCAC CATGTGCAC CATGTGCAC CAGTGGAT CCAGTGGAT TCCCCGGATGAT TCCCCGGTAAT TCCCCGGTAAT TCCCCGGTAAT TCCCCGGTAAT TCCCCGGTAAT CTATGAGATGA	120 180 240 300 300 1eukemia 60 120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50 55 60 65	INHVIVILILI DLGCLSFGFS YIVAPAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac; Coding sequence GCCCGCCTGC GCACGGCCCC GCACGGATGC GCACGGATGC TGCCCGGCTGC AATTCCTTTGG TTAAGAGCA ATTCCTTTGG TTAGCAGTCT AATTTACAGG GTGGAGGAGC GTGGAGGAGC GTGGAGCAGC GTGGAGCAGC GTGGAGAGC GTGTGAGAG ACGTGCAAGG GTGTGACAGG GTGTGACAGG GTGTGACAGG GCTGCAAGG GTGACCCCG TATGTGGTGA GAGGAAGACG GGAATAGGTA	TALRSAATAR PSVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL TGQVHELRDL TGQVHELRDL TGQVHELRDL TGQVHELRDL TGQVHELRDL TGQVHELRDL TGQCGTGC TGCCTCCGGGGTCC CTGACTCCGT GCACTTCTGG GTCGGCGTCC CTGACTCCGT GCACTTTTQA TTGGGGATTTT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTT TATCTAACTA AAATCCTGCA ACACCTGGG CAGGAGAGGA ACACCTGGG GCCCCGGGA ACACCTGGG GCCCCCGGGA ACACCTGGG GCCCCCGGGA ACACCTGCGCAA CAGGTCACCG CGCTCCGCAA TTGGTGAATT	LPRPLAKRCC GMAVPRDIAA VGILVLPHD LKVLYATSHC REYDTAEAQS 9	LOPRDAAKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL OF recepto: 5228 31	ESAWKPLFYIL HSIYATLYMD LNIYFKSRGG YFFFNALLLL RNGLVKDKRF (avian er (avian er	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWFL 2throblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGAC TCATCGGGGCTC TAACAAGCTC TCATCGTC AGTGGAGCGA CCTGTGCGAC CCTGTGCGAC CCTGTGCGAC CATGCGAT CCATGCGAC GCCATGCGAC GTGTGCTGCA TAGCAGAGCC TCCCGTAGA TCCCCGTAGA TCCCCGTAGA AGTGGAGGC CCAGATGGAT TCCCCGTAGAT TCCCCGTAGAT TCTATGAGAT AGTGTGTAC	120 180 240 300 1eukemia 60 120 180 240 300 360 420 480 540 660 720 660 720 900 900 1020 1080 1140 1200
50 55 60 65 70	INHVIVILILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nu Nucleic Ac: Coding sequence GCCGCGCTGC AGGCCACCTC GCACGGCCCC GCAGGGCCCC TTAAAGACCA ATTCCTTTGG TTAAGACCA ATTTCCTTTGG TTGGGGGTG TGGCTGGGGTG TGGCTGGGGTG TGGTGGGGTG TGGTGGGGTG TGGTGGGGTG TGGTGAGCCA ATTTACAGG TTGTGAGACCC TTAAGGACCA GGTTCCAGA ACGTGCAAGG ACGTGCAAGG ACGTGCAAGG ACGTGCAAGG ACGTGCAAGG ACGTGCAAGG ACGTGCAAGG ACGTGCAAGG ACGTGCAAGG TTATTATGTGA AGGGAAGACC GGAATAGGTA TTCAAAAACT	TALRSAATAR PSSVPTDWTP VSSYAPRYHEN WFWFRLYWFP TGQVHELRDL E 10 spidermal nber: Hs.77 Id Accession Lence: 187 II GCCGGAGTCC CTGACTCCGG GTCGGCGTCC CTGACTCCGG GTCCTCCGG GTCCTCTGG GTCTCTCGG GTCCTCTGG ACACTTTMA TTGGGAATTT TCCAGGAGTC AAAACCTGCA ACACTGCA TCCAGTGGC ACCACTGGG GCCCCCGGGA ACACTGCCC AGGGCAAATA ACAGATCACGG GCCTCCGCAA TTGGTGAATT GCACCTCCCAT GCCCTCCCAT GCCCTCCCAT GCCCTCCCAT GCCCTCCCAT TGGTGAATT GCACCTCCCAT TGGTGAATT GCACCTCCCT	LPRPLAKRCC GMAVPRDIAA VGILVLPHD LRVLYATSHC REYDTAEAQS growth faci 7432 growth faci 7432 li	LOPRDAAKMP AYLLOGSFYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL FOR recepto: 5228 31 CCGGCGCCGC CCGCCTCGCC TCGGGAGAGC CTCAGCTCC TATGTGCAGA AGTCTCATTG GGAAATATGT AAAACCGACC CGGTTGAGCA AGCAGTGACT CGGTCAGCA AGCAGTGACT CTCTATGACCA CGGTCACCC CTCTACACC CCTCTACACC CCCTCCCCACACC CCACCTGCG CCAAGCGGC CCAACCTGCG CCAAGCGGC CCAACCTGCG CCAACCTGCAACA CCCCAACCTCCC CCACCTCCAACA CCCCACCTCCAACA CCCCACCTCCACACC CCCCACCTCCACACC CCCCCACCTCCCACACC CCCCCCCACACC CCCCCCCC	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YPFFNALLLI RNGLVKDKRF (avian er; (avian er	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWPL 51 ACCGGACGAC CAACCACCCAC TCTTCGGGGA GGCTGCGCTC TAACAAGCTC CAATAACTGT TCTTTCCTTC AGTGGAGCGA TCCTATGCAC CCACTAGGA CCTGTGCAAC CCATGGAGCGA GTGTGCTGCA CCAGGAGGAGC CTGCCAGCAG GTGTGCTGCA CCAGGAGGAGC TCCCAGGAGGAGC TCCCAGGAGGAGC TCCCAGGAGGAT TCCCCGTAAT TCCCCGTAAT TCATGAGATC TATGAGATC TATTAGAGATC TATTAGAGATC TATTAGAGATC TATTAGAGATC TATTAGAGATC TATTAGAGATC TATTAGAGATC TATTAGAGATC TATTAGAGATC	120 180 240 300 1eukemia 60 120 180 240 300 360 420 480 540 660 720 660 720 900 900 1020 1080 1140 1200
50 55 60 65 70	INHVIVILILI DLGCLSFGPS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac; Coding sequence GCCGCGCTGC AGGCCACTC GCAGGCCC GCAGGGCCC GCAGGATGC TGCCCGGGGG TGCCCGGGGG TGCCCGGGGG TGCCCGGGGG TTAGCAGTC TTAAAGACCA ATTCTTTGG TTAGCAGTC TATTCAGGG GGCTGCCAGGG GGCTGCACAG GCTGCAGGG GGTGCACAG GCTGCAGGG GGTGCACAG GCTGCAGGG GGGTGCACAG GGGTGCACAG GGGTGCACAG GGGTACACG GGATTCAGGAC GGATTCTGGTGA GGGATAGGTA TTCAAAAACT TTCAAAAACT GGCTCTTCA	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL E 10 epidermal nber: Hs.77 Id Accession GCCGGAGTCC GTCGGGGTCC CTGACTCCGT GACCTCCGG GTCGGCGTCC CTGACTCCGT GACCTTCGG GTCGGCGTCC CTGACTCCGT GACCTCCGG GTCGGCGTCC CTGACTCCGT GACCTCCGG GTCGGCGTCC GACCTCCGG ACCACTGGG ACCACTGGG ACCACTGGG CCGGGAATAA AAATCCTGCA ACACTGCG ACGAGTAGGA ACACTGCC AGGGCAAATA CAGATCACGC AGGGCAAATA CAGATCACGC GCGTCGCAA TTGGTGAATT GCACTCCTCA	LPRPLAKRCC GNAVPRDIAA VGILVLPHD LKVLYATEHC REYDTAEAQS growth fact 7432 growth fact 7432 growth fact 7432 li #: NM_00: -3819 21 CGAGCTAGCC GCCCGAGTCC CCCAGTATGA GACGCCGGG GGAAATTACC GGCTGGTAT GGAAATTACC GGCTGGTAT TGATCATCAGA TGATGCAGAT TGATCATCAGA GAACTGCCAG CAAGTCCCC GAGCGACTGC CCCACTCATG CCACTCATG CCCCTTGGT CTCCTGGTC CTGTTAGAAAG TAAAGACTCA CAGTTGCGAT CAGCTTAGGT CCCCTGTGTTAAGAAG TAAAGACTCA CAGTTGCGAT CAGCTTGGTT CTCTTGGTT CAGCTTCGGTT CAGCTTCGGTT CTCTTGGTT CAGCTTGCGTT CAGCTTGCGTT CTCTTGGTT CAGCTTGCGTT CAGCTTCGGTT CTCTTCGGTT CAGCTTGCGTT CAGCTTGCGTT CTCTTCGGTT CAGCTTCGGTT CAGCTTCGGTT CTCTTCTGGTT CCTCTTCGGTT CCTCTTCGGTT CCTCTTCGGTT CCTTCTGGTT CCTCTTCGGTT CCTCTTCTTCTT CCTCTTCTTCT CTTCTTCTTCTT	LOPRDAKMP AYLLOGSPYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL TOT receptor 5228 31 CCGGCGCCCC CCGCCCCCCC CCGCCCCCCCC CCAGCCC CCAGCCC TATGTGCAGA GCAGTCACT AAGTTTGCC TATGTGCAGA AGCAGTGACT AAGTTCACC CCGCACCCC CCCCCCCCCC	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian erg 41 GGCCGCCCAG GCCAACGCCA CGGAGCGAG CGAACGCCA AGGAGCTGCT AAGGCATGTT GGAATTATGA CCCTCAACAC ACTACAACAC CTCAACAC CACACCTGC CAAACCTGC CAAACCTGC CACACCAGCA CAAACCTGC CACACCAGCA CACACCAGCA CACACCAGCA CACACCAGCA GCAAATTCAC GCACAACCA GCAAATTCAC GCACACCA GCAAATTCAC CTCACACCA CTCACACCA CTCACACCA CTCACACCA CCACCACCA CCACCACCA CCACCACCA CCACCA	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWFL STHRHALAA LTLMNLYWFL STHRHALAA LTLMNLYWFL STHRHALAA LTLMNLYWFL STHRHALAA LTLMNLYWFL STHRHALAA LTLMNLYWFL STHRHALAA CCAGGACGAC CCAGGACGAC CCAATACACTOT TCTTTCCTTC AGTGGAGCAC CCATGTGAAC CCAGATGAT TCCCCGTAAT TCCCCGTAAT TCCCCGTAAT TCCCCGTAAT TTATGAGATG AGTGTGTAAA CTATTAAACAC ATTTAGGGGT	120 180 240 300 1eukemia 60 120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020 1080 1140 1200 1260 1320
50 55 60 65 70	INHVIVILILI DLGCLSFGPS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac; Coding sequence GCCGCGCTGC AGGCCACTC GCAGGCCC GCAGGGCCC GCAGGATGC TGCCCGGGGG TGCCCGGGGG TGCCCGGGGG TGCCCGGGGG TTAGCAGTC TTAAAGACCA ATTCTTTGG TTAGCAGTC TATTCAGGG GGCTGCCAGGG GGCTGCACAG GCTGCAGGG GGTGCACAG GCTGCAGGG GGTGCACAG GCTGCAGGG GGGTGCACAG GGGTGCACAG GGGTGCACAG GGGTACACG GGATTCAGGAC GGATTCTGGTGA GGGATAGGTA TTCAAAAACT TTCAAAAACT GGCTCTTCA	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL E 10 epidermal nber: Hs.77 Id Accession GCCGGAGTCC GTCGGGGTCC CTGACTCCGT GACCTCCGG GTCGGCGTCC CTGACTCCGT GACCTTCGG GTCGGCGTCC CTGACTCCGT GACCTCCGG GTCGGCGTCC CTGACTCCGT GACCTCCGG GTCGGCGTCC GACCTCCGG ACCACTGGG ACCACTGGG ACCACTGGG CCGGGAATAA AAATCCTGCA ACACTGCG ACGAGTAGGA ACACTGCC AGGGCAAATA CAGATCACGC AGGGCAAATA CAGATCACGC GCGTCGCAA TTGGTGAATT GCACTCCTCA	LPRPLAKRCC GNAVPRDIAA VGILVLPHD LKVLYATEHC REYDTAEAQS growth fact 7432 growth fact 7432 growth fact 7432 li #: NM_00: -3819 21 CGAGCTAGCC GCCCGAGTCC CCCAGTATGA GACGCCGGG GGAAATTACC GGCTGGTAT GGAAATTACC GGCTGGTAT TGATCATCAGA TGATGCAGAT TGATCATCAGA GAACTGCCAG CAAGTCCCC GAGCGACTGC CCCACTCATG CCACTCATG CCCCTTGGT CTCCTGGTC CTGTTAGAAAG TAAAGACTCA CAGTTGCGAT CAGCTTAGGT CCCCTGTGTTAAGAAG TAAAGACTCA CAGTTGCGAT CAGCTTGGTT CTCTTGGTT CAGCTTCGGTT CAGCTTCGGTT CTCTTGGTT CAGCTTGCGTT CAGCTTGCGTT CTCTTGGTT CAGCTTGCGTT CAGCTTCGGTT CTCTTCGGTT CAGCTTGCGTT CAGCTTGCGTT CTCTTCGGTT CAGCTTCGGTT CAGCTTCGGTT CTCTTCTGGTT CCTCTTCGGTT CCTCTTCGGTT CCTCTTCGGTT CCTTCTGGTT CCTCTTCGGTT CCTCTTCTTCTT CCTCTTCTTCT CTTCTTCTTCTT	LOPRDAKMP AYLLOGSPYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL TOT receptor 5228 31 CCGGCGCCCC CCGCCCCCCC CCGCCCCCCCC CCAGCCC CCAGCCC TATGTGCAGA GCAGTCACT AAGTTTGCC TATGTGCAGA AGCAGTGACT AAGTTCACC CCGCACCCC CCCCCCCCCC	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian erg 41 GGCCGCCCAG GCCAACGCCA CGGAGCGAG CTGAGCGAA AGGGAGCTGT AAGGCATGTG CCACACGCA ACACCTGC CTCAACAC CACACCTGC CACACCTGC CACACCTGC CACACCTGC CACACCTGC CACACCTGC CACACCTGC CACACCTGC CACACCTGCC CACACCTGC CCACACCTGC CCACACCTGC CCACACCTGC CCACACCTGC CCACACCTGC CCACACCTGC CCACACCTGC CCACACCTGC CCACACCTGC CCACCTGCC CCACCTGCC CCACCTGCC CCACCTGCC CTCGCCCCACA TGCCCGCACA TGCCCGCCACA TGCCCGCCCC TCCACTTCCCCCCACA TGCCCCCCCC TCCACTTCCCCCCACA TGCCCGCCCC TCCACTTCCCCCCACA TGCCCCCCCC TCCACTTCCCCCCACA TGCCCCCCCCC TCCACTTCCCCCCACA TCCCCCCCCC TCCACTCCCCCCC TCCACTCCCCCCC TCCACCCCCCCC	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWFL STHRLHALAA LTLMNLYWFL /*CHIODIASTIC CAACACCAC CCACCCAC TCTTCGGGGA GGCTGCGCTC TAACAAGCTC CAATAACTGT TCTTTCCTTC AGTGGAGCAC CCTGTGCAAC CCTGTGCAAC CCATGTGGAGC CATGTGGAGC CATGTGGAGC CCAGTGGAT CAATGGAGC TCCCCAGTGGAT CAATGGAGC AGACGAAGCA ATTCCACTTAGA AGTGGAGC TCCCCGTAT TCCCCCGTAT TCCCCGTAT TCCCCGTAT TCCCCGTAT TCCCCCTAT TCCCCTAT TCCCCCTAT TCCCCTAT TCCCCCTAT TCCCCTAT TCCCCTAT TCCCCCTAT TCCCCTAT TCCCCTA	120 180 240 300 leukemia 60 120 180 240 300 420 480 540 600 660 720 780 840 900 960 1020 1080 1140 1200 1260 1320 1380
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50 55 60 65 70	INHVIVILILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nu Nucleic Ac: Coding sequence GCCGCGCTGC AGGCCACCTC GCACGGCGC TGCCCGGCGATGC TGCCCGGCGATGC TTAAAGACCA ATTCCTTTGG GTTAGCAGTTTACAGG GTTAGCAGTTTACAGG GTTAGCAGTTTACAGG GTTAGCAGTTTGG TTAGCAGTTTGG GTTAGCAGTTTGGTAGACCCA ACTTCCAGA ACGTTCCAGA GCTTCCAGA ACGTTCAGAG ACGTTCAGAG ACGTTCAGAG ACGTTCAGAG ACGTTCAGAG ACGTTCAGAG ACGTTCAGAG GGAATAGGTA TTCAAAAACT GACTCCTTCA AAGGAAAAACT GACTCCTTCA AAGGAAATACAA	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WFWFRLYWFP TGQVHELRDL E 10 epidermal nber: Hs.77 Id Accession lence: 187 II GCCGGAGTCC GTCGGCGTCC GTCGGCGTCC GTCGGCGTCC GTCGGCGTCT GACCTTCGG GTCGGCTCT GACCTTTTAA TTGGAATTT TCCAGGAGT TATCTAACTA AAATCCTGCA TCCAGTGGG GCCCCGGGA ACACCTGCCC AGGGCAAATA CAGATCACGG GCCCCCGGGA TGTGGGAATT CAGATCACGC CGCTCCGCAA TTGGTGAATT GCACCTCCCC CAGGGTTATC CACATACTCC CACAGTGTTT CCCAGGGTTTTA CACATACTCC CAGGGTTTTA CACTACTCC CAGGGTTTTA CACATACTCC CAGGGTTTTA CACTACTCC CAGGGTTTTA CCCAGGATTTT CCCAGGGTTTTA CCCAGGATTTT CCCAGGTTTTA CCCAGGATTTT CCCAGGATTT CCCAGGATTT CCCAGGATTT CCCAGGATTTT CCCAGGATTT CCCAGGATTT CCCAGGATTT CCCAGGATTT CCCAGGATTT CCCAGGATTT CCCAGGATTT CCCAGGATT CCCAGGAT CCCAGCAGAT CCCAGGATT CCCAGGATT CCCAGGATT CCCAGGAT CCCAGGAT CCCAGCAGAT CCCAGGAT CCCAGCAG CCCCCAGGAT CCCAGGAT CCCAGCAG CCCCAGGAT CCCAGCAG CCCCCAGGAT CCCAGCAG CCCCCAGAT CCCAGCAG CCCCCAGAT CCCAGCAG CCCCCAGC CCCCAGC CCCCCAGC CCCCCCAGC CCCCCCAGC CCCCCCCC	LPRPLAKRCC GMAVPRDIAA VGILVLPHD LKVLYATSHC REYDTAEAQS growth faci 7432 gf #: NM_00: -3819 21 CGAGCTAGCC GCCCGAGTCC CCCAGTATTGA GACGCCUGG GGAGATAGC GGCTGGTTAT GATCATCAGA TGATGCAGA TGATGCAGA TGATGCAGA CAGTGCCAA GACTGCCAG CAAGTCCCC GAGCGCTTGCCAG CAAGTCCCC CAGTGCTAT CAGCTGCCAA CAGTGCCAG CAAGTCCCCC CAGTGCCAC CAGTGCCAC CCCACTCATG CAGCTTTGGT CTCTGTGCTC CTCTGTGCTT CTGTTTTGAG CAGTTGCGAT TCATGGGCAT TCATGGGCAT TCATGGGCAT TCATGGGCAT TCCTCTGGAT CCTCTTGGAT GCTTATTCAG	LOPRDAKMP AYLLOGSFYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL TO recepto: 5228 31 CCGGCGCCGC CCGCCTCGCC CCGCGCTCGCC GCAGCGCTCC GCAGCGCTCC AAAGTTTGCC AAACTGAC AGCAGTCAC AGCAGTCAC CGGTCAGC AAGTGACC CGGTCAGC CGGTCAGC CGGTCAGC CGGTCAGC CGGTCAGC CTCAGCAAGC GCCACTGGC CCACAGGAAC CTCCACATCC CCCACAGGAAC GCTTGGCC CCACAGGAAC GCTTGCCAACC CCCACAGGAAC GCTTGCCAACC CCCACAGGAAC GCTTGCCACAC	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YFFFNALLIL RNGLVKDKRF (avian erg (avian er	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWPL 51 ACCGGACGAC CAACACCGC CAACACCGC TCTTCCGGGA GGCTGCGCT TAACAAGCTC CAATAACTGT TCTTTCCTTC AGTGGAGC GCCATGAGA CCTGTGCAAC CCAGTGCGAC GGCCAGGAG TCCAGTAGA TCCTATGCC CCAGTAGGAG TCCCAGTAGA TCCATTGCAC TAGAGAGAC TCCCGTAAT CTATGAGATG TCTATGAGATG TCTATGAGATG TCTATGAGATG TATTAGAGTT AGTGTGTAAC TATTAGAGTT AGTGTGTAAC TATTAGAGTT GGAAACCT TCAGAGT GGAACCTCCAT	120 180 240 300 leukemia 60 120 180 240 300 420 480 540 600 660 720 780 840 900 960 1020 1080 1140 1200 1260 1320 1380
50 55 60 65 70	INHVIVILILI DLGCLSFGPS YIVAPAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Aci Coding sequence GCCCGGCTGC AGGCCACT GCACGGCCC GCACGGCCCC GCACGGCTGC AGGCATGC TAAAGACCA ATTCCTTGA ATTTACAGG TTAGCAGTCT AATTTACAGG GTGGAGAGCA GCTGCCACAG ACGTCCAGGCC GGACTGCACAG GTGCAAGG GTGCAAGG GTGCAAGG TTAGCAGAT TTCAGAAACT TTCAAAAACT TTCAAAAACT TTCAAAAACT TTCAAAAACT TTCAAAAACT TTCAAAAACT TTCAAAAACT TTCAAAAACT GCCTTTGAGA AGGAAATCA GCCTTTGAGA AGGAAATCA GCCTTTGAGTA AGGAAATCA	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL EE 10 epidermal nber: Hs.77 Id Accession GCCGGAGTCC GTCGGGGTCC GACCTTCGG ACCCTCCGG ACCCTCCGG ACCACTGGG CAGGAGAGT TATCTAACTA AAATCCTGCA TATCTAACTA AAATCCTGCA ACACTGCG ACCACTGGG GCCCCGGGA ACACTGCG GCCCCGGGA TTGGTGAATT GCACTTCTT ACCTTCAAATT ACCTTGAAAT ACCTTGAAAT ACCTTGAAATT ACCTAGAAAT ACCTTGAAAT ACCTTGAAATT ACCTAGAAAT ACCTTGAAATT ACCTTGAATT ACCTTGAATT ACCTTGAAATT ACCTT	LPRPLAKRCC GMAVPRDIAA VGILVLPHD LKVLYATSHC REYDTAEAQS growth faci 7432 gr	LOPRDAAKMP AYLLOGSPYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL TO receptor CCGGCGCCCCC CCGCCCCCCC CCGCCCCCCC CCGCGCGCCCCC CCGCGCGCCCC CCGCGCGCCCC CCGCGCCCCC CCAGCCCCC CCAGCCCCC CCAGCCCCC CCAGCCCCC CCAGCCCCC CCACCCCC CCACCCCC CCCCCCCC	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian erg 41 GCGCCGCCCAG GCCAACGCCA CGGAGCGAG CTGAGCAG AGAGCTGTC AAGACATGTC AAAACATGCAACAC GCCAACAC GCCAACAC ACACACAC GCAACAC ACACACAC	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWFL /throblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGA GGCTGGGCTC TAACAAGCTC CAATAACTGT TCTTTCGTTC AGTGGAGCA GCCCATGAGA CCTGTGCAAC CATGTGGAAC CATTAGAGGT GAAAACCGTA GGACTCCAT GGTCTCCAT GTTTTCTCTT CATTTTCTCTT CATTTCTCTT CATTTTCTCTT CATTTCTCTT CATTTCTT CATTTCTT CATTTCTT CATTTCTT CATTTCTT CATTTCTT CATTTCTT CATTTCT CATTTCT CATTTCT CATTTCT CATTTCT CATTTCT CATTT CATTTCT CATTTCT CATTTCT CATTTCT CATTT CATT	120 180 240 300 240 300 240 120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020 1140 1200 1260 1320 1380 1440 1500
50 55 60 65 70	INHVIVILILI DLGCLSFGFS YIVAPAAKVL DNA SEQUENG Gene name: Unigene nur Nucleic Ac; Coding sequence (Coding sequence) (Codi	TALRSAATAR PSSVPTDWTP VSSYAPRYHEN WFWFRLYWFP TGQVHELKDL E 10 epidermal nber: Hs.77 id Accession lence: 187 il GCCGGAGTCC GTCGGGGTCC CTGACTCCGG GACCCTCCGG GACCCTCCGG GACCCTCCGG GACCCTCCGG AAAACCTGCA TATCTAACTA AAATCCTGCA ACACCTGCG ACGAGGAGGA ACACCTGCG ACGAGGAGGA ACACCTGCC AGGGCAATCC AGGGCAATCC CCAGTGGTC CCCGGA ACACCTGCC CCGGGA TTGGTGAATT CCACCTCAT ACCTAGAAAT CCCTGAAAT TATTTCAGG	LPRPLAKRCC GMAVPRDIAA VGILVLPHD LKVLYATSHC REYDTAEAQS growth fact 7432 a. #: NM_00: -3819 21 CARGCTAGCC GCCCGAGTCC CCCAGTATTGA GACGCCGGG GGAGTATTGA GATCATTCAGA TGATGCAAA AGATCACTC CAGCTGCCA GAGCAATGCC CAGCTGCCAA GAACTGCCAG CAAGTCCCCC CAGCTGCTAT CAGCTTGGTC CTCCTGGTC CTCCTGGTC TCCTTGGTT TCCTGGTC CAGCTGCGAA CAGTGCCAA CAGTCCCTC CAGATCCCGC CAACATCCTTG AAACAACATCCTTG AAACAAAAAAA	LOPRDAAKMP AYLLOGSFYG 1SDVQLEPTK SLRTVPDIPF ENFSKAEKPL FOR recepto: 5228 31 CCGGCGCCCCC CCGCCCCCCC CTCGGCGAGGCTCCC AAAGTTTGCC CAAAGTTTGCC CAAAGTTTGCAGA AGCAGTGATC AGGATAACT AAGTGATCA CCGTTCAGCA CCGTTCAGCA CCGTTCAGCA CCGTTCAGCA CCGTTCAGCA CCGTTCAGCA CCGTTCAGCA CCGTTCAGCA CCGCTCCCTACAACC CCCACTGGC CCACACGGG CCACTCGC CCACAGGAAC CCCACAGGAAC GCTTGGCCT AGGACCAAGC GCTTGGCCT CCACAGGAAC GCTTGGCCT TGCACAGCAGC CTTGGCCT TGCACAGCAGC CTTGGCCT TGCACAGCAGC CTTGGCCT TGCACAGGAAC CTCCATAA	ESAWKPLFYIL HSIYATLYMD LNIYFKSRGG YFFFNALLLI RNGLVKÖKRF (avian er; (avian er	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWPL 2 throblastic 51 ACCGGACGAC CAACCACCOC TCITCGGGGA GGCTGCGCTC TAACAAGCTC TCATTAGGAC AGTGGAGC CCATGAGGA CCTGTGCAAC CATGTCGATG CCAGGAG GTTGCTGCAC CATGTCGAT CCAGGAG GTTGCTGCAC CATGTCGAT CCAGGAG GTTGTGCAC CATGTGGAT CCAGGAG GTTGTGCAC CATGTGGAT CCAGGAG GTTGTGCAC CATGTGGAT CCAGGAG GTTGTCTGCA AGACGAAGC CATTAGAGAC CATTAGAGAC CATTAGAGAC GAAACCGTA GGACCTCCAT GATAAGTGAT GTTTTCTTT GATAAGTGAT	120 180 240 300 1e leukemia 60 120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020 1140 1200 1260 1320 1380 1440 1500 1560
50 55 60 65 70	INHVIVILILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac; Coding sequence GCCGCGCTGC AGGCCACTC GCAGGGCCC GCAGGGATGC TGCCGGGGGCACT TAAGACACT TAAGACACT TAAGACACT AATTTCATTGG GTGGAGGGCA GACTTCCAGA GACTTCAGA GACTTCAGA GACTTCAGA GACTTCAGA TCCAGACA GACTTCAGA TCCAGACA GACTTCAGACA GACTTCAGACA GACTTCAGA TCCAGACA GAGGAAGAC GGAATAGAA TCCAAAAACT TAAAAACT GACTCCTTCA AAGGAAATAG GCATTCAGA GCATTCAGA GCATTCAGA GCATTCTG GAGGAATTCA AAGGAATTCA AAGGAATTCA AAGGAATTCA GACTCTTCA AAGGAATTCA GACATTTTG GACTCTTCA AAGGAATTCA GACATTTTTG GACTCTTCA AAGGAATTCA GACATTTTTTTTTT	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WFWFRLYWFP TGQVHELRDL E 10 epidermal nber: Hs.77 Id Accession lence: 187- 11 GCCGGGTCC CTGACTCCGT GACCTTCCGG GTCGGCTCT GCACTTTTGA TTGGGAATTT TCCAGGGGTCT TACAGGAGT AAACCTGCA TCCAGTGGG ACCCCGGGG ACCCCGGGG ACCCCGGGG ACCCCGGGA ACACCTGCC AGGGCAAATA TCAGTGAATT GCACTCCCC AGGGTAATT CACGGATTTCAGGA TTGGGAATT CACGATCACG TCACTCCCCAGGGTTTT ACCTAGAAT GCCTCACAT TACTTCAGAT TACTTCAGAT TACTTCAGAT TACTTCAGAT TACTTCAGAT TTACTTCAGGAT TTACTTCCAGGAT TCCACCCCAGGAT TCCACCCCAGAT TTACTCCCAGGAT TTACTCCCAGGAT TTACTCCAGGAT TTACTCCCAGGAT TTACTCCCAGGAT TTACTCCCAGGAT TTACTCCCAGGAT TTACTCCAGGAT TTACTCCCAGGAT TTACTCCCAGGAT TTACTCCCAGGAT TCCACCCCCAGA TTCCCCCAGGAT TCCCCCACAC TTCCCCCACAC TTCCCCCACAC TTCCCCCACAC TTCCCCCACAC TTCCCCCACAC TTCCCCCCACAC TTCCCCCCACAC TTCCCCCCACAC TTCCCCCACAC TTCCCCCACAC TTCCCCCACAC TTCCCCCACAC TTCCCCCACAC TCCCCCCCACAC TTCCCCCACAC TCCCCCCCACAC TCCCCCCACAC TCCCCCCCACAC TCCCCCCCACAC TCCCCCCCC	LPRPLAKRCC GNAVPRDIAA VGILVLPHD LKVLYATEHC REYDTAEAQS growth faci 7432 gt %: NM_009 -3819 21 CGAGCTAGCC GCCCGAGTCC CCCAGTATTGA GACGCCCGG GGAAATTACC GGCTGCTAT GGACATAGCC GGCTGCCAA GACGCCCGC CAGGCCCCAG CAGCTGCCAA GACGCCCCCA CAGCTGCCAA CAGCTGCCAA CAGCTGCCAA CAGCTGCCAA CAGCTGCCAA CAGCTGCCAC CAGCTGCCAA CAGCTGCCAC CCCACTCATG CACCTCCTGGC CTCCTGCGCT CTCTGTGCTC CTCTTGGT TAGCAGGC AACATCCTTG AAACATCCTTG AAACATCCTTG AAACAAAAAT TCAGCAAAAAT TCAGCAAAAAT TCAGCAAAAAT TCAGCAAAAAAT TCAGCAAAAAT TCAGCAAAAAAT TCAGCAAAAAT TCAGCAAAAAT TCAGCAAAAAAT TCAGCAAAAAT TCAGCAAAAT TCAGCAAAAAT TCAGCAAAAAT TCAGCAAAAT TCAGCAAAAT TCAGCAAAT TCAGCAAAT TCAGCAAAAT TCAGCAAAAT TCAGCAAAT TCAGCAAAT TCAGCAAAAT TCAGCAAAT TCAGCAAAAT TCAGCAAAAAT TCAGCAAAAAT TCAGCAAAAAT TCAGCAAAAT TCAGCAAAAAT TCAGCAAAAAT TCAGCAAAAAAT TCAGCAAAAAT TCAGCAAAAT TCAGCAAAAAT TCAGCAAAAAT TCAGCAAAAAT TCAGCAAAAAT TCAGCAAAAT TCAGCAAAAAT TCAGCAAAAT TCAGCAAAAT TCAGCAAAAT TCAGCAAAAT TCAGCAAAAAT TCAGCAAAAAT TCAGCAAAAT TCA	LOPRDAAKMP AYLLOGSPYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL TO recepto: 5228 31 CCGGCGCCGC CCGCCTCGCC CCGCCTCGCC GCAGCGCTCC TAGGGAGGCCTCC TAGGGAGGCCTC TAGGGAGGCTCC TAGGGAGGCTCC AAAGTTTGCC GAAAAACCGGAC CGGTTCAGCA AGGAGTGACT AAGTGTGATC AAGTGTGATC CTGGTCTGCC CCTCTACACC GCCACTGCG CCACAGGAC CTCCACATCA CTCCACATCA GCTTTGCCTAGC AGGACCAGGC GCTTGGCT AGGACCAGGC CCACAGGAC GCTTGGCT AGGACCAGC GCTTGGCT AGGACCAGC GCTTGGCT AGGACCAGC GCTTGGCT AGGACCAAGC GCTTGGCT AGGACCAAGC GCTTGGCT AGGACCAAGC GCTTGGCTATG AGGACCAAGC GCTTTGCCTATA AGGACCAAGC GGATTACGCT TTGTGCTATA	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian erg (avian er	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWPL STHRIHALAA LTIMNLYWPL STHRIHALAA LTIMNLYWPL STHRIHALAA LTIMNLYWPL STHRIHALAA LTIMNLYWPL STHRIHALAA STHRIHALAA TCTATGGGGA GGCTGGGCTC TAACAAGCTC CAATAACTGT TCTTTCCTTC AGTGGAAG CCTGTGCAAC TCCTGTGCAAC TCCTGTGCAAC TCCTGTGCAAC TCCCAGCAG GTGTGCTGCA AGACGAAGCC TCCCCGTAAT CTATGAGATG CCAGTGGAAT CTATGAGATG AGTGTGTAAC TATTAAACAC ATTTAAACAC ATTTAAACAC ATTTAAACAC TATTAAACAC TATTAAACAC TATTAAACAC TATTAAACAC TTTTCTCTT GATAAGTGT AAACTGGAAA	120 180 240 300 300 120 180 240 300 360 420 480 540 600 660 720 780 840 900 91020 1020 1020 1020 1140 1200 1260 1320 1380 1440 1500 1560 1620
50 55 60 65 70	INHVIVILILI DLGCLSFGFS YIVAPAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac; Coding sequence GCCCGCGCTGC AGGCCACTC GCACGGCCCC GCACGGCCCC GCACGGCTGC AGGCACTC GCACGGCCCC TAAAGACCA TTAGCAGTCC TAAAGACCA ATTCCTTGG TTAGCAGTCC TAATTACAGG GTGGAGAGCA GCTTCCAGA TGCTGGGGTG GTGGAGAGCA GCTTCCAGA TGCTGGGGTG GTGAACCCCG TATGTGGGGT GGAACCCCG TATGTGGGAC GCATTCAGA ACGTTCAAAACT TCAAAAACT GCCTTTGAGA GCAGTCGTCA GCACTTTGAGA ACGATATCA GCACTTTGAGA ACGACTTTTG TGCAAGGCCA TGCAGAGCCA TGCAGCCA TGCAGAGCCA TGCAGAGCCA TGCAGAGCCA TGCAGAGCCA TGCAGAGCCA TGCAGCCA TGCAGAGCCA TGCAGCCA TGCAGCC	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL EE 10 epidermal nber: Hs.77 Id Accession lence: 187- 11 GCCGGAGTCC GTCGGCGTCC CTGACTCCGT GACCTCCGG GTCGGCGTCC CTGACTCCGT GACCTTCGG TCGGGGTTC GCACTTTGA TTGGGAATT TCCAGGAGTT TCCAGGAGGT TATCTAACTA AAATCCTGCA TATCTAACTA AAAATCCTGCA TATCTAACTA AAAATCCTGCA ACACTGGG GCCCCCGGGA ACCACTGGG GCCCCCGGGA ACACTGCC AGGGCAATTA CAGATCACGC CAGGTGAATT GCACTCCAT GCACTCCAT TACTTCAGAAT TACTTCAGAAT TACTTCAGG GGACCTCCGG GCAGCTCCGGG TCCCTAGAAT TACCTAGAAAT TACCTAGAACT TAATTTCAGG GCAGCTCCGGG CAGGCTCCCGGG CAGGCTCCGGG TTATTTCAGG CAGGCTCCGGG TAATTTCAGG CAGGCTCCGGG CAGCTCCGGG CAGCTCCGGG CAGCTCCGGG CAGCTCCGGG CAGCTCCGCG CAGCTCCGC CAGCTCCGCG CAGCTCCCGC CAGCTCCCCGC CAGCTCCCGC CAGCTCCCCCCCCCC	LPRPLAKRCC GMAVPRDIAA VGILVLPHD LKVLYATEHC REYDTAEAQS growth fact 7432 #: NM_00: -3819 21 CGAGCTAGCC GCCCGAGTCC CCAGTATTGA GRACGCCGGG GGAGAAAAG GGACTAGCC GGCTGGTTAT GGAAATTACC GGCTGGTAT GGAAATTACC GGCTGGTAT CAGCTGCCAA TGATCACAGA TGATCACAGA TGATCACAGA TCATCAGA CAGTGCCAC CAGCTGCTAT CCAGCTGCTAC CAGCTGCTAT CCAGCTGCTAC CAGTGCGAT CCTCTGGT CTCTGGT CTCTGGT CTCTGGT CAACTCCAG CATACGCGC AACATCCTTG AACAAAAAT TCAGAAAAC TCAGAAAAC CTGCAACACCTTC CTCTGGAT CCTGCAACACCTTC CAGCAAAAAAT CCTGCAACACCTTC CAGCAAAAAAT CCTGCAACACCTTCC CTCCTAGCACC CTCCAACACCTCC CTCCAACACCCTCC CTCCCAACCCTCC CTCCCAACCCCCCC CTCCCAACCCCCCCC	LOPRDAAKMP AYLLOGSPYG AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL COF receptor CCGGCGCCCCC CCGCCCCCCC CCGCCCCCCC CCGCCCCCC	ESAWKPLFYIL HSIYATLYMD LNIYFKSRGG YFFFNALLLL RNGLVKDKRF (avian erg 41 GCGCCGCCCAG GCCAACGCCA GGCAACGCCA AGAGCGAG AGAGGAGC AAGAGAGAAA TGAAGGAGC TTCTAGGAA TGAAGGAGC TTCTAGGAA GCAAACTACTG GCCACACTGC AAATCATCTG GCCACAACCA GCAAATTCOG CCACCACGTA TGAAGAGTGT GCGCACACCA GCAAATTCOG CCACCACGTA AGCAGGTGCC TGAGAGA TGAAGAGTGT GCGCACACCA GCAAATTCOG CCACCACGTA AAACAGGTC TGGATATTCT AAAACAGGA ACATGGTCA CCACACGTCA CCACACGTCA CCACACGTCA CCACACGTCA ACATGGTCA CCACACGTCA CCACACCA C	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWFL SHIPLHALAA LTIMNLYWFL STACKACCACCAC CAACCACCAC CAACCACCAC CAACCACCA	120 180 240 300 300 120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020 1140 1200 1260 1320 1380 1440 1500 1620 1660 1620
50 55 60 65 70	INHVIVILILI DLGCLSFGFS YIVAPAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac; Coding sequence GCCCGCGCTGC AGGCCACTC GCACGGCCCC GCACGGCCCC GCACGGCTGC AGGCACTC GCACGGCCCC TAAAGACCA TTAGCAGTCC TAAAGACCA ATTCCTTGG TTAGCAGTCC TAATTACAGG GTGGAGAGCA GCTTCCAGA TGCTGGGGTG GTGGAGAGCA GCTTCCAGA TGCTGGGGTG GTGAACCCCG TATGTGGGGT GGAACCCCG TATGTGGGAC GCATTCAGA ACGTTCAAAACT TCAAAAACT GCCTTTGAGA GCAGTCGTCA GCACTTTGAGA ACGATATCA GCACTTTGAGA ACGACTTTTG TGCAAGGCCA TGCAGAGCCA TGCAGCCA TGCAGAGCCA TGCAGAGCCA TGCAGAGCCA TGCAGAGCCA TGCAGAGCCA TGCAGCCA TGCAGAGCCA TGCAGCCA TGCAGCC	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL EE 10 epidermal nber: Hs.77 Id Accession lence: 187- 11 GCCGGAGTCC GTCGGCGTCC CTGACTCCGT GACCTCCGG GTCGGCGTCC CTGACTCCGT GACCTTCGG TCGGGGTTC GCACTTTGA TTGGGAATT TCCAGGAGTT TCCAGGAGGT TATCTAACTA AAATCCTGCA TATCTAACTA AAAATCCTGCA TATCTAACTA AAAATCCTGCA ACACTGGG GCCCCCGGGA ACCACTGGG GCCCCCGGGA ACACTGCC AGGGCAATTA CAGATCACGC CAGGTGAATT GCACTCCAT GCACTCCAT TACTTCAGAAT TACTTCAGAAT TACTTCAGG GGACCTCCGG GCAGCTCCGGG TCCCTAGAAT TACCTAGAAAT TACCTAGAACT TAATTTCAGG GCAGCTCCGGG CAGGCTCCCGGG CAGGCTCCGGG TTATTTCAGG CAGGCTCCGGG TAATTTCAGG CAGGCTCCGGG CAGCTCCGGG CAGCTCCGGG CAGCTCCGGG CAGCTCCGGG CAGCTCCGCG CAGCTCCGC CAGCTCCGCG CAGCTCCCGC CAGCTCCCCGC CAGCTCCCGC CAGCTCCCCCCCCCC	LPRPLAKRCC GMAVPRDIAA VGILVLPHD LKVLYATEHC REYDTAEAQS growth fact 7432 #: NM_00: -3819 21 CGAGCTAGCC GCCCGAGTCC CCAGTATTGA GRACGCCGGG GGAGAAAAG GGACTAGCC GGCTGGTTAT GGAAATTACC GGCTGGTAT GGAAATTACC GGCTGGTAT CAGCTGCCAA TGATCACAGA TGATCACAGA TGATCACAGA TCATCAGA CAGTGCCAC CAGCTGCTAT CCAGCTGCTAC CAGCTGCTAT CCAGCTGCTAC CAGTGCGAT CCTCTGGT CTCTGGT CTCTGGT CTCTGGT CAACTCCAG CATACGCGC AACATCCTTG AACAAAAAT TCAGAAAAC TCAGAAAAC CTGCAACACCTTC CTCTGGAT CCTGCAACACCTTC CAGCAAAAAAT CCTGCAACACCTTC CAGCAAAAAAT CCTGCAACACCTTCC CTCCTAGCACC CTCCAACACCTCC CTCCAACACCCTCC CTCCCAACCCTCC CTCCCAACCCCCCC CTCCCAACCCCCCCC	LOPRDAAKMP AYLLOGSPYG AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL COF receptor CCGGCGCCCCC CCGCCCCCCC CCGCCCCCCC CCGCCCCCC	ESAWKPLFYIL HSIYATLYMD LNIYFKSRGG YFFFNALLLL RNGLVKDKRF (avian erg 41 GCGCCGCCCAG GCCAACGCCA GGCAACGCCA AGAGCGAG AGAGGAGC AAGAGAGAAA TGAAGGAGC TTCTAGGAA TGAAGGAGC TTCTAGGAA GCAAACTACTG GCCACACTGC AAATCATCTG GCCACAACCA GCAAATTCOG CCACCACGTA TGAAGAGTGT GCGCACACCA GCAAATTCOG CCACCACGTA AGCAGGTGCC TGAGAGA TGAAGAGTGT GCGCACACCA GCAAATTCOG CCACCACGTA AAACAGGTC TGGATATTCT AAAACAGGA ACATGGTCA CCACACGTCA CCACACGTCA CCACACGTCA CCACACGTCA ACATGGTCA CCACACGTCA CCACACCA C	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWPL 2 throblastic 51 ACCGGACGAC CAACCACCOC TCITCGGGGA GGCTGCGCTC TAACAAGCTC TCATTAGGAC AGTGGAGC CCATGAGGA CCTGTGCAAC CATGTCGATG CCAGGAG GTTGCTGCAC CATGTCGAT CCAGGAG GTTGCTGCAC CATGTCGAT CCAGGAG GTTGTGCAC CATGTGGAT CCAGGAG GTTGTGCAC CATGTGGAT CCAGGAG GTTGTGCAC CATGTGGAT CCAGGAG GTTGTCTGCA AGACGAAGC CATTAGAGAC CATTAGAGAC CATTAGAGAC GAAACCGTA GGACCTCCAT GATAAGTGAT GTTTTCTTT GATAAGTGAT	120 180 240 300 240 300 120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020 1140 1200 1320 1340 1200 1340 1200 1340 1500 1440 1500 1620 1660

	TGCAAGCTTC TGGAGGGTGA GCCAAGGGAG TTTGTGGAGA ACTCTGAGTG CATACAGTGC 1860 CACCCAGAGT GCCTGCCTCA GGCCATGAAC ATCACCTGCA CAGGACGGGG ACCAGACAAC 1920
	TGTATCCAGT GTGCCCACTA CATTGACGGC CCCCACTGCG TCAAGACCTG CCCGGCAGGA 1980
_	GTCATGGGAG AAAACAACAC CCTGGTCTGG AAGTACGCAG ACGCCGGCCA TGTGTGCCAC 2040
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	AAAATTCCCG TCGCTATCAA GGAATTAAGA GAAGCAACAT CTCCGAAAGC CAACAAGGAA 2460
	ATCCTCGATG AAGCCTACOT GATGGCCAGC GTGGACAACC CCCACGTGTG CCGCCTGCTG 2520
,	GGCATCTGCC TCACCTCCAC CGTGCAACTC ATCACGCAGC TCATGCCCTT CGGCTGCCTC 2580
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	GCCAAACTGC TGGGTGCGGA AGAGAAAGAA TACCATGCAG AAGGAGGCAA AGTGCCTATC 2820 AAGTGGATGG CATTGGAATC AATTTTACAC AGAATCTATA CCCACCAGAG TGATGTCTGG 2880
	AGCTACGGGG TGACCGTTTG GGAGTTGATG ACCTTTGGAT CCAAGCCATA TGACGGAATC 2940
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	TCTTCCATTC CATTGTTTTG AAACTCAGTA TGCCGCCCCT GTCTTGCTGT CATGAAATCA 4620
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50	TTCTCGCAAA AACGTATCTC CTAATTTGAG GCTCAGATGA AATGCATCAG GTCCTTTGGG 4800
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55	CCTTACGCTT TGTCACACAA AAAGTGTCTC TGCCTTGAGT CATCTATTCA AGCACTTACA 5040
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60	TECAATTTAT CAAGGAAGAA ATGGTTCAGA AAATATTTTC AGCCTACAGT TATGTTCAGT 5400
	CACACACAC TACAAAATGT TCCTTTTGCT TTTAAAGTAA TTTTTGACTC CCAGATCAGT 5460
	CAGAGCCCCT ACAGCATTGT TAAGAAACTA TTTGATTTTT GTCTCAATGA AAATAAAACT 5520
	ATATTCATTT CC
65	Protein sequence 10
	Gene name: epidermal growth factor receptor (avian erythroblastic leukemie
	Unigene number: Hs.77432
	Protein Accession #: NP_005219
70	Signal sequence: 1-27
70	Pfam domain: Recep_L_domain [57-190, 372-492]
	Transmembrane domains: 646-668 1 11 21 31 41 51
~-	MRPSGTAGAA LLALLAALCP ASRALBEKKV CQGTSNKLTQ LQTFEDHFLS LQRMPNNCEV 60
75	VLGNLEITYV QRNYDLSFLK TIQEVAGYVL IALNTVERIP LENLQIIRGN MYYENSYALA 120
	VLSNYDANKT GLKELPMRNL QEILRGAVRP SNNPALCNVE SIQWRDIVSS DPLSNMSMDF 180
	QNHLGSCQKC DPSCPNGSCM GAGEENCQKL TKIICAQQCS GRCRGKSPSD CCHNQCAAGC 240
	TGPRESDCLV CRKFRDEATC KDTCPPLMLY NPTTYQMDVN PEGKYSFGAT CVKKCPRNYV 300
80	VTDHGSCVRA CGADSYEMEE DGVRKCKKCE GPCRKVCNGI GIGEFKDSLS INATNIKHFK 360 NCISISGDLH ILPVAFRGDS FTHTPPLDPQ ELDILKTVKE ITGFLLIQAW PENRTDLHAF 420
	ENLBIRGET KOHGOPSLAV VSLNITSLGL RSLKEISDGD VIISGNKNLC YANTINWKKL 480
	PGTSGQKTKI ISNRGENSCK ATGQVCHALC SPEGCWGPEP RDCVSCRNVS RGRECVDKCK 540
	LLEGEPREFV ENSECIÇCHP ECLPQAMNIT CTGRGPDNCI QCAHYIDGPH CVKTCPAGVM 600
	GENNTLVWKY ADAGHVCHLC HFNCTYGCTG PGLEGCPING PKIPSIATGM VGALLLLLVV 660

5	ALGIGLFMRR RHIVRKRTLR RLIQERELVE PLTPSGEAPN QALLRILKET EFKKIKVIGS 720 GAFGTYYKGL WIPEGEKVKI PVAIKELREA TSPKANKEIL DEAYVHASVD NPHYCRLIGI 780 CUTSTVQLIT QLMPFGCLLD YVREHKDNIG SQYLLMWCVQ IAKGMYLED RRLVHRDLAA 840 RNVLVKTPQH VKITDFGLAK LLGAEEKEYH ADGKVPIKW MALESILHRI YTHGSDWSY 900 GUTVWELMTF GSKEYDGIPA SEISSILEKG ERLPQPPICT IDVYMIMVKC WMIDADSRPK 960 FRELIIEFSK MARDPGRYLV IQGDERMHLP SPTDSHFYRA LMDEEDMDDV VDADEYLIPQ 1020 GQFFSSPSTS RTPLLSSLSA TSMNSTVACI DRNGLQSCPI KEDSFLQRYS BDPTGALTED 1080 SIDDTFLPVP EYINQSVPKR PAGSVQNFVY HNQPLNPAPS RDPHYQDPHS TAVGNPEYLN 1140 TVQPTCVNST FDSPAHWAQK GSHQISLDNP DYQQDFPPKE AKPNGIFKGS TAENAEYLRV 1200
15	DNA sequence 11 Gene; name: claudin 5 (transmembrane protein deleted in velocardiofacial syndrome) Unigene number: Hs.110903 Probeset Accession #: AW245805 Nucleic Acid Accession #: NM_003277 Coding sequence: 121-777
20	1 11 21 31 41 51 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
25	CTGATCCTGG GGTGGGGGT GCCCATGTGG CAGGTGACCG CCTTCCTGGA CCACAACATC 240 GTGACGGCGC AGACCACCTG GAAGGGCCTG TGGATGTCGT GCGTGGTGCA GAGCACCGGG 300 CACATGCAGT GCAAAGTGTA CGACTCGGTG CTGGCTCTGA GCACCACGGT GCAGGCGGCG 360 CGGGGGGTCA CCGTGAGGCC CGTGCTGCTG GCGTTCGTTG CGCTCTTCGT GACCCTGGCG 420 GGCGGCAGT GCACCACCTG CGTGGCCCCG GGCCGGCCA AGGGGGGTGT GGCCCTACG 480
30	GGAGGGFIGE TCTACCTETT TIGGGGGFIG CTGGGGCTG GGCACTCTG CTGGTTCGCC 540 AACATTGTCG TCCGCGAGIT TTACGACCCG TCTGTGCCCG TGTCGCAGAA GTACGAGCTG 600 GGCGCAGCGC TGTACATCGG CTGGGCGGC ACCGCGCTGC TCATGGTAGG CGGCTGCCTC 660 TTGTGCTGGG GGCCCTGGGT CTGCACCGGC GTCCCGACC TCAGCTTCCC CGTGAAGTAC 720 TCAGCGCCGC GGCGCCCAC GGCCACCGGC GACTACGACA AGAAGAACTA CGTCTGAGGG 780 CGCTGGGCAC GGCGGCCC CTCCTGCCAG CACGGCCTTGC GAGGGGTTGG ATAAGCCTGG 840
35	GGAGCCCGGC ATGGACCGG GCTTCCGCCG GGTAGCGCGG GCGCCAGGCT CCTCGGAACG 900 TCCGGCTCTG CGCCCGACG CGCTCCTG ATCCGCTCCT GCCTGCGCCC GCAGCTGACC 960 TCCCGCCCGA ATGAGCCCGG CCCTGCCCTT AACAGACGGA ATGAAGTTTC CTTTTCTGTG 1020 CGCGCGCGTT TTTCCATAGG CAGAGCGGGT GTCAGACTGA GGATTTCGCT TCCCCTCCAA 1080 GACGCTGGGG GTCTTGGCTG CTGCCTTACT TCCCAGAGGGC TCCTGCTGAC TTCGGAGGGG 1140
40	CGGATGCAGA GCCCGGGCC CCCACCGGAA GATGTGTACA GCTGGTCTTT ACTCCATCGG 1200 CAGGCCCGAG CCCAGGGACC AGTGACTTGG CCTGGACCTC CCGGTCTCAC TCCAGCATCT 1260 CCCCAGGCAA GGCTTGTGGG CACCGGAGCT TGAGAGAGGG CGGGAGTGGG AAGGCTAAGA 1320 ATCTGCTTAG
45	Protein sequence 11 Gene name: claudin 5 (transmembrane protein deleted in velocardiofacial syndrome) Unigene number: Hs.110903 Protein Accession #: NP_003268
50	Signal sequence: none found Pfam domain: PMP22 Claudin [4-181] Transmembrane domains: 5-27, 74-96, 123-145, 164-186 Cellular Localization: plasma membrane 1 11 21 31 41 51
55	MGSAALEILG LVLCLVCWGG LILACGLPMW QVTAPLDENI VTAQTTWKGL WMSCVVQSTG 60 HMQCKVYDGV LALSTEVQAA RALTVSAVLL AFVALFVTLA GAQCTTCVAP GPAKARVALT 120 GGVLYLFCGL LALVPLCWFA NIVVRBFYDP SVPVSQKYEL GAALYIGWAA TALLMVGGCL 180 LCCGAWVCTG RPDLSFFVKY SAPRRPTATG DYDKKNYV
60	DNA sequence 12
65	Gene name: vascular endothelial junction-associated molecule Unigene number: Hs.54650 Probeset Accession #: AA410345 Nucleic Acid Accession #: AF255910
65	Gene name: vascular endothelial junction-associated molecule Unigene number: Hs.54650 Probeset Accession #: AA410345 Nucleic Acid Accession #: AF255910 Coding sequence: 241-1137 1 11 21 31 41 51 TTACCATTGT GTTGGGCTGC GAGAAGACGA CAGAAGGGGG ACCCGCCTCT TGGCAGCCAG 60
65 70	Gene name: vascular endothelial junction-associated molecule Unigene number: Hs.34650 Probeset Accession #: AA410345 Nucleic Acid Accession #: AF255910 Coding sequence: 241-1137 1 11 21 31 41 51
	Gene name: vascular endothelial junction-associated molécule Unigene number: Hs.54650 Probeset Accession #: AAA10345 Nucleic Acid Accession #: AF255910 Coding sequence: 241-1137 1 11 21 31 41 51

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CTCCACTTTA GAGATACACC AAAGCCACCG TTGTTACACA AGTTATTAAA CTATTATAAA 1200
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                           Protein sequence 12
Gene name: vascular endothelial junction-associated molecule
Unigene number: Hs.54650
 10
                         Protein Accession 8: AAP81223
Signal sequence: 1-22
Igc2 domain: 41-116, 146-221
Transmembrane domains: 239-261
Callular Localization: plasma membrane
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                           MARRSHRILL LLLLRYLVVA LGYHKAYGFS APKDQQVVTA VEYQEAILAC KTPKKTVSSR
LEMKKLGRSV SFVYYQQTLQ GDFKNRAEMI DFNIRINNT RSDAGKYRCE VSAPSEQGN
LEEDTVILEV LVAPAVPSCE VPSSALSGTV VELRCQDKEG NPAPEYTWFK DGIRLLENPR
LGSQSTNSSY TWNTKTGTLQ FNTVSKLDTG EYSCEARNSV GYRRCPGKEM QVDDLNISGI
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                           IAAVVVVALV ISVCGLGVCY AQRKGYFSKE TSFQKENSSS KATTMSENDF KHTKSFII
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                           DNA sequence 13
                            Gene name: solute carrier family 11 (proton-coupled divalent metal ion
                           Unigene number: Hs.182611
Probeset Accession #: D50402
Nucleic Acid Accession #: NM_000578
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                           Coding sequence: 1-1653
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                         ANTGGETTE TGARCAAGGT CGTCACCTET TOCATCATG TGCTAGTETG CACCATCAAG
CTCTACTTCG TGGTCAGCTA TCTGCCCAGC CTGCCCACC CTGCCTACT CGGCCTTGCA
GCCTTGCTGG CCGCAGCCTA CCTGGGCCTC AGCACCTACC TGGTCTGGCA CTGTTGCCTT
GCCCACGGAG CCACCTTTCT GGCCCACAGC TCCCACCACC ACTTCCTGTA TGGGCTCCTT
GAAGAGGACC ACAAAGGGGA GACCTCTGGC TAG
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60
                           Protein sequence 13
                           Gene name: solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1 Unigene number: Hs.182611
65
                           Protein Accession #: NP_000569
                           Signal sequence: none found
                          Pfam domain: Nramp [78-463]

Transmembrane domains: 58-80, 88-110, 159-181, 195-217, 284-306, 349-379, 394-416, 432-454, 468-490, 501-523

Cellular Localization: plasma membrane

1 21 31 41 51
70
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                           DNA sequence 14
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Gene name: solute cerrier family 7 (cationic amino acid transporter, y+

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Unigene number: Hs.184601
Probeset Accession #: AP104032
Nucleic Acid Accession #: NM_003486
Coding sequence: 53-1576
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CCTGACCCTG CAGCGGAACA TCACGCTGCT CAACGGCGTG GCCATCATCG TGGGGACCAT
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CTACGGCTCG CTGCCCGCCT TCCTCAAGCT CTGGATCGAG CTGCTCATCA TCCTGGCCTTC
ATCGCAGTAC ATCGTGGCCC TGGTCTTCGC CACCTACCTG CTCAAGCCGC TCTTCCCCAC
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CGCCGTGAC TCATCACAGC TGAAGGCCGC CACCCAGGTC CAGGATGCC TTGCCGCCGC
CAAGCTCCTG GCCTGGCCC TGATCATCT TGAAGGCAC AAACTGGATG TGGGAACAT
TGTGCTGGCA TTATCAGCG GCCTCTTTCCT CTATGAGGCAC AAACTGGATG TGGGAACAT
TGTGCTGGCA TTATCAGCG GCCTCTTTCC CTATCAGGAGA TGGAATTACT TGAAGTTCCT
CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCCTG GCCATCATCA TCTCCCTGCC
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                    CCCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC
 35
                    Protein sequence 14
Gene name: solute carrier family 7 (cationic amino acid transporter, y+
                   Gana name: solute carrier ramily 7 (cationic amino acid transporter, y* Unigene number: Hs.184601
Protein Accession #: NP_003477
Pfam domain: as permeases [46-481]
Transmembrane domains: 52-74, 82-104, 120-142, 145-167, 169-191, 200-222, 237-259, 275-297, 323-345, 371-393,
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                    398-419, 430-452, 455-476
Cellular Localization: plasma membrane
1 11 21 31
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                    DNA sequence 15
                    Gene name: Glutamate receptor subunit
Unigene number: Hs.249141
                    Nucleic Acid Accession #:
Coding sequence: 1-2943
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                  GGGTGGAGT TCAACAGCAA AGGGCAGAGAA ACCAACTACA CCCTGGGGAT CCTAGAAAAG
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GCCACCACCC TGGACATCAA CCTGTCGCAG ACACTGGCCA ACAAACCCT GGTCGTGACA
ACCATCCTGG AGAACCCATA CGTCATGCGC CGGCCCAACT TCCAGGGCCT GTTGGGGGAAC
GAACGCTTCG AGGGCTTCTG CGTGGGACAT CTGCGGGAGC TGGCCGAGCT GCTGCGGTAC
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	TGGACGGGCA 1						1500
	ACCATCACAG (1560
5	CCCTTCTCCC						1620 1680
	CTGTTTCTGG (1740
	GCACGCCCCC I	ACATCCTGGA	GAACCAGTAC	ACGCTGGGCA .	ACAGCCTGTG	GTTTCCCGTG	1800
	GGGGGCTTCA 1						1860
10	AGCOGRAGICI (1920
10	CAGACCAACA						1980 2040
	TCACGGTACC						2100
	TTCGTCAAGA (GCACAGAAGA	GGGCATTGCC	GCCGTCCTCA	ACTCCCGCTA	CGCCTTCCTG	2160
15	CTCGAGTCCA						2220
13	GGACTCCTCG :						2280 2340
	AAGTGGTGGG						2400
	ATGGAGAACA						2460
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20	GTGTGCCAGG						2580
	TCCCGCCGGC						2640 2700
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	CCCGCCGCCC						2820
25	GCGCTGCGGG						2880
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	TGA						
	Protein seg	nence 15					
30	Gene name:		receptor s	ubunit			
	Unigene num						
	Protein Acc						
	Signal sequ			4001 - PRPs de	omain [416-	785, 799-838	1
35	Transmembra	ne domains	297-319,	544-566, 6	24-646, 803	-825	•
	Cellular Lo	calization	plasma m	embrane			
	1	11	21	31	41	51	
	 	WARA CRECON		PROFFIGURE]		
40	ARVEVDIPEL	ORDSOYETTO	TMCOILPEGU	DDQTVQGRGE VSVLGP6SSP	ASASTVENIC	GEKEIPHIKV	60 120
, •				RILKSPNYPS			180
				VSTILIDANA			240
•				NTSHPFYPEP			300
45				PLACTSANIW			360
43				WYSNRTLAMN LRELABLLPF			· 420 480
						RKPGYPSPLD	540
	PFSPAVWLFM	LLAYLAVSCV	LFLAARLSPY	EWYNPHPCLR	ARPHILENQY	TLONSLNPPV	600
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						RRBABSEEVS	840
						YSAGAGGDAG	900
55				RVCQECRRIQ	ALRASGAGAP	PRGLGVPABA	960
33	TSPPRPRPOP	AGPRELAEHE					
	DNA sequen	CO 16					
			A3 recepto	or			
60	Unigene nu	mber: Hs.2	58				
60			NM_00067				
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65						CGTGCAAGAA	
						TTTTTTGTTC	
						GCAGAAAGAT CTGGTCCCTG	
						TCATGGCTCC	
70	TCTTCTGCTC	TTTCCATCT	TTTGCTGAG	A GTTCTGAGC	CTGTACTIC	TCTTGGCCCA	360
						CAAAAAGCCA	
						AGCAGCACTT ATGTGCGGTG	
						A AGGGTTTCCA	
75						A GACTGTCACT	
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80						C AGCCTGCAGA T GGGGTGCTGG	
						C AGCTGCCTTT	
	TTATGACTT	3 CCTACTGCT	T ATCTTTACC	C ACCCTCCA	T CATGTCCTT	G CTGGCCATCG	1080
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5 10	CCATGITTIGG CATGCCAATT GGAACAAACT AGTTCAAGAC CTTTATCTAT ACATGGCAT AAATAAAGAA CCTCTGATTC ACTCTGTTCC GGCCAAGGGA	CCCCTGGTT CAGTCTGAAC GGCTAAGTCC CATCAACTGC CCTGCTGTCC GTTCAAGGAA TTTGGACACA ATTGACCTTC	ATGAGAATGG GTCATGTGCG TTATCTAACT TTGTTTCTGG ATCATCTACT CATGCCAACT ACCTACCTTT AGCATTGAGA AGGATTCCCCA	CCATCTATCT CCAAAGAGAC ITCTTTTCTT ITAATGGTGA CCATGATGAA CCATGATGAA AGAATTCTGA TCAACAAACA	ATACTTCAGC TGACATCTTT AGGTGCATTT GTTTGCTCTG GGTACCACAG CCCTATCGTC AGCCTGTGTG GTAGTTATCC CTTGAGGGCC	TTCCTCACCT TACATCATTC TATGGACGGG TCATGGCTGC CITGTGCTGT TATGCCTATA GTCTGCCATC ATCAGAGATG TGTATGCCTGC	1260 1320 1380 1440 1500 1560 1620 1680 1740 1800
15	CCCAATTATA TTCTCTCTAA GTCTGTTTTC ACTTACTGAC GCCATTGTGG	TCTCCCCAC TTCAGTGTTT CTTCTTCCA AAAAGGCTCT AATTGAGCAG AACTGAGTTT	TCCACTACTC TGGAGGCCTG ATAGAAGAAT AGTTGGGCTG AGAACCTGCT AAGGGGGACT	TCTTCCTCCA ACTTGGGGAC AAGTCATGGA AACATGTGTG CTCGGAGGAT	CTTCATTTTT AACGTATTAT GCCTGAAGGG TGGTGGTGAC GCCTAGAAGA	CCTTTGTCCT TGATATTATT	1920 1980 2040 2100 2160
20	Protein seg Gene name: Unigene num Protein Acc	adenosine ber: Hs.25 ession #:	NP_000668				
25	Signal seque Pfam domain Transmembra Cellular Lo	: 7tm_1 (2 ine domains: calization;	9-282]	-72, 86-108 mbrane 31	, 120-150,	179-201, 22 51	9-251
30	VGVLVMPLAI VTTHRRIWLA SPLTWIPIPL	VVSLGITIHE LGLCWLVSFL VVMCAIYLDI	FIGLCALVON YSCLFMTCLL VOLTPMFOWN PYLIRNKLSL	LIFTHASIMS MKLTSEYHRN NLSNSKETGA	LLAIAVDRYL VTFLSCQFVS FYGREFKTAK	RVKLTVRYKR VMRMDYMVYP SLPLVLPLPA	60 120 180 240
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		glypican 1					
40	Probeset Ac Nucleic Act Coding sequ	ience: 222-	X54232 1 #: NM_003 -1898				
	1 l	11	21 1	31	41	51	
45	CGGGACCTTG	GTCTCCGCCT	TCGCGGGGGGG	CGCCGCCTCT	GGACCGCGAG	OGCCGCCGCC CCGCGCGCGC AGGATCCGAG CGGGCCCGAG	60 120 180
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	CCTGCTGCAC	CCAGGCGGAG CAGCGAGATG	GAGGAGAACC	TGGCCAACCG	CAGCCATGCC	GAGCTGGAGA	480
55	CCTGCTGCAC CCGCGCTCCG TCGATGACCA CCGGCGCCTT AGCTGCGCCT GGGCCCGCCT	CAGCGAGATG GGACAGCAGC CTTCCAGCAC CGGAGAGCTG GTACTACCGC GCTCGAGGGCC	GAGGAGAACC CGCGTCCTGC CTGCTGAACG TACACGCAGA GGTGCCAACC CTCTTCAAGC	TGGCCAACCG AGGCCATGCT ACTCGGAGCG ACGCGAGGGC TGCACCTGGA AGCTGCACCC	CAGCCATGCC TGCCACCCAG GACGCTGCAG CTTCCGGGAC GGAGACGCTG CCAGCTGCTG	GAGCTGGAGA CTGCGCAGCT GCCACCTTCC CTGTACTCAG GCCGAGTTCT CTGCCTGATG	480 540 600 660 720 780
55 60	CCTGCTGCAGA CCGGCCTCCG CCGGCGCCTT AGCTGGCCTT AGCTCGGCCGCT AGCTCGGA GAGAGCTGCG CGAGAGCTGC CCTGCCCTGA	CAGCAGATE GGACAGCAGC CTTCCAGCAC CGGAGAGCTG GTACTACCGC GCTCCGAGCGC CTGCCTGGGCC CAGCAGAGCTG CATGAAGCTG CTATTGCCGA	GAGGAGAACC CGCGTCCTGC CTGCTGAACG TACACGCAGA GGTGCCAACC CTCTTCAAGC AAGCAGGCCG ACCCGTGCCT GTCCGGAAAG GTCTACTGTG AATGTGCTCA	TGGCCAACCE AGGCCATGCT ACTCGGAGGG ACGCGAGGGC TGCACCTGGA AGCTGCACCC AGGCGCTGCG TCGTGGCTGC TGGCTCACTGCCT AGGGCTGCCT	CAGCATGCC TGCCACCAG GAGCTGCTGG GGAGACGCTG GGAGACGCTG GCCCTTCGGG TCGCTCCTT CCCCTGGGC GGGAGTCCC TGCCAACCAG	GAGCTGGAGA CTGCGCAGCT GCCACCTTCC CTGTACTCAG GCCGAGTTCT CTGCCTGATC GAGCCCCGA GTGCAGGGCC CCGGAGTGCT GCCCAGGCCAGG	480 540 600 660 720 780 840 900 960 1020 1080
	CCTGCTGCAC CCGCGCCTCCG TCGATGACCA CCGGCGCCTT AGTTGGCCTGG GGGCCGGCT ACTACCTGGA GAGAGCTGGC TGGGCTTGGC TGGCCTGAC ACTGCACTGA ACGCCGACTG CCTCCAGGA ACGTCAACCC GGGAGAGGCC	CAGCAGATG GSACAGCAGC CTTCCAGCAC CGGAGAGCTG GTACTACCGC GCTCGAGGGC CTGCCTGGGCC CAGCAGAGCTG CATGAGGTG CATGAGGTG CATGAGGTG CAACAGGTGC CAACAGGGCC CAACAGGGCC CAACAGGGCC CAACAGGGCC CAACAGGGCC CAACAGGGCC CCAACAGGCCC AACAGGGCC ACCTTCAAGG	GAGGAGAACC CGGGTCCTGC CTGCTGAACG CTGCTGAACG CTCTTCAAGC CTCTTCAAGC AAGCAGGCC AACCAGGCC ATCCGGAAAG GTCTACTGTCA ATTGTGCTCA ATTGTGCTCA ACGCTCACGG GGGCCTGACGG GGGCCTGACGG ACGCTTGAGA	TGGCAACCG AGGCGATGCT ACTCGGAGGG AGGCGAGGGC TGGACCTGGA AGCTGCACCC AGGCGCTGGC TGGTGCTGC TGGCTGCT TGGACTGCT TGGACTGCT TGGACTGCT TGGACTGCT TGGACTGCT TGGACTGCT TGGACTGCT TGGACTGCT AGAGCTGCCT AGAGCTGCCT AGAGCTGCT AGAGCGTCAT AGAAGCGGCG AGGTGGTCTC	CAGCCATECC TGCCACCACA GAGGCTGCAG GAGACTGCAG CTTCCGGGAC GGAGACGCTGCTC GCCCTTCGGG GGGGTGCCC TGCCACCAG CACGACAAG CCTGCACACAG CCTGCACACAG CCTGCACAAG CCAGCACAAG CCAGGCCAG CCAGGCCAG CCAGGCCAG CCAGGCCAG TGAGCCACAG TGAGCCACAG TGAGCCACAG TGAGCCACAG TGAGCCACAG TGAGCCACAG TGAGCCACAG TGAGCCACA	GAGCTGGAGA CTGGCAGCTTCC CTGTACTCAG GCCAGCTTCC CTGTACTCAG GAGGCCCCAG GTGCAGGCC CCGAGTGCT GCCGCAGGC GCCAACCTGG TTCTGGGGTA GCCATCAACG GCGAACCCCA CTGGCCCCAG GCGCAGCCCA CTGGCCCCAG CCGCAGCTCC	480 540 600 720 780 840 900 1020 1080 1140 1260 1320 1380
60	CCTGCTGCACC CCGCGCCTCG TCGATGACCA CCGGCCCCTCT ACTACCTGGA ACTACCTGGA ACGCCGCCT ACGCCTGGC TCGGCCTGGC TCGGCCTGGC CCGAGAGCTGT CCTCCCCTGA ACGCCGAGTG CCCTCAGGA ACGCCGAGTG CCCTCAGGA ACGCCAGCTCA TGAGCACTCCA TGAGCACTCCA TGAGCACTGC ACGCCGGA TGCCCAGGA ACGCCGGA TGCGCAGGCC CCAGCCGCGCA TGCCCAGGA	CAGCAGATTG GGACAGCCCC GGACAGCCCC GCTCCAGCCC GCTCGAGCCC GCTCGAGCCC CCTGCCGGCC CCTGCGGCC CAGCGACGTG CATGAAGCTG CATGAAGCTG CATGAAGCTG CAACAGGACCTC CAACAGGGCCCT ACCTTCAGGC CGACTTCAGGC CGACTTCTGG CGACTTCTGG CGATGATGATGACCTC CATGACCATC CATGACCATC CTACAACGGCCTG CATGACCATC CTACAACGGC	GAGGAGAACC CTGCTGACG CTGCTGACG CTGCTGACG CTGCTGACG GGTGCCAACC CTCTTCAAGC AAGCAGGCG ACCCGTGCCT ATCAGGAAAG GTCTACTGTG AATGTGCTA ATCAGCAGCG ACGCTGAGG AACGACCAGA AACAACCAGA AACAACCAGA AACAACCAGA AACAACCAGA AACAACCAGG	TGGCCAACCG AGGCCATGCT ACTGGAGGG AGCGGACTGGA AGCTGCACCC AGGGGCTCACGGT TGGTCACTGCT AGGGTGCTCACTGCT TGGTCACTGCT AGGGTGCTCACTGCT TGGTCACACGT TGGTCACACGT TGGTCACACGT CCAAGGTCAT AGAGCGGC AGCTGGTCAC AGAGGACACT CAAGGACACT TCAATGAGC TCAATGAGC TCAATGAGC TCAATGAGC TCAATGAGC TCAATGAGC TCAATGAGC TCAATGAGC TCAATGAGC TCAATGAGGC TCAATGAGGG AGCTGCTCCAGGGA	CAGCCATGCC TGCCACCAGG GAGCCTGCAG CTTCCGGAC GGAGACGCTG CCACCTGCTG GCCTTCGGG GGGAGTCCCC TGCCAACCAG GCCACCAGG GCGACACAG GCTGCGGGC GCACCAG GCGGGGCAC GCGGGGCAG GTGCAGCAG GTGCAGGGCGC CAGGGCTGC CAGGCCAGC CAGGCTGCAG CAGGCTGCAG CAGGCTGCAG CAGGCCAGC CAGCCAGC	CAGCTGGAGA CTGCGCAGCTTCC CTGTACTCAG GCCAGCTTCT CTGCTGATC GAGGCCCGA GTGCAGGCC GCCAGCTCG GCCACCTCG GCCACCTCC AGAACCCCA ACGACTCC GCCAGCTCC AAGATGCCC GCCAGCTCC AAGATGCCC GCCAGCTCC AAGATGCCCA ACGACCCCA GCCAGCTCC AAGATGCCCA GCCAGCTCC AAGATGCCCC GCCAGCTCC AAGATGCCCC GCCAGCTCC AACACCGC GCCAGCACCC GCCAGCACCCC GCCAGCACCC GCCAGCACCC GCCAGCACCC GCCAGCACCC GCCAGCACCC GCCAGCACCC GCCAGCACCC GCCAGCACCC GCCAGCACCC GCCAGCACCG GCCAGCACC	480 540 660 720 780 900 900 1020 1140 1260 1320 1340 1500 1560 1560
60 65	CCTGCTGCAC CCGCGCCTCCG TCGATGACCA TCGGCGCCCT ACTACCTGGA ACTACCTGGA ACGCCGCCT TCGGCGCTGCC TCGGCGCTGCC TCGGCGCTGCC TCGGCGTGCC TCGGCGTGC ACGCCGGA ACGCCGGA ACGCCGGA ACGCCGGA ACGCCGGA ACGCCGGA ACGCCGGA ACGCCGGA ACGCCGGA ACGCCCGGA ACGCCCGGA ACGCCCGGA TGCGCACGC TCGGCACGC ACGCCCGGA TCCGCCCGC AGAAGACCTC AGAAGACCTC AGAAGACCTC AGAAGACCTC AGAAGACCTC AGAAGACCTC AGAAGACCTC AGAAGACCTC AGAAGACCAAG	CAGCAGATTG GACAGC CTTCCAGCAC GGAGAGCTG GTACTACCGC GCTCGAGGGC CCTGCAGGGC CAGCACATG CATGAAGCTG CATGAAGCTG CATGAAGCTG CATGAAGCTG CATGAAGCTG CAACAGGACCTC CAACAGGGAC CCAGGGCCCT ACCTTCAGG CGACTTCTGG CAGTGATGAC CAGGGCCTT CAGGGCCT CAGCAGCCTC CAGCAGCTCC CACAGCAGCT CACAGCAGCAGCT CACAGCAGCAGCT CACAGCAGCAGCT CACAGCAGCAGCT CACAGCAGCAGCT CACAGCAGCAGCT CACAGCAGCAGCT CACAGCAGCAGCT CACAGCAGCAGCC CACAGCAGCAGCC CACAGCAGCAGCC CACAGCAGCAGCC CACAGCAGCAGCAGCC CACAGCAGCAGCAGCAGCAGCACACACA	GAGGAGAACC CGGGTGCTGCACG CTGCTGAACG CTGCTGAACG CTGCTGAACG CTCTTCAAGC AAGCAGGCGG ACCGTGCTGCT GTCCGGAAAG GTCTACTGTG AATCAGGCGG ACGCTCACGG ACGCTGACG ACGCTGAGG ATCAGCGTCGGAGG ATCAGCTCC CGCTGCTGGATG TGCCCCAGG TGTCCCGATG TGCCCCAGG ACGCCACCAGG ACGCACCAGG ACGCCACCAGG ACGCCACCAGG ACGCCACCAGG ACGCCCCAGG TGCCCCCAGG ACGCCCCAGG ACGCCCCAGG ACGCCCCAGG ACGCCCAGG ACGCCCCAGG ACGCCCCAGG ACGCCCCAGG ACGCCCCAGG ACGCCCCAGG ACGCCCAGG ACGCCCAGG ACGCCCAGG ACGCCCAGG ACGCCCCAGG ACGCCCCAGG ACGCCCCAGG ACGCCCAGG ACGCCCAGG ACGCCCAGG ACGCCCAGG ACGCCCAGG ACGCCCAGG ACGCCACAGT ACGCCCAGG ACGCCACAGT ACGCCCAGG ACGCCACAGT ACGCCCAGG ACGCCCAGG ACGCCCAGG ACGCCCAGG ACGCCCAGG ACGCCCAGG ACGCCACAGT ACGCCACAGT ACGCCCACAGT ACGCCACAGT ACGCCAC	TGGCCAACCG AGGCCATGCT ACTGGAGGGC AGCGGAGGGC AGCGCACCTGGA AGCTGCACCC AGGCGTTGCACCC AGGCGTTGCACCCT TGGCTCACTGCT TGGCTCACTGCT TGGTGCTCAT TGCACACCGT TGGTGCTCAT TGCACACCGT TGGTGCTCAT AGGAGTGAT AGAAGCGGC AGCTGGTCT ACGGGATGC TCAACAACCT ACCGGATCAC ACTTCCAGGA ACCTCTGCGG ACCTCTTCCAGGA ACCTCTGCGG CCCCGACCTT GGCGGAACCT GGCGGAACCT GGCGGAACCT ACCACGACCT ACCACACC ACCACCACCT ACCACGACCT ACCACGACCT ACCACACC ACCACACAC ACCACACACAC ACCACACACAC ACCACACACAC ACCACACACAC ACCACACACACAC ACCACACAC	CAGCCATGCC GAGCCATGCC GAGCCTGCAG CTTCCGGAC GGAGACGCTG GCCCTTCGGG GGGAGTCCTT CCCCTGGGC GGGAGTCCCAC CACCAG CACCAG CACCAG CACCAG CACGACACAG CAGGGCAAG CAGGGCAAG CAGGGCAAG CAGGGCAAG CAGGGCAAG CAGGGCAAG CAGGGCAAG CAGGAGTGCAG CAGAGGCAG CAGAGGCAG CAGAGGCAG CAGAGGTGAAG CCCGAAGGCAG CCCTCCTGCCC CCCCACGCC CCCCACGCC CCCCACGCC CCCCACGCC CCCCACGCC CCCCACGCC CCCCACGCC CCCCACGCC CCCCACGCC CCCCACCACCAC CCCCACCCC CCCCACGCC CCCCACCCC CCCCACCCC CCCCACCCC CCCCACCCC CCCCACCCC CCCCACCCC CCCCACCCC CCCCACCCC CCCCACCCC CCCCACCC CCCCCACCC CCCCACCC CCCCCACCC CCCCACCC CCCCCC	GAGCTGGAGA CTGCCACTTCC CTGTACTCA GCCAGCTTCT CTGCTGATC GAGGCCCGA GTGCAGGGC GCCAGGC GCCACCTGATC GAGGCCCGC GCCAGCCC AGATGGCC AAGATGCCC AAGATGGCC AAGATGGCC ACCACCGC GCCAGCCC ACCACCGC GCCAGCCC CCCAGGCC CTCCCCCC CTGGACATCC CCCAGGAGAGC CCCCAGGAGAGC CCCACCGC CCCACCGC CCCAGGAGAGAC CCCAGGAGAGAC CCCCCCCTCT CCCAGGGACA	480 540 660 720 840 900 1020 1140 1200 1320 1380 1450 1560 1680 1740 1860 1920
60 65 70	CCTGCTGCACA CCGCGCCTCCG TCGATGACCA CCGGCGCCTTCG ACTACCTGGA GAGACCTGCG ACTACCTGGA GAGACCTGCC CCGAGACCTGCACA ACGCCACAT ACTACCTGAA ACGCCACAT CCTCCCCTCA ACGCCACAT CACCCAGGA ACGTCAACCC GGGACGTCCA TGAGCACGCC TGAGCACTCCA TGAGCACGC GCTCCAGCC TGAGCCCGA TGAGCACGC TGAGCCCGA TGAGCACGC GCTCCAGCC TCCTCCACCC TCCTCCCCCC TCCTCCCCCC TCCTCCCCCC TCCTCC	CAGCAGATE GSACAGCAGC CTTCCAGCAC CGGAGAGCTG GTACTACCGC GCTGCAGGGCC CTGCCTGGGCC CAGCAGAGTGC CATTGCCGA GAGGACCTC CAACAGGACCT CAACAGGGCC CAGCAGCC CAGCAGCC CAGCAGCC CAGCAGCC CAGCAGCC CAGCAGCC CAGCAGCC CATGACCAGC CATGACCAGC CAGCAGCC TACACTGCC CATGACCTC TACACAGGC TACACTGCC TACACTGCC TACACTGCC TACACTGCC GCCTCCAGC GGGAGCCCAGT TAGCCCTCCC GGCCTCCAGC GGCCTCCAGC GGCCTCCAGC GGCCCCCCCC GGCCCCCCCC GGCCCCCCCC GGCCCCCC	GAGGAGAACC COGGTTCCTGC CTGCTGAACG CTGCTGAACG CTGCTGAACG CTGCTGAACG CTGCTGAACG CTGCTGAACG AAGCAGGCC AAGCAGGCC AAGCAGGCC AATCAGCACACACAGA ACCAGTGCCA ACGCTGACTCA CGGCAGCAGA ACGACTGAGA ACGACTGAGA ACGACTGAGA TCAGCCTCC CGCAGCAGA ACGACCAGA CGGCAGCAGA ACGACCAGA CGGCAGCAGA CGGCAGCAGA CGGCAGCAGA CGCCAGCCCCCCCC	TGGCAACGG AGGCGATGCT ACTCGGAGGG AGGCGAGGGC AGGCGCTGGA AGCTGCACCC AGGCGCTGGC TGGTGCTGC TGGTGCTGC TGGTGCTCC TGGTGCTCC TGGTGCTCC TGGTGCTCACT TGCACAGGT CCAAGGTCAT ACAGGGACACT ACTGCAGGACACT ACTCCAGGA ACCTCTGCGG CCCCAAGGCTACT GGCCGAACCT TGCACAGCC TCATGCAGCT TTTCTGCGT TTTCTGCCT TTTCTGCCT TTTCTGCCT TTTCTGCCCG GAGCCCCAGG CCCAAGCCCG GAGCCCCAGG CCCAAGCCCCG GAGCCCCAGG ACCCCACGCCCG GAGCCCCAGCCCCG AGGCCCACAGC ACCCCACGCCCCG GAGCCCCACGCCCCCCCC	CAGCCATEGE CAGCCATEGE GAGACCCAGE GAGACCCAGE GAGACCCAGE GAGACCCAGE CCAGCTGCCAG CCAGCTGCCAG CCCAGCAGGA CCAGCACCAG CCCAGCACCAG CCCAGCACCAG CCCAGCACCAG CCAGCACCAG CCAGCACCAGC CCCCCAAGGC ATATTTAGT CCAGCAGGACCT TCAGGGACCT TCAGGGACCT CCAGAAGCACG CCAGAGCACC CCAGACC CCAGAGCACC CCAGAGCACC CCAGACC CCAGACC CCAGACC CCAGACC CCAGACC CCAGACC CCAGACC CCAGACC CCACC CCCC CCCC CCCC CCCCACC CCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC	GAGCTGGAGA CTGGCAGCTTCC CTGTACTCAG GCCAGCTTCC CTGTACTCAG GAGGCCCCAG GTGCAGGGCC CCGGAGTGCT GCCGAGCTGG TTCTGGGGTA GCCATCAC GCGAGCTCC AAGATGGCCCA CTGGCCCAG TCCTCCCC AAGATGGCC TACCTCCCCG GTGGACATCA ACCAACCGC GACGGCAGGA ACCAACCGC GACGGCAGGA ACCAACCGC CAGGAAGAAC CAGGAAGGA	480 540 660 720 840 900 1020 1140 1200 1320 1380 1440 1560 1680 1740 1860 1920 2040 2160 2220 2280

	CTGCGCCCTT GAGGGGCCCC AGCGTCTGCA GGGTGACGCC TGAGACAGCA CCACTGCTGA 25	160 320 580
5	GGGGCACTG ACCACCTGC GCTTCTGCTG GAGGAGGGA AGCTGGGCCC AAAGGCCCAG 28 GGAGGCAGC TGGGCTCTGC CAATGTGGGC TGCCCCTGC ACACAGGGCT CACAGGGCAG 25 GCCTTGCTGG GGTCCAGGGC TGTTGGAGGA CCCCGAGGGC TGAGGAGCAG CCAGGACCG 27	540 700 760 820
10	CAGGGCTCAG AGTGACCCTC GGCTGTCACC TGCTCACAGG GATGCTGGTG GCTGGTGAGA 20 CCCCCGCACTG CACACGGGAA TGCCTAGGTC CCTTCCCGAA CCAGCCAGCT GCACACGAGG 2 GCACGGGGAC CTGGATAGTT AAGGGCTTTT CCAAACATGC ATCCATTAC GAGACTTCC 3	880 940 000 060
16	CACCITIGAC CONSTRACT CACTORAGEC ATLAGGACC TECCOCAGE 3: CTGCACGGC CUTCCTTCC TECTOTECC CACCITICAG GISECCCTG GAAGGGGTG 3: TOTGGTGTTG GAAGGGGTC CTGCACGGG AGAAGGACT GAAGGGTCT GAGGGCAGCTG 3:	120 180 240
15	CHARACTER ACCIDENCE CONTINUES OF CARGACTE CARGACTER TOTAL ACCIDENCE CONTINUES ACCIDENCE CONTINUES ACCIDENCE CONTINUES ACCIDENCE OF CONTIN	300 360 420 480
20	TCTCTGGAAG GGGCAGCCCT GAGTGGTCAC TGGTCAGGGC AGTGGCCAAG CCTGCTGTGT 3	540 600 660
25	Protein sequence 17 Gene name: glypican 1 Unigene number: Hs.2699 Protein Accession #: NP_002072	
30	Signal sequence: none found Pfam domain: Glypican protein [2-490] Transmembrane domains: none found Cellular Localization: plasma membrane 1 11 21 31 41 51	
35		60 120 180 240
40	PLGPECSRAV MKLVYCAHCL GVPGARPCPD YCRNVLKGCL ANQADLDAEW RNLLDSMVLI TOKFMGTSGV ESVIGSVHTW LAEAINALQD NRDTLTAKVI QGCGNPKVNP QGPGPEEKRR RGKLAPRERP PSGTLEKLVS EAKAQLRDVQ DFWISLPGTL CSEKMALSTA SDDRCWNGMA RGYLPEVMG DGLANQINNP EVEVDITKPD MTIRQQIMQL KIMTNRLRSA YNGNDVDFQD ASDDGSGSGS	300 360 420 480
45	DNA sequence 18 Gene name: NY-REN-24 antigen Unigene number: Hs.128425 Nucleic Acid Accession #: AF155102	
	Coding sequence: 27-908	
50	1 11 21 31 41 51 GCSAGGGCGA GGGCG GTGCTCATGG AGGAGGACCT GATCCAGCAG AGCCTGGACG ACTACCACGC CGGCAGGTAC AGCCCGCGGC TGCTCACGGC GCACGAGCTG CCACTGGACG	60 120
55	CECACGTECT GRANCCEGAT GAGARCETEC AGCGCCTECA GCTCTGGGGC CAGCAGCTCC AGGTCACGG AGACGCCAG GAGARGGGCC AGGACTCTT CTTCCGGGGG GCCAAGGAGG GCATGGGCCA GGACGAGGGGC CAGTTCAGCG TEGAGATGC ACTCACCGGC AAGGCTTACC TOTGGGCCGA CAAGTACCGG CCACGCAAGC CGCGCTTCTT CAACCGCGTG CACACGGGCT TCGAGTGGAA CAAGTACAAC CAGACGCACT ACGACTTCTT CAACCACCG CCCAAGATCG	180 240 300 360 420 480
60	TECAGGATA CAAGTICAAC ATCITICIACE COJACCICAT CGACAAGGGC TCCACGCCGG AGTACTICCT GGAGGCCTGC GCCGACAACA AGGATITCGC CATCCTGCG TCCACGCGG GCCGCCTACG AGGACATCGC TITCAAGGATC GTCAACCGC AGTGGGAATA CTCGCACCGC CACGGCTTCC GCCGGCTTACG GCCCTGGGGA ACGGCAGCC AGGAGGCCC AGGGCCCACAC GGGTGCCACA GCCCAGGTCG GAGTGGCCA GCCGGCAGGC TTGTCTTCA GCATCCGACG GGGTGCCACA GCCCAGGTCG GAGTGGCCA GCCGGCAGGC TTGTCTTCA GCATCCGACG	540 600 660 720 780
65	GGAACATCTC CAACAGAAGC AAAACGGAAA GTGCCTCCCG GACCCCAGA GGGCCACCCA ACCTCACCAG TCACCAGCCC CAGACCACCC ACAGCCCCTC CCAGACACCC CGCCTCATCT GGAAATAGTT COTTTGTTT CTCTAAAAAG ACTTGTAGGT GGGAAAAAAA ATCTTTTGTT CTCATGGAAT TGGCCTATTG GCAAGATCGC ATGTTTTTTT AATAAACGTT GTATTTTAGA ATAAAAA	900 960 1020
70	Protein sequence 18 Gene name: NY-REN-24 antigen Unigene number: Hs.128425 Protein Accession #: AAD42868	
75	Signal sequence: none found Transmembrane domains: none found Cellular Localization: plasma membrane 1 11 21 31 41 51	

	DNA sequenc	e 19					
	Unigene num	tumor necr	osis factor	receptor e	uperfamily,	member 1A	
5	Probeset Ac	cession #:	BE295782	065			
	coding sequ	ence: 256-	1623				
	1	11	21 i	31 1	41	51	
10	CGGCCCAGTG	ATCTTGAACC	CCAAAGGCCA	GAACTGGAGC	CTCAGTCCAG	AGAATTCTGA	60
10	GAAAATTAAA	GCAGAGAGGA	GGGGAGAGAT	CACTGGGACC	AGGCCGTGAT	CTCTATCCCC	120
	CUGGAAGCCC	CCTCAACTGT CAGCACTGCC	GCTGCCACAC	TGCCCTGAGC	CCAAATGGGG	GAGTGAGAGG	180 240
	CCATAGCTGT	CTGGCATGGG	CCTCTCCACC	GTGCCTGACC	TECTECTECC	COCCOCC	300
15	GACAGGGAGA	TGGTGGGAAT AGAGAGATAG	ATACCCCTCA	GGGGTTATTG	GACTGGTCCC	TCACCTAGGG	360
	TOTATTICET	GTACCAAGTG	CCACAAAGGA	ACCTACTTOF	ACAATGACTG	TOTAGGGGGGG	420
	GGGCAGGATA	CGGACTGCAG	DAINTENTEACE	ACCCCCTCCT	TO COOPER	80888888	540
^^	TCTTGCACAG	GCCTCAGCTG TGGACCGGGA	CACCGTGTGT	GGCTGCAGGA	ACABACCAGEA	CCCCC A TOTATO	600
20	I CONGIGUANA	ACCITITICCA	GTGCTTCAAT	TGCAGCCTCT	CCCTCAATGG	GACCCATCAC	660 720
	CICICCIGCC	AGGAGAAACA GTGTCTCCTG	GAACACCCCTC	TGCACCTGCC	ATCC N C/2TTMT	Constant and a con-	780
	CTACCCCAGA	TIGAGAATGT	TAAGGGCACT	DATTARDARD	GCACCACAGT.	COTOTOCOCO	840 900
25	CIGGICATII	TOTTIOUTE	TIGOLTTITA	TCCCTCCTCT	TCATTCGTTT	AATCTATOCO	960
	GAGGGGGAGC	GGAAGTCCAA TTGAAGGAAC	TACTACTOC	ATTOTTTGTG	GGAAATCGAC	ACCTGAAAAA	1020
	ACTUCAGGCT	TCACCCCCAC	CCTGGGCTTC	AGTCCCGTGC	CCAGTTCCAC	CALLOS CALLOS	1080 1140
	MUCTUCACCT	ATACCCCCGG	TCACTGTCCC	AACTTTGCGG	CTCCCCCAC	AGAGGTOOCK	1200
30	AMCCCCCCTTC	AGAAGTGGGA	GGACAGCGCC	CACAAGCCAC	AGAGCCTAGA	CCCCATCCCC	1260 1320
	CELGCGACGC	TOTACGCCGT	GGTGGAGAAC	CTCCCCCCTT	TOTAL	CONTRACTO	1380
	CTGCGCGAGG	CGCAATACAG	CATGCTGGG	GATCGGCTGG ACCTGGAGGC	AGCTGCAGAA	CGGGCGCTGC	1440
35	GCCACGCTGG	AGCTGCTGGG	ACCCGTGCTC	CGCGACATOG	ACCOMMON	CTCCCTCCAC	1500 1560
23	GACATCGAGG	AGGCGCTTTG	OGGCCCCCCCC	GCCCTCCCCC	CCCCCCCAC	TOTOTOTOROR	1620
	ACTITITET	CCCCTGCGGG GGAAAGGAGG	GGTCCTGCAG	GGGCAAGCAG	CACCTACCAC	CCCCCT CCT	1680 1740
	GGIGCIMACC	CUICGATUTA	CATAGCTTTT	CTCAGCTGCC	TOTOTOTO	CCRCRCRCRC	1800
40	CGCTGTGCGC	GCGGAGAGAG	GTGCGCCGTG	GGCTCAAGAG	CCTGAGTGGG	TGGTTTGCGA GGCTGCTCGG	1860
	GGGCCCCTGG	TTCGTCCCTG	VCC. Labelander	みぐみながなでみずみ	ACC BOTTON		1920 1980
	1111611116	TITIGITIT	AAATCAATCA	TGTTACACTA	ጉ ተግልልልልሴቸል	COLOR CANADANA	2040
	GARCAATGGG	GCCTTCAGCT	GGAGCTGTGG	ACTITICITAC	CTAAGGCAGG	GGCGAGCACG ATTCTGAAGT	2100
45	T				AIACACIAAA	ATTCIGAAGT	2160
	Protein sec	ruence 19					
	Gene name:	tumor necr	rosis factor	receptor s	superfamily,	member 1A	
50	Protein Acc	ber: Hs.15 ession #:	59 NP_001056				
-	Signal sequ	ence: 1-25	, –				
	TNPR domain	1: 44-81, 6	94-125, 127	-166, 168-19) 5		
	Cellular L	ne domains	211-234	mhrane			
55	+	11	21	31	41	51	
	MGLSTVPDLL	LPLVLLELLV	GIVECUITO		1	1	
	WCURGIILIN	DCPGPGODTD	CRECESCSFT	ASENHI DHCL	SCSKCDKDAG	CHETPOCHEN	60 120
60	AD I V CGCRRN	OYKHYWSENT.	FOCENCES CT.	NGTEVAL GOVD	TOWNS ICEPTAIN	COMP Designation	180
•	SKLYSIVCGK	CTKLCLPQIE STPEKEGELE	MVKGTEDSGT	PSPSDTDGPT	OLCLLSLLFI DTLOPERING	GLMYRYQRWK	240
	PUDCENTE	KKEAVBBAOG	ADPILATALA	SDPIPNPLOK	MED SATINDAS	LOTTODDATEV	300 360
	WA A ETGA & & PUC	WKEPVRRLGL LGCLEDIBEA	SUHEIDRLEL	QNGRCLREAG	YSMLATWRRR	TPRREATLEL	420
65			ICGPARLYPA	PSULR			
	DNA sequence						
	Unigene num	prominin mber: Hs.li	(MOUSE)-11k: 12360	e 1			
70	Probeset Ad	cession #:	R40057				
70	Nucleic Act	d Accession	#: NM_00	6017			
	1	11	21	31	41	51	
	000000000	1	i -	1	1	4	
75	GTTGCTGCTA	CCTCATGTTT GGGCTGTGCG	GGAGGATCTT	GCTAGCTATG	GCCCTCGTAC	TOGGCTCCCT	60
7	TCCTAAGGCT	TGGAATTATG	AATTGCCTGC	AACAAATTAT	GAGACCCAAG	ACTOCOATAA	120 180
	ACCTOCACCE.	ATTUGCATTC	TCTTTGAACT	AGTGCATATC	THE RIPORT PROPERTY.	TOOTROLOGO	240
00	TGATTATGAC	CCAGAAGATA AAGCCAGAAA	CTGTAATCTT	AGGTCTABAG	AAGGCATATG	AATCCAAAAT	300
80	GWIIWIICIW	TGCTGTGTCC	TGGGGGCTGCT	GTTTATTATT	Literature States	TOTOTOTOTO	360 420
	TITCTTTTGT	ATGTGTCGTT	CCTYTTAACAA	ATYTTYT/TYT/A	CARAMOORO	10001000	480
	MATAMOLATT	GGCATCTTCT	ATGOTTTTOT	GGCAAATCAC	<u> </u>	COCTOR MORE	540 600
	AAGGAGTCGG	AAACTGGCAG	ATAGCAATTT	CAAGGACTIG	CGAACTCTCT	TGAATGAAAC	660

	TCCAGAGCAA ATCAAATATA TATTGGCCCA GTACAACACT ACCAAGGACA AGGCGTTCAC 720	
	AGATCTGAAC AGTATCAATT CAGTGCTAGG AGGCGGAATT CTTGACCGAC TGAGACCCAA 780	
	CATCATCCCT GTTCTTGATG AGATTAAGTC CATGGCAACA GCGATCAAGG AGACCAAAGA 840	
_	GGCGTTGGAG AACATGAACA GCACCTTGAA GAGCTTGCAC CAACAAAGTA CACAGCTTAG 900	
5	CAGCAGTCTG ACCAGCGTGA AAACTAGCCT GCGGTCATCT CTCAATGACC CTCTGTGCTT 960	
	GGTGCATCCA TCAAGTGAAA CCTGCAACAG CATCAGATTG TCTCTAAGCC AGCTGAATAG 1020 CAACCCTGAA CTGAGGCAGC TTCCACCCGT GGATGCAGAA CTTGACAACG TTAATAACGT 1080	
	CAACCCTGAA CTGAGGCAGC TTCCACCCGI GGATGCAGAA CTTGACAACG TTAATAACGI 1080 TCTTAGGACA GATTTGGATG GCCTGGTCCA ACAGGGCTAT CAATCCCTTA ATGATATACC 1140	
	TGACAGAGTA CAACGCCAAA CCACGACTGT COTAGCAGGT ATCAAAAGGG TCTTGAATTC 1200	
10	CATTGGTTCA GATATCGACA ATGTAACTCA GCGTCTTCCT ATTCAGGATA TACTCTCAGC 1260	
	ATTCTCTGTT TATGTTAATA ACACTGAAAG TTACATCCAC AGAAATTTAC CTACATTGGA 1320	
	AGAGTATGAT TCATACTGGT GGCTGGGTGG CCTGGTCATC TGCTCTCTGC TGACCCTCAT 1380	
	CGTGATTTTT TACTACCTGG GCTTACTGTG TGGCGTGTGC GGCTATGACA GGCATGCCAC 1440 CCCGACCACC CGAGGCTGTG TCTCCAACAC CGGAGGCGTC TTCCTCATGG TTGGAGTTGG 1500	
15	ATTAAGTTTC CTCTTTTGCT GGATATTGAT GATCATTGTG GTTCTTACCT TTGTCTTTGG 1560	
	TGCAAATGTG GAAAAACTGA TCTGTGAACC TTACACGAGC AAGGAATTAT TCCGGGTTTT 1620	
	GGATACACCC TACTTACTAA ATGAAGACTG GGAATACTAT CTCTCTGGGA AGCTATTTAA 1680	
	TARATCARAR ATGRAGCTCA CTTTTGARCA AUTTTACAGT GACTGCARAR ARRATAGAGG 1740	
20	CACTTACGGC ACTCTTCACC TGCAGAACAG CTTCAATATC AGTGAACATC TCAACATTAA 1800	
20	TGAGCATACT GGAAGCATAA GCAGTGAATT GGAAAGTCTG AAGGTAAATC TTAATATCTT 1860 TCTGTTGGGT GCAGCAGGAA GAAAAAACCT TCAGGATTTT GCTGCTTGTG GAATAGACAG 1920	
	AATGAATTAT GACAGCTACT TGGCTCAGAC TGGTAAATCC CCCGCAGGAG TGAATCTTTT 1980	
	ATCATTIGCA TATGATCTAG AAGCAAAAGC AAACAGTTIG CCCCCAGGAA ATTIGAGGAA 2040	
25	CTCCCTGAAA AGAGATGCAC AAACTATTAA AACAATTCAC CAGCAACGAG TCCTTCCTAT 2100	
25	AGAACAATCA CTGAGCACTC TATACCAAAG CGTCAAGATA CTTCAACGCA CAGGGAATGG 2160	
	ATTGTTGGAG AGAGTAACTA GGATTCTAGC TTCTCTGGAT TTTGCTCAGA ACTTCATCAC 2220 AAACAATACT TCCTCTGTTA TTATTGAGGA AACTAAGAAG TATGGGAGAA CAATAATAGG 2280	
	ATATTTTGAA CATTATCTGC AGTGGATCGA GTTCTCTATC AGTGAGAAAG TGGCATCGTG 2340	
••	CAAACCTGTG GCCACCGCTC TAGATACTGC TGTTGATGTC TTTCTGTGTA GCTACATTAT 2400	
30	CGACCCCTTG AATTTGTTTT GGTTTGGCAT AGGAAAAGCT ACTGTATTTT TACTTCCGGC 2460	
	TCTAATTTT GCGGTAAAAC TGGCTAAGTA CTATCGTCGA ATGGATTCGG AGGACGTGTA 2520	
	CGATGATGTT GAAACTATAC CCATGAAAAA TATGGAAAAT GGTAATAATG GTTATCATAA 2580	
	AGATCATGTA TATGGTATTC ACAATCCTGT TATGACAAGC CCATCACAAC ATTGATAGCT 2640 GATGTTGAAA CTGCTTGAGC ATCAGGATAC TCAAAGTGGA AAGGATCACA GATTTTTGGT 2700	
35	AGTITICIGG TCTACAAGGA CTTTCCAAAT CCAGGAGCAA CGCCAGTGGC AACGTAGTGA 2760	
	CTCAGGCGGG CACCAAGGCA ACGGCACCAT TGGTCTCTGG GTAGTGCTTT AAGAATGAAC 2820	
•	ACAATCACGT TATAGTCCAT GGTCCATCAC TATTCAAGGA TGACTCCCTC CCTTCCTGTC 2880	
	TATTTTTGTT TTTTACTTTT TTACACTGAG TTTCTATTTA GACACTACAA CATATGGGGT 2940	
40	GTTTGTTCCC ATTGGATGCA TTTCTATCAA AACTCTATCA AATGTGATGG CTAGATTCTA 3000 ACATATTGCC ATGTGTGGAG TGTGCTGAAC ACACACCAGT TTACAGGAAA GATGCATTTT 3060	
40	GTGTACAGTA AACGGTGTAT ATACCTTTTG TTACCACAGA GTTTTTTAAA CAAATGAGTA 3120	
	TTATAGGACT TTCTTCTAAA TGAGCTAAAT AAGTCACCAT TGACTTCTTG GTGCTGTTGA 3180	
	AAATAATCCA TTTTCACTAA AAGTGTGTGA AACCTACAGC ATATTCTTCA CGCAGAGATT 3240	
45	TTCATCTATT ATACTTTATC AAAGATTGGC CATGTTCCAC TTGGAAATGG CATGCAAAAG 3300	
43	CCATCATAGA GAAACCTGCG TAACTCCATC TGACAAATTC AAAAGAGAGA GAGAGATCTT 3360	
	GAGAGAGAAA TGCTGTTCGT TCAAAAGTGG AGTTGTTTTA ACAGATGCCA ATTACGGTGT 3420 ACAGTTTAAC AGAGTTTTCT GTTGCATTAG GATAAACATT AATTGGAGTG CAGCTAACAT 3480	
	ACAGITITAAC AGAGITITICI GITGCATTAG GATAAACATI AATIGGAGIG CAGCIAACAI 3480 GAGIATCATC AGACIAGIAI CAAGIGITCI AAAAIGAAAI AIGAGAAGAI CCIGICACAA 3540	
	TTCTTAGATC TGGTGTCCAG CATGGATGAA ACCTTTGAGT TTGGTCCCTA AATTTGCATG 3600	
50	AAAGCACAAG GTAAATATTC ATTTGCTTCA GGAGTTTCAT GTTGGATCTG TCATTATCAA 3660	
	AAGTGATCAG CAATGAAGAA CTGGTCGGAC AAAATTTAAC GTTGATGTAA TGGAATTCCA 3720	
	GATGTAGGCA TTCCCCCCAG GTCTTTTCAT GTGCAGATTG CAGTTCTGAT TCATTTGAAT 3780	
	AAAAAGGAAC TTGGC	
55	Protein sequence 20	
	Gens name: prominin (mouse)-like 1	
	Unigene number: Hs.112360	
	Protein Accession #: NP_006008	
60	Signal sequence: 1-21	
00	Transmembrane domains: 105-127, 157-179, 438-460, 482-504, 784-806 Cellular Localization: plasma membrane	
	1 11 21 31 41 51	
65	MALVLGSLLL LGLCGNSFSG GQPSSTDAPK AWNYELPATN YETQDSHKAG PIGILFELVH 60)
65	IPLYVVQPRD PPEDTLRKFL QKAYESKIDY DKPETVILGL KIVYYEAGII LCCVLGLLFI 120	
	ILMPLVGYPP CMCRCCNKCG GEMEQRQKEN GPPLRKCPAI SLLVICIIIS IGIFYGPVAN 180	
	HQVRTRIKRS RKLADSNPKD LRTLLNETPE QIKYILAQYN TTKDKAPTDL NSINSVLGGG 240 ILDRLRPNII PVLDEIKSMA TAIKETKEAL ENMNSTLKSL HQQSTQL888 LTSVKTSLRS 300	
	SINDPLCIVE PSSETCHSIR LSLSQLNSNP ELRQLPPVDA ELDNVNNVLR TDLDGLVQQG 360	
70	YQSLNDIPDR VQRQTTTVVA GIKRVLNSIG SDIDNVTQRL PIQDILSAPS VYVNNTESYI 420	
	HRNLPTLEEY DSYMWLGGLV ICSLLTLIVI FYYLGLLCGV CGYDRHATPT TRGCVSNTGG 480)
	VFLMVGVGLS FLPCWILMII VVLTFVFGAN VEKLICEPYT SKELFRVLDT PYLLNEDWEY 540	
	YLSCKLFNKS KMKLTPEQVY SDCKKNRGTY GTLHLQNSFN ISEHLMINEH TGSISSELES 600 LKVNLNIFLL GAAGRKNLQD FAACGIDRWN YDSYLAQTGK SPAGVNLLSF AYDLEAKANS 660	
75	LPPGNLENSL KRDAQTIKTI HQQRVLPIEQ BLSTLYQSVK ILQRTGNGLL ERVTRILASL 720	
	DPAQNFITNN TSSVIIEETK KYGRTIIGYF EHYLQWIEFS ISEKVASCKP VATALDTAVD 780	
	VPLCSYIIDP LNLFWFGIGK ATVFLLPALI FAVKLAKYYR RMDSEDVYDD VETIPMKNME 840	
	NGNNGYHKDH VYGIHNPVMT SPSQH	
80	MIN COMPANY 21	
30	DNA sequence 21 Gene name: G protein-coupled receptor 39	
	Unigene number: Hs.85339	
	Nucleic Acid Accession #: NM_001508	
	Coding sequence: 1-1362	

	1	11	21	31	41	51		
	ATGGCTTC	AC CCAGCCTC	CC GGGCAG	 TGAC TGCTCCCAAA	TCATTGATCA	 CACTCATOTYC	60	
•	CCCGAGTT	TG AGGTGGCC	AC CIGGAI	CAAA ATCACCCTTA	TTCTGGTGTA	CCTGATCATC	120	
5	AAAGGATA	GG GCCTTCTC	GG GAACAG	CGCC ACCATTCGGG AGAC CACATGGTGA	TCACCCAGGT	GCTGCAGAAG	180 240	
	TIGGIGIT	CC TCATCGGG	CAT GCCCAT	GGAG TTCTACAGCA	TCATCTGGAA	TCCCCTGACC	300	
	ACGTCCAG	CT ACACCCTO	STC CTGCAA	GCTG CACACTTTCC CAGC TTTGAGCGCT	TCTTCGAGGC	CTGCAGCTAC	360	
10	TTCAGGTA	CA AGGCTGTC	STC GGGACC	TTGC CAGGTGAAGC	TGCTGATTCG	CTTCGTCTCG	420 480	
	GTCACCTC	co cccreare	IGC ACTGCC	CTIG CIGITIGCCA	TGGGTACTGA	GTACCCCCTG	540	
	CAGCCCGA	GC CCAGCCAC GA CCTCCAA1	CCG GGGTCT	CACT TECAACOGCT	CCAGCACCCG	CCACCACGAG	660	
1.5	CAGTCCAG	CA TCTTCCGC	ogc crross	GGTC TACCTCGTGG	TCCTGCTCTC	CGTAGCCTTC	720	
15	ATGTGCTG	GA ACATGATO	CA GGTGCT	CATG AAAAGCCAGA XXXXX AGCGAAGAGA	AGGGCTCGCT	GGCCGGGGGC	780	
	ACCATCAT	CT TCCTGAGG	CT GATTGT	TGTG ACATTGGCCG	TATGCTGGAT	GCCCAACCAG	840 900	
	ATTOGGAG	GA TCATGGCT	rgc ggccaz	ACCC AAGCACGACT	GGACGAGGTC	CTACTTCCGG	960	
20	CCGCTCCT	GT ACACGGT	TC CTGGC	GGAG ACGTTTTCT	TGTTCAGCTC	GGTCATCAAC	1020 1080	
	TGCCGCCT	GT CGCTGCAC	GCA CGCCAJ	CCAC GAGAAGCGCC	TGCGCGTACA	TGCGCACTCC	1140	
				GCGC CCGTTGCTCT				
36	TCTAAGTC	CC AGTCATIO	BOTTOGA	LGTCA CTAGAGCCCA	ACTCAGGCGC	GAAACCAGCC	1260 1320	
25	AATTCTGC	TG CAGAGAA	IGG TTTTC	GGAG CATGAAGTTI	GA			
	Protein	sequence 2	1					
				d receptor 39				
30		number: He Accession		1508, NP 001409				•
	Signal s	equence:	none found	1 -				
	Transmen	mains: 7tm	_1 (72-17; ins: 32-4	2, 224-344] 54, 68-90, 111-1	33. 151-173	221-243 5	200-201	320-342
35	Cellular	: Localizat:	ion: pla:	sma membrane	,	,	100-301,	320-342
33	1	11	21	31	41	51 1		·
	MASPELPO	SD CSQIIDH	SHV PEPEV	ATWIK İTLILVYLI	FVMGLLGNSA	TIRVTQVLQK	60	
	KGYLQKEV	TTD EMVSLAC	SDI LVFLI	GMPME PYSIIWNPLT VSGPC QVKLLIGPV	TSSYTLSCKI	HTPLPEACSY	120	
40	VNVPSHRO	LT CNRSSTR	HHE QPETS	NMSIC TNLSSRWTVI	OSSIFGAPV	YLVVLLSVAF	180 240	
	HCWNMMQV	/LM KSQKGSL	AGG TRPPQ	lrkse seesrtarr(TIIFLRLIV	TLAVCWMPNQ	300	
				LPFSE TFFYLSSVII RFVQR PLLFASRRQ:				
45		LES LEPNSGA						
43								
	TABLE 8A: A	ABOUT 1260 GEN	NES UP-REGU	LATED IN GLIOBLASTO	MA COMPARED 1	O NORMAL ADUL	TISSUES	
_0	Table 8A list	is about 1260 gen	es up-regulated	l in glioblastoma comoan	tinhs isomon of be	issues. These wen	a eplacted fro	om 59680 probesets on the Affymetrix/Eos Hu03 GeneChi e "average" glioblastoma level was set to the 75th percent
50	amongst var	nous guodiasioma	umors. The "	everage" norma) aduli (is:	sua taval was set t	o the 85th cercentile	amonosi va	rious non-malianant fissues. In order to remove nene-
	before the ra	kground levels of : silo was evaluated	non-specific hy 1	bridization, the 10th perce	entile value emong	st the non-malignan	il lissues was	subtracted from both the numerator and the denominator
	Pkey:	Unique f	Eos probeset ld					
55	ExAcon: UnigenelD:			mber, Genbank accessio	n number			
55	Unigene Titl	e: Unigene	number gene title					
	R1:			turnor to 85th percentile	normal body tissue			
	Pkey	ExAcon L	InigenelD U	ilgane Tille			R1	
60	431917	D16181 F	ts.2868 pe	ripheral myelin protein 2			75.2	
				olein kinase C binding pr RY (sex determining regic			74.6	
	428321			ripheral myelin protein 2	11 17-00.2		74.2 71.6	
65	412719 449494		ts.129911 E	STS	00755		70.7	
03	415817			omo sapiens cDNA: FLJ2 otein tyrosine phosphata			66.3 64.3	
	413472	BE242870 F	ls.75379 sc	dute carrier family 1 (glial			60.1	
	456759 435147			elta (Drosophila)-like 3 omo saplens mRNA; cDN	A DKF7n761C171	216	52.3 46.7	
70	425842	Al587490 F	Hs.159623 N	K-2 (Drosophila) homolog		2 (1	40.1	
	412733 418375			IAA0080 protein	and a second		39.0	
	453392			maptosomal-associated p RY (sex determining regi			38.7 37.2	
75	423849	AL157425 I	Hs.133315 H	omo sapiens mRNA; cDl	IA DKFZp781J132	4 (f	36.8	
15	413333 416829			oroblast growth factor 1 (a stanin (cadharin-associat			32.8	
	431941	AK000106 I	Hs.272227 H	omo sapiens cDNA FLJ2			31.8 31.8	
	436878 426325		Hs.47448 E	STs			31.4	
80	425057			yelin-essociated oligoder chaete-scute complex (O			30.9 30.4	
	448711	AF169692 1	Hs.12450 p	rotocadherin 9	. ,		30.2	
	439415 430838			STs ypothetical protein FU12	015		28.3 26.9	
				, p-2100000 proton - 1012			20.3	

	429466	M85835	Hs.12827	ESTs	25.9
	447004 424581	AW296968 M62062	Hs.157539	ESTs	25.3
	452744	M02002 Al267652	Hs.150917 Hs.30504	catenin (cadherin-associated protein), a	24.8
5	441285	NM_002374	Hs.167	Homo sepiens mRNA; cDNA OKFZp434E082 (ir microtubule-essociated protein 2	24.8
-	453642	Al370936	Hs.34074	dipeptidylpeptidase Vi	24.3 24.3
	424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	24.3
	450133	AW969769	Hs.105201	ESTs	24.2
10	408562	AJ435323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	23.3
10	448672	AI955511	Hs.225106	EST8	22.7
	435708 407034	Al362949 U84540	Hs.75169	ESTs	22.0
	407168	R45175	Hs.117183	gb:Human dystrobrevin isoform OTN-3 (DTN ESTs	21.9
	431019	NM_005249	Hs.2714	forkhead box G1B	21.7
15	409049	AJ423132	Hs.146343	ESTs	21.5 21.4
	433896	AW294729	Hs.274461	ESTs	21.1
	445041	T64183	Hs.282982	solute carrier	21.0
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	20.4
20	444378	R41339	Hs.12569	ESTa	20.0
20	411305 437414	BE241596 AW894071	Hs.69547 Hs.48448	myelin basic protein	19.9
	441016	AW138653	Hs.25845	hypothetical protein DKFZp547C176 ESTs	19.8
	440435	AL042201	Hs.21273	transcription factor NYD-sp10	19.6 18.5
0.5	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transi	18.4
25	452461	N78223	Hs.108106	transcription factor	18.1
	409395	U48745	Hs.54435	dystrobrevin, alpha	18.1
	417183	R52089	Hs.172717	EST8	18.0
	409638 428392	AW450420 H10233	Hs.21335 Hs.2265	EST _B	18.0
30	449611	Al970394	Hs.197075	secretory granule, neuroendocrine protei ESTs	18.0
	446692	Z44514	Hs.156829	Homo sapiens mRNA for KIAA1763 protein,	17.0
	425088	AA663372	Hs.169395	hypothetical protein FLJ12015	16.9 16.9
	444471	A8020684	Hs.11217	KIAA0877 protein	16.8
35	421659	NM_014459	Hs.106511	protocadherin 17	16.7
22	431725	X65724	Hs.2839	Norte disease (pseudoglioma)	16.6
	429276 416892	AF056085 L24498	Hs.198612 Hs.80409	G protein-coupled receptor 51	16.6
	441440	AI807981	Hs.30495	growth arrest and DNA-damage-inducible, ESTs	16.5
	449433	A1672096	Hs.9012	ESTs, Weakly similar to S26650 DNA-bindi	15.7
40	421264	AL039123	Hs.103042	microtubule-associated protein 1B	15.7 15.5
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	15.3
	413597	AW302885	Hs.117183	ESTS	15.1
	424945	AI221919	Hs.173438	hypothetical protein FLJ10582	14.9
45	447414 426269	D82343 H15302	Hs.18551 Hs.168950	neuroblastoma (nerve tissue) protein	14.9
	416857	AA188775	Hs.292453	Homo sapiens mRNA; cDNA DKFZp566A1046 (f ESTs	14.8
	419721	NM_001650	Hs.288650	equeporin 4	14.7 14.6
	411078	AI222020	Hs.182364	CocoaCrisp	14.4
50	453924	R49295	Hs.24886	ESTS	14.4
30	409389	A8007979	Hs.301281	Homo saplens mRNA, chromosome 1 specific	14.3
	430130 410909	AL137311 AW898161	Hs.234074	Homo saplens mRNA; cDNA DKFZp761G02121 (14.1
	412266	N59006	Hs.53112 Hs.26133	ESTs, Moderately similar to ALUB_HUMAN A ESTs	14.0
	412986	X81120	Hs.75110	cannablnoid receptor 1 (brain)	14.0
55	424790	AL119344	Hs.13326	ESTs, Weakly similar to 2004399A chromos	14.0 14.0
	439239	AI031540	Hs.235331	ESTs	14.0
	441497	R51084	Hs.23172	ESTs	14.0
	445495 414245	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypotheti	14.0
60	429900	BE148072 AA460421	Hs.75850 Hs.30875	WAS protein family, member 1	13.7
	448595	AB014544	Hs.21572	ESTs KIAA0644 gene product	13.6
	449605	AW138581	Hs.198416	ESTs	13.6 13.6
	452526	W38537	Hs.280740	hypothetical protein MGC3040	13.6
65	420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA he	13.3
Ų3	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	13.3
	420077 424120	AW512260 T80579	HS.87767	ESIS	13.2
	456965	AW131888	Hs.290270 Hs.172792	ESTs Worldw closiles to humalhadical and	13.2
	423361	AW170055	Hs.47628	ESTs, Wealdy similar to hypothetical pro ESTs	13.2
70	428409	AW117207	Hs.98523	ESTs	13.1 12.9
	417160	N76497	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	12.6
	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	12.5
	411379 436954	A1816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	12.5
75	430691	AA740151 C14187	Hs.130425	ESTs	124
	433551	A1985544	Hs.103538 Hs.12450	protocadherin 9	124
	422544	AB018259	Hs.118140	KIAA0716 gene product	124
	427540	R12014	Hs.20976	ESTs	12.2 12.1
80	435624	AF218942	Hs.24889	formin 2	12.1
90	415849	R20529	Hs.6806	ESTs	12.1
	428845 442671	AL157579 AI005668	Hs.153610	KIAA0751 gene product	11.9
	444396	T65213	Hs.134779 Hs.4257	EST ESTs	11.9
			10.72.01	COM	11.8
				. 160	

	452752	AW044058	Hs.33578	KIAA0820 protein	11.8
	425523	AB007948	Hs.158244	KIAA0479 protein	11.8
	416072	AL110370	Hs.79000	growth associated protein 43	11.7
5	440184 428976	AB002297	Hs.7022	dedicator of cyto-kinesis 3	11.7
,	444783	AL037824 AK001468	Hs.194695	ras homolog gene family, member !	11.6
	448299	AA497044	Hs.62180	anillin (Drosophila Scraps homolog), act	11.6
	414214	D49958	Hs.20887 Hs.75819	hypothetical protein FLJ10392	11.6
	428982	NM_005097	Hs.194704	glycoprotein M6A feucine-rich, glioma inactivated 1	11.5
10	405238		110.104104	Compared Reported Institute 1	11.5
	420352	U79734	Hs.97206	huntingtin interacting protein 1	11.4
	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (C/EBP),	11.4
	424918	R13982	Hs.169309	myelin-essociated oligodendrocyte basic	11.4
	434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	11.4 11.4
15	451952	AL120173	Hs.301663	ESTs	11.3
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	11.3
	424278	AK000723	Hs.144517	hypothetical protein FLJ20716	11.3
	429418	AI381028	Hs.118769	ESTs	11.3
20	429918	AW873986	Hs.119383	ESTs	11.3
20	443912	R37257	Hs.184780	ESTs	11.3
	448743	AB032962	Hs.21896	KIAA1136 protein	11.3
	420092 408081	AAB14043	Hs.88045	EST ₈	11.2
	411642	AW451597 NM_014932	Hs.167409	ESTs	11.2
25	415170	R44386	Hs.71132 Hs.164578	neuroligin 1 ESTs	10.9
	426320	W47595	Hs.169300	transforming growth factor, beta 2	10.9
	450568	AL050078	Hs.25159	Homo sapiens cONA FLJ10784 fis, clone NT	10.8
	425799	T08133	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	10.8
20	423853	AB011537	Hs.133466	stil (Drosophila) homolog 1	10.8 10.7
30	400293	N51002	Hs.306480	Homo sapiens mRNA; cDNA DKFZp761E2112 (I	10.7
	447773	Al423930	Hs.36790	ESTs. Weakly similar to putative p150 [H	10.7
	448321	NM_005883	Hs.20912	adenomatous polyposis coti like	10.5
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	10.5
35	440684	AI253123	Hs.127358	ESTs, Highly similar to S21424 nestin (H	10.3
33	444017 438380	U04840	Hs.214	neuro-oncological ventral antigen 1	10.3
	440471	T05430 AA886146	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	10.3
	413063	AL035737	Hs.307944 Hs.75184	ESTs	10.2
	439978	BE139460	Hs.124873	chitinase 3-like 1 (cartilage glycoprote Homo sapiens cDNA FLJ 11477 fis, clone HE	10.1
40	448902	Z45998	Hs.22543	Homo saplens mRNA; cDNA DKFZp76111912 (f	10.1
	424932	R14070	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	10.1 9.9
	431721	AB032996	Hs.268044	KIAA1170 protein	9.9
	419088	AJ538323	Hs.52620	integrin, beta 8	9.8
45	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	9.8
73	436511 414696	AA721252	Hs.291502	ESTs	9.8
	449539	AF002020 W80363	Hs.76918	Niemann-Pick disease, type C1	9.7
	412959	D87458	Hs.58446 Hs.75090	ESTs KIAA0282 protein	9.7
	412811	H06382	Hs.21400	ESTs	9.6
50	449300	AI656959	Hs.222165	ESTs	9.6 9.6
	426344	H41821	Hs.322469	transcriptional activator of the c-fos p	9.5
	419271	N34901	Hs.238532	ESTs	9.5
	419078	M93119	Hs.89584	insulinoma-associated 1	9.4
55	451516	AI800515	Hs.12024	ESTs	9.4
"	422656	AI870435	Hs.1569	LIM homeobox protein 2	9.3
	449318	AW236021	Hs.78531	Homo saplens, Similar to RIKEN cDNA 5730	9.3
	414175 415279	Al308876	Hs.103849	hypothetical protein OKFZp761D112	9.3
	428784	F04237 Y12851	Hs.1447 Hs.193470	glial fibrillary acidic protein	9.2
60	429903	AL134197	Hs.93597	purinergic receptor P2X, ligand-gated to	9.2
	424641	AB001106	Ha.151413	cyclin-dependent kinase 5, regulatory su glia maturation factor, beta	9.2
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	9.1
	449448	D60730	Hs.57471	ESTs	9,1
~-	408508	AI806109	Hs.135736	KIAA1580 protein	9.1 9.0
65	452785	AL359942	Hs.298434	erythroid differentiation and denucleati	9.0
	448986	H42169	Hs.18653	hypothetical protein FLJ14627	8.9
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	8.9
	433800	AI034361	Hs.135150	tung type-I cell membrane-associated gly	8.9
70	408926 449625	AF217525	Hs.49002	Down syndrome cell adhesion molecule	8.8
	400292	NM_014253 AA250737	Hs.23796 Hs.72472	odz (odd Oz/ten-m, Drosophila) homolog 1	8.8
	417404	NM_007350	Hs.82101	ESTs	8.7
	420345	AW295230	Hs.25231	pleckstrin homology-like domain, family ESTs	8.7
76	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brein)	8.7 9.7
75	437528	N59648	Hs.169745	crumbs (Orosophila) homolog 1	8.7 8.7
	440152	AB002376	Hs.7006	KIAA0378 protein	8.7
	451099	R52795	Hs.25954	Interleukin 13 receptor, alpha 2	8.6
	400780	4 4 04 2000	11. 45555		8.6
80	434891 449277	AA814309 AA001064	Hs.123583	ESTs	8.6
	415709	AA001064 AA649850	Hs.172976 Hs.278558	ESTs ESTs	8.6
	439947	AB005627	Hs.6788	astrotaciin	8.5
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	8.5
				2	8.5

	400040	*****			
	433042 416370	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	8.4
	452786	N90470	Hs.203697	ESTs, Weakly similar to 138022 hypotheti	8.4
		R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	8.4
5	415796 428271	R87548	Hs.78854	ATPase, Na+/K+ transporting, beta 2 poly	8.3
,	408947	AF028547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	8.3
	419863	AL080093	Hs.49117	Homo sapians mRNA; cDNA DKFZp584N1682 (f	8.3
	433447	AW952691 U29195	Hs.93485	Homo septens mRNA; cDNA DKFZp761D191 (fr	8.3
	431467	N71831	Hs.3281	neuronal pentrada II	8.3
10	409327	L41162	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (I	8.3
10	414300	Al304870	Hs.53563 Hs.188680	collagen, type IX, alpha 3	8.3
	407728	AW071502	Hs.175931	ESTs ESTs	8.2
	422798	R92347	Hs.34574		8.2
	419704	AA429104	Hs.45057	ESTs, Weakly similar to ALU1_HUMAN ALU S ESTs	8.2
15	429007	D80642	16,45037		8.2
	442710	AI015631	Hs.23210	gb:HUM092E09B Human fetal brain (TFujiwa ESTs	8.1
	425048	H05468	Hs.164502	ESTs	8.1
	429149	AW193360	Hs.197982	ESTs, Weakly similar to I38022 hypotheti	8.1
	445740	T78281	Hs.13226	Homo sapiens clone 25181 mRNA sequence	8.0
20	418771	AA807881	Hs.25329	ESTs	8.0
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	7.9 7.9
	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	7.9 7.9
	448408	AA322866	Hs.21107	neuroligin	7.9
~-	455384	H72176	Hs.4273	hypothetical protein FLJ13159	7.9
25	446819	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	7.9
	435501	AW051819	Hs.129908	KIAA0591 protein	7.8
	423600	A1633559	Hs.310359	ESTA	7.8
	450625	AW970107		gb:EST382188 MAGE resequences, MAGK Homo	7.8
20	415314	N88802	Hs.5422	glycoprotein M6B	7.7
30	420036	R60336	Hs.52792	Homo sapiens mRNA; cDNA DKFZo586I1823 (f	7.7
	427687	AW003867	Hs.1570	histamine receptor H1	7.7
	449328	A1962493	Hs.197647	ESTs	7.7
	419249	X14767	Hs.89768	gamma-aminobutyric actd (GABA) A recepto	7.7
25	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	7.7
35	419103	Z40229	Hs.95423	hypothetical protein FLJ23033	7.6
	438779	NM_003787	Hs.6414	nucleolar protein 4	7.6
	433532	AW975367		gb:EST387475 MAGE resequences, MAGN Homo	7.6
	448555	A1536697	Hs.159863	ESTs	7.5
40	439662	H97552	Hs.269060	ESTs	7.5
70	448543	AW897741	Hs.21380	Homo saplens mRNA; cDNA DKFZp586P1124 (f	7.5
	410099 431592	AA081630	Hs.169387	KIAA0036 gene product	7.5
		R69016	Hs.213194	hypothetical protein MGC10895	7.4
	409731 405819	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.4
45	407886	AW969688	Hs.100826	cor.	7.4
	437416	AL359605	Hs.283851	ESTs	7.4
	437698	R61837	Hs.7990	Homo sepiens mRNA; cDNA DKFZp547G036 (fr	7.4
	408604	D51408	Hs.21925	ESTs, Moderately similar to 184505 catcl ESTs	7.4
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	7.4
50	447499	AW262580	Hs.147674	protocadherin beta 16	7.3
	454036	AA374756	Hs.93560	Homo saplens mRNA for KIAA1771 protein,	7.3
•	409746	NM_004794	Hs.56294	RAB33A, member RAS oncogene family	7.3
	410037			TWO OW CHICAGO I WAS CHICAGO I CONTROL	
			Hs.58009	KIAA0918 protein	7.2
55	419318	AB020725 AW969742	Hs.58009 Hs.291005	KIAA0918 protein	7.2 7.2
	424051	AB020725 AW969742 AL110203		KIAA0918 protein ESTs	7.2 7.2 7.2
	424051 442028	AB020725 AW969742	Hs.291005	KIAA0918 protein ESTs Homo sapiens mRNA; cDNA DKFZp586J1922 (f	7.2 7.2 7.2 7.2
	424051 442028 448243	AB020725 AW969742 AL110203 Al243749 AW369771	Hs.291005 Hs.138411	KIAA0918 protein ESTs	7.2 7.2 7.2 7.2 7.2
	424051 442028 448243 436281	AB020725 AW969742 AL110203 Al243749 AW369771 AW411194	Hs.291005 Hs.138411 Hs.8074	KIAA0918 protein ESTs Homo sepiens mRNA; cDNA DKFZp586J1922 (f brain-specific anglogenesis bhilbitor 3 integrin, beta 8 myetotil leukemia factor 1	7.2 7.2 7.2 7.2 7.2 7.2
60	424051 442028 448243 436281 426429	AB020725 AW969742 AL110203 Al243749 AW369771 AW411194 X73114	Hs.291005 Hs.138411 Hs.8074 Hs.52620 Hs.85195 Hs.169849	KIAA0918 protein ESTs Home septens mRNA; cDNA DKFZp586J1922 (f brain-specific angiogenesis inhibitor 3 integrin, beta 8	7.2 7.2 7.2 7.2 7.2 7.2 7.2
60	424051 442028 448243 436281 426429 407182	AB020725 AW969742 AL110203 Al243749 AW369771 AW411194 X73114 AA312551	Hs.291005 Hs.138411 Hs.8074 Hs.52620 Hs.85195 Hs.169849 Hs.230157	KIAA0918 protein ESTs Homo sapiens mRNA; cDNA DKF2p586J1922 (f brain-specific anglogenesis inhibitor 3 integrin, beta 8 myeloid leukemia factor 1 myosin-binding protein C, slow-type ESTs	7.2 7.2 7.2 7.2 7.2 7.2
60	424051 442026 448243 436281 426429 407182 415293	AB020725 AW969742 AL110203 Al243749 AW369771 AW411194 X73114 AA312551 R49462	Hs.291005 Hs.138411 Hs.8074 Hs.52620 Hs.85195 Hs.169849 Hs.230157 Hs.106541	KIAA0918 protein ESTs Homo sapiens mRNA; cDNA DKFZp586J1922 (f brain-specific anglogenesis inhibitor 3 integrin, beta 8 myeloid leukemia factor 1 myosin-binding protein C, slow-type ESTs ESTs	7.2 7.2 7.2 7.2 7.2 7.2 7.2 7.2
60	424051 442026 448243 436281 426429 407182 415293 422764	AB020725 AW969742 AL110203 A1243749 AW369771 AW411194 X73114 AA312551 R49462 AI767727	Hs.291005 Hs.138411 Hs.8074 Hs.52620 Hs.85195 Hs.169849 Hs.230157 Hs.106541 Hs.47522	KIAA0918 protein ESTs Homo sepiens mRNA; cDNA DKFZp586J1922 (f brain-specific anglogenesis inhibitor 3 integrin, beta 8 myetoif leutkemia factor 1 myosin-binding protein C, slow-type ESTs ESTs ESTs ESTs	7.2 7.2 7.2 7.2 7.2 7.2 7.2 7.2 7.2
60	424051 442026 448243 436281 426429 407182 415293 422764 451592	AB020725 AW969742 AL110203 AI243749 AW369771 AW411194 X73114 AA312551 R49462 A1767727 AI805416	Hs.291005 Hs.138411 Hs.8074 Hs.52620 Hs.85195 Hs.169849 Hs.230157 Hs.106541 Hs.47522 Hs.213897	KIAA0918 protein ESTs Homo septens mRNA; cDNA DKFZp586J1922 (f brain-specific anglogenesis inhibitor 3 integrin, beta 8 myetolid leukemia factor 1 myosin-binding protein C, slow-type ESTs ESTs ESTs ESTs ESTs	7.2 7.2 7.2 7.2 7.2 7.2 7.2 7.2 7.1
	424051 442026 448243 436281 426429 407182 415293 422764 451592 429469	AB020725 AW969742 AL110203 AI243749 AW369771 AW411194 X73114 AA312551 R49462 A7767727 AI805416 M64590	Hs.291005 Hs.138411 Hs.8074 Hs.52620 Hs.85195 Hs.169849 Hs.230157 Hs.106541 Hs.47522 Hs.213897 Hs.27	KIAA0918 protein ESTs Homo sapiens mRNA; cDNA DKFZp586J1922 (f brain-specific anglogenesis inhibitor 3 integrin, beta 8 myeloid leutemia factor 1 myosin-binding protein C, slow-type ESTs ESTs ESTs ESTs ESTs glycine dehydrogenase (decarboxylating;	7.2 7.2 7.2 7.2 7.2 7.2 7.2 7.2 7.1 7.1
60 65	424051 442028 448243 436281 426429 407182 415293 422764 451592 429469 415734	AB020725 AW969742 AL110203 A1243749 AW369771 AW411194 X73114 AA312551 R49462 A767727 AI805416 M64590 NM_014747	Hs.291005 Hs.138411 Hs.8074 Hs.52620 Hs.85195 Hs.169849 Hs.230157 Hs.166541 Hs.47522 Hs.213897 Hs.27 Hs.78748	KIAA0918 protein ESTs Homo sepiens mRNA; cDNA DKFZp586J1922 (f brain-specific anglogenesis inhibitor 3 integrin, beta 8 myetoti leutkemia factor 1 myosin-binding protein C, slow-type ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	7.2 7.2 7.2 7.2 7.2 7.2 7.2 7.2 7.1 7.1 7.1
	424051 442028 448243 436281 426429 407182 415293 422764 451592 429469 415734 434149	AB020725 AW969742 AL110203 AL243749 AW369771 AW411194 X73114 AA312551 R49462 A1767727 AI805416 M64590 NM, 014747 Z43829	Hs.291005 Hs.138411 Hs.8074 Hs.52620 Hs.85195 Hs.169849 Hs.230157 Hs.165541 Hs.47522 Hs.213897 Hs.27 Hs.78748 Hs.19574	KIAA0918 protein ESTs Homo septens mRNA; cDNA DKFZp586J1922 (f brain-specific anglogenesis inhibitor 3 integrin, beta 8 myetolid leukemia factor 1 myosin-binding protein C, slow-type ESTs ESTs ESTs ESTs ESTs gycine dehydrogenase (decarboxytating; KIAA0237 gene product hypothetical protein MGC\$469	7.2 7.2 7.2 7.2 7.2 7.2 7.2 7.1 7.1 7.1 7.1 7.1
	424051 442028 448243 436281 426429 407182 415293 422764 451592 429469 415734 434149 438726	AB020725 AW969742 AL110203 AL243749 AW369771 AW411194 X73114 AA312551 R49462 AI767727 AI805416 M64590 NM_014747 Z43829 AA324975	Hs.291005 Hs.138411 Hs.8074 Hs.52620 Hs.85195 Hs.169849 Hs.230157 Hs.106541 Hs.213897 Hs.27 Hs.78748 Hs.19574 Hs.128993	KIAA0918 protein ESTs Homo sapiens mRNA; cDNA DKFZp586J1922 (f brain-specific angiogenesis inhibitor 3 integrin, beta 8 myeloid leukenia factor 1 myosin-binding protein C, slow-type ESTs ESTs ESTs ESTs ESTs eylcine dehydrogenase (decarboxylating: KIAA0237 gene product hypothetical protein MGC5469 ESTs, Weady stimilar to T00079 hypothetii	7.2 7.2 7.2 7.2 7.2 7.2 7.2 7.1 7.1 7.1 7.0 7.0
	424051 442028 448243 436281 426429 407182 415293 422764 451592 429469 415734 434149 436726 417632	AB020725 AW969742 AL110203 Al243749 AW369771 AW411194 X73114 AA312551 R49462 AI767727 AI805416 M64590 NM_014747 Z43829 AA324975 R208555	Hs.291005 Hs.138411 Hs.8074 Hs.52620 Hs.85195 Hs.169849 Hs.230157 Hs.106541 Hs.47522 Hs.213897 Hs.78748 Hs.128993 Hs.128993	KIAA0918 protein ES1's Homo sepiens mRNA; cDNA DKFZp586J1922 (f brain-specific anglogenesis binibitor 3 integrin, beta 8 myetoti leutemia factor 1 myosin-binding protein C, slow-type ES1's ES1	7.2 7.2 7.2 7.2 7.2 7.2 7.2 7.1 7.1 7.1 7.0 7.0
65	424051 442028 448243 436281 426429 407182 415293 422764 451592 429469 415734 434149 436726 417632 422421	AB020725 AW969742 AL110203 AL243749 AW369771 AW411194 X73114 AA312551 R49462 AI767727 AI8055416 M64590 NM_014747 X43829 AA324975 R20855 AA325138	Hs.291005 Hs.138411 Hs.8074 Hs.52620 Hs.86195 Hs.169849 Hs.230157 Hs.106541 Hs.213897 Hs.27 Hs.78748 Hs.128993 Hs.128993 Hs.128593	KIAA0918 protein ESTs Homo septens mRNA; cDNA DKFZp586J1922 (f brain-specific anglogenesis inhibitor 3 integrin, beta 8 myetolid leukemia factor 1 myosin-binding protein C, slow-type ESTs ESTs ESTs ESTs ESTs ESTs Gycine dehydrogenase (decarboxytating; KIAA0237 gene product hypothetical protein MGC5469 ESTs, Weathy similar to T00079 hypotheti glycoprotein MSB hypothetical protein FLJ22672	7.2 7.2 7.2 7.2 7.2 7.2 7.1 7.1 7.1 7.0 7.0 7.0 7.0
	424051 442026 448243 436281 426429 407182 415293 422764 451592 429469 415734 434149 436726 417632 422421 435267	AB020725 AW969742 AL110203 AL243749 AW369771 AW411194 X73114 AA312551 R49462 AT67727 AI805416 M64590 NM_014747 Z43829 AA324975 R20855 AA325138 N23797	Hs.291005 Hs.138411 Hs.8074 Hs.52620 Hs.85195 Hs.169849 Hs.230157 Hs.106541 Hs.47522 Hs.213897 Hs.78748 Hs.78748 Hs.128993 Hs.5422 Hs.235673 Hs.110114	KIAA0918 protein ESTs Homo sapiens mRNA; cDNA DKFZp586J1922 (f brain-specific angiogenesis inhibitor 3 integrin, beta 8 myeloid leukenia factor 1 myosin-binding protein C, slow-type ESTs ESTs ESTs ESTs ESTs eSTs eylcine dehydrogenase (decarboxylating: KIAA0237 gene product hypothetical protein MGC5469 ESTs, Weatdy stimilar to T00079 hypothetic glycoprotein M68 hypothetical protein FLJ22672 ESTs	7.2 7.2 7.2 7.2 7.2 7.2 7.1 7.1 7.1 7.0 7.0 7.0 7.0 8.9
65	424051 442028 448243 436281 426429 407182 415293 422764 451592 429469 415734 434149 436726 417632 422421 435267 437117	AB020725 AW969742 AL110203 Al243749 AW369771 AW411194 X73114 AA312551 R49462 AI767727 AI805416 M64590 NM_014747 Z43829 AA324975 R20855 AA325138 N23797 ALD49256	Hs. 291005 Hs. 138411 Hs. 8074 Hs. 52620 Hs. 85195 Hs. 16554 Hs. 230157 Hs. 16554 Hs. 47522 Hs. 213897 Hs. 78748 Hs. 19574 Hs. 128993 Hs. 5422 Hs. 236873 Hs. 110114 Hs. 110114	KIAA0918 protein ES1s Homo sepiens mRNA; cDNA DKFZp586J1922 (f brain-specific anglogenesis inhibitor 3 integrin, beta 8 myetotil leukemia factor 1 myosin-binding protein C, slow-type ES1s ES1s ES1s ES1s ES1s ES1s ES1s ES1s	7.2 7.2 7.2 7.2 7.2 7.2 7.1 7.1 7.1 7.0 7.0 7.0 6.9 6.9
65	424051 442028 448243 436281 426429 407182 415293 422764 451592 429469 415734 434149 436726 417632 422421 435267 437117 445523	AB020725 AW969742 AL110203 AL243749 AW369771 AW411194 X73114 AA312551 R49462 A1767727 A1805416 M54590 NM_014747 X43829 AA324975 R20855 AA325138 N23797 AL049256 Z30118	Hs.291005 Hs.138411 Hs.8074 Hs.52620 Hs.86195 Hs.169849 Hs.230157 Hs.106541 Hs.213897 Hs.27 Hs.27 Hs.78748 Hs.128993 Hs.2693 Hs.236873 Hs.110114 Hs.122593 Hs.22593 Hs.22593	KIAA0918 protein ESTs Homo sapiens mRNA; cDNA DKFZp586J1922 (f brain-specific angiogenesis inhibitor 3 integrin, beta 8 myeloid leukemia factor 1 myosin-binding protein C, slow-type ESTs ESTs ESTs ESTs ESTs glycine dehydrogenase (decarboxylating; KIAA0237 gene product hypothetical protein MGC\$469 ESTs, Wealdy similar to T00079 hypothetic glycoprotein M5B hypothetical protein FLJ22672 ESTs ESTs ESTs ESTs ESTs ESTs ESTs, Moderately similar to unnamed prot	7.2 7.2 7.2 7.2 7.2 7.2 7.1 7.1 7.1 7.0 7.0 7.0 7.0 6.9 6.9
65 70	424051 442024 448243 436281 426429 407182 415293 422764 451592 429469 415734 434149 436726 417632 427632 427632 437117 4455267 437117 445520	AB020725 AW969742 AL110203 AL243749 AW369771 AW411194 X73114 AA312551 R49462 AT67727 AI805416 M64590 NM_014747 Z43829 AA324975 R20855 AA325138 N23797 AL049266 Z30118 AF070628	Hs. 291005 Hs. 138411 Hs. 8074 Hs. 52620 Hs. 85195 Hs. 169849 Hs. 230157 Hs. 169849 Hs. 23157 Hs. 169849 Hs. 213897 Hs. 78748 Hs. 19574 Hs. 128993 Hs. 5422 Hs. 236873 Hs. 110114 Hs. 122593 Hs. 13429 Hs. 13429	KIAA0918 protein ESTs Homo sapiens mRNA; cDNA DKFZp586J1922 (f brain-specific angiogenesis inhibitor 3 integrin, beta 8 myeloid leukenia factor 1 myosin-binding protein C, slow-type ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	7.2 7.2 7.2 7.2 7.2 7.2 7.1 7.1 7.1 7.0 7.0 7.0 7.0 8.9 8.9 8.9
65	424051 442024 448243 436281 426428 407182 415293 422764 451592 429469 434149 436726 417632 422421 435217 445523 445900 445745	ABIZO725 AW969742 AL110203 AI243749 AW369771 AW411194 X73114 AA312551 R49462 AI767727 AI805416 M64590 NM_014747 Z43829 AA324975 R20855 AA325138 N23797 ALD49256 Z30118 AF0770528 AB007924	Hs. 291005 Hs. 138411 Hs. 8074 Hs. 52620 Hs. 85195 Hs. 169849 Hs. 2301557 Hs. 165541 Hs. 475522 Hs. 213897 Hs. 78748 Hs. 19574 Hs. 128993 Hs. 5422 Hs. 236873 Hs. 110114 Hs. 128993 Hs. 293788 Hs. 13429 Hs. 13429	KIAA0918 protein ESTs Homo septens mRNA; cDNA DKFZp586J1922 (f brain-specific anglogenesis inhibitor 3 integrin, beta 8 myetold leukemia factor 1 myosin-binding protein C, slow-type ESTs ESTs ESTs ESTs ESTs ESTs Hydine dehydrogenase (decarboxytating: KIAA0237 gene product hypothetical protein MGC5469 ESTs, Weathy similar to 100078 hypotheti hypothetical protein FLJ22672 ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	7.2 7.2 7.2 7.2 7.2 7.2 7.2 7.1 7.1 7.1 7.0 7.0 7.0 8.9 8.9 8.9 6.9
65 70	424051 442028 448243 436281 426428 407182 415293 427182 429469 415739 42741 436726 417632 422421 435267 437117 445523 445900 445745	AB020725 AW969742 AL110203 AL243749 AW369771 AW411194 X73114 AA312551 R49462 A1767727 A1805416 M64590 NM_014747 XX329 AA324975 R20855 AA3253138 N23797 AL049266 Z30118 AF070628 AB007924 NM_002914	Hs.291005 Hs.138411 Hs.8074 Hs.52620 Hs.86195 Hs.169849 Hs.230157 Hs.106541 Hs.213897 Hs.27 Hs.213897 Hs.78748 Hs.19574 Hs.126993 Hs.5422 Hs.235873 Hs.110114 Hs.122593 Hs.13429 Hs.13429 Hs.13429	KIAA0918 protein ESTs Homo sapiens mRNA; cDNA DKFZp586J1922 (f brain-specific angiogenesis inhibitor 3 integrin, beta 8 myeloid leukemia factor 1 myosin-binding protein C, slow-type ESTs ESTs ESTs ESTs glycine dehydrogenase (decarboxylating; KIAA0237 gene product hypothetical protein MGC\$469 ESTs, Wealdy similar to T00079 hypotheti glycoprotein MSB hypothetical protein FLJ22672 ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	7.2 7.2 7.2 7.2 7.2 7.2 7.1 7.1 7.1 7.0 7.0 7.0 7.0 6.9 6.9 6.9
65 70	424051 442024 448243 436281 426429 407182 415293 422764 451692 429469 415734 434149 436726 417632 427421 435267 437117 445523 445745 42469 445745 42469 42588	AB020725 AW969742 AL110203 AL243749 AW369771 AW411194 X73114 AA312551 R49462 AT67727 AI805416 M64590 NM_014747 Z43829 AA324975 R20855 AA325138 N23797 AL049266 Z30118 AF070628 AB007924 NM_002914 F12101	Hs. 291005 Hs. 138411 Hs. 8074 Hs. 52620 Hs. 85195 Hs. 169849 Hs. 230157 Hs. 106541 Hs. 47522 Hs. 213897 Hs. 78748 Hs. 19574 Hs. 129593 Hs. 5422 Hs. 236873 Hs. 2425 Hs. 13245 Hs. 13245 Hs. 13245 Hs. 185701	KIAA0918 protein ESTs Homo sapiens mRNA; cDNA DKFZp586J1922 (f brain-specific angiogenesis inhibitor 3 integrin, beta 8 myelotid leutemia factor 1 myosin-binding protein C, slow-type ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	7.2 7.2 7.2 7.2 7.2 7.2 7.1 7.1 7.1 7.1 7.0 7.0 7.0 7.0 8.9 8.9 8.9 8.9
65 70	424051 442024 448243 436281 426428 407182 415293 422764 451592 429469 415732 42421 434149 436728 417632 422421 435267 437117 445523 44590 445745 424085 424085 426723 426723	AB020725 AW969742 AL110203 AL243749 AW369771 AW411194 X73114 AA312551 R49462 A1767727 A1805416 M64590 NM_014747 XX329 AA324975 R20855 AA3253138 N23797 AL049266 Z30118 AF070628 AB007924 NM_002914	Hs. 291005 Hs. 138411 Hs. 8074 Hs. 52620 Hs. 85195 Hs. 169849 Hs. 230157 Hs. 166541 Hs. 47522 Hs. 213897 Hs. 78748 Hs. 19574 Hs. 128993 Hs. 5422 Hs. 236873 Hs. 110114 Hs. 128993 Hs. 13226 Hs. 13226 Hs. 139226 Hs. 139226 Hs. 139226 Hs. 139226 Hs. 185701	KIAAUS18 protein ESTs Homo septens mRNA; cDNA DKFZp586J1922 (f brain-specific anglogenesis inhibitor 3 integrin, beta 8 myetolid leukemia factor 1 myosin-binding protein C, slow-type ESTs ESTs ESTs ESTs ESTs eycline dehydrogenase (decarboxytating: KIAAU237 gene product hypothetical protein MGC\$469 ESTs, Weatky similar to T00079 hypotheti glycoprotein MSB hypothetical protein FLJ22672 ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	7.2 7.2 7.2 7.2 7.2 7.2 7.2 7.1 7.1 7.1 7.0 7.0 7.0 6.9 6.9 6.9 6.9
65 70 75	424051 442024 448243 436281 426429 407182 415293 422764 451692 429469 415734 434149 436726 417632 427421 435267 437117 445523 445745 42469 445745 42469 42588	ABIZO725 AW969742 AL110203 Al243749 AW369771 AW411194 X73114 AA312551 R49462 AI767727 AI805416 M64590 NM_014747 Z43829 AA324975 R20855 AA325138 N23797 ALD49256 Z30118 AF070628 AB007924 NM_002914 F12101 AA620400	Hs. 291005 Hs. 138411 Hs. 8074 Hs. 52620 Hs. 85195 Hs. 169849 Hs. 230157 Hs. 106541 Hs. 213897 Hs. 27 Hs. 27 Hs. 213897 Hs. 27 Hs. 213897 Hs. 125993 Hs. 125993 Hs. 13429 Hs. 135701 Hs. 100717 Hs. 300717 Hs. 193222	KIAA0918 protein ESTs Homo sapiens mRNA; cDNA DKFZp586J1922 (f brain-specific angiogenesis inhibitor 3 integrin, beta 8 myeloid leukemia factor 1 myosin-binding protein C, slow-type ESTs ESTs ESTs ESTs Gycine dehydrogenase (decarboxylating; KIAA0237 gene product hypothetical protein MGC\$469 ESTs, Wealdy similar to T00079 hypotheti glycoprotein MSB hypothetical protein FLJ22672 ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	7.2 7.2 7.2 7.2 7.2 7.2 7.1 7.1 7.1 7.0 7.0 7.0 7.0 6.9 6.9 6.9 6.9 6.9
65 70	424051 442024 448243 436281 426429 407182 415293 422469 4157592 429469 415732 42469 417632 42421 435267 437117 445523 445904 445744 44574	AB020725 AW969742 AL110203 AL243749 AW369771 AW411191 X73114 AA312551 R49462 A1767727 A1805416 M64590 NM_014747 X3829 AA324975 R20855 AA325138 N23797 ALD49256 Z30118 AF070628 AB007924 NM_002914 F12101 AA620400 A199268	Hs. 291005 Hs. 138411 Hs. 8074 Hs. 52620 Hs. 85195 Hs. 169849 Hs. 230157 Hs. 165541 Hs. 78748 Hs. 19574 Hs. 19574 Hs. 122593 Hs. 235873 Hs. 2422 Hs. 13245 Hs. 13245 Hs. 13245 Hs. 139226 Hs. 185701 Hs. 300717 Hs. 133029	KIAA0918 protein ESTs Homo sapiens mRNA; cDNA DKFZp586J1922 (f brain-specific angiogenesis inhibitor 3 integrin, beta 8 myeloid leukemia factor 1 myosin-binding protein C, slow-type ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	7.2 7.2 7.2 7.2 7.2 7.2 7.1 7.1 7.1 7.0 7.0 7.0 7.0 8.9 8.9 8.9 8.9 8.9
65 70 75	424051 442024 448243 436281 426429 407182 415293 427562 451592 451592 435726 437454 435267 437117 445526 44745 427	AB020725 AW969742 AL110203 AL243749 AW369771 AW411194 X73114 AA312551 R49462 AT67727 AI805416 M54590 NM_014747 Z43829 AA324975 R20855 AA325138 N23797 AL049266 Z30118 AF070628 AB007824 NM_002914 F12101 AA520400 A199268 A1049268	Hs. 291005 Hs. 138411 Hs. 8074 Hs. 52620 Hs. 85195 Hs. 169549 Hs. 230157 Hs. 106541 Hs. 47522 Hs. 213897 Hs. 78748 Hs. 128993 Hs. 2422 Hs. 235873 Hs. 110114 Hs. 122593 Hs. 283788 Hs. 13429 Hs. 13429 Hs. 13429 Hs. 133229 Hs. 133229 Hs. 133229 Hs. 133229	KIAAUS18 protein ESTs Homo septens mRNA; cDNA DKFZp586J1922 (f brain-specific anglogenesis inhibitor 3 integrin, beta 8 myetold leukemia factor 1 myosin-binding protein C, slow-type ESTs ESTs ESTs ESTs eSTs gycine dehydrogenase (decarboxylating: KIAAU237 gene product hypothetical protein MGC5469 ESTs, Weatky similar to T00079 hypotheti glycoprotein MSB hypothetical protein FLJ22672 ESTs ESTs ESTs ESTs, Moderately similar to unnamed prot Homo septens clone 24787 mRNA sequence KIAAU455 gene product replication factor C (activator 1) 2 (40 Homo septens mRNA full lempt insert cDN sodium charnet, vollage-gated, type III, Homo septens, Similar to RIKEN cDNA 2010 ESTs ESTs	7.2 7.2 7.2 7.2 7.2 7.2 7.2 7.1 7.1 7.1 7.0 7.0 7.0 7.0 8.9 8.9 8.9 6.9 6.9 6.9
65 70 75	424051 442024 448243 436281 426429 407182 415293 427764 451592 429469 415734 436726 417632 42745 4274	AB020725 AW969742 AL110203 AL243749 AW369771 AW411194 X73114 AA312551 R49462 AT67727 AI805416 M64590 NM_014747 Z43829 AA324975 R20855 AA325138 N23797 AL049266 Z30118 AF070628 AB007924 NM_002914 F12101 AA620400 AL199268 AW022228 AW022228 AW022228 AW022284 AW022228 AW022284 AL049884 AW022228 AW022284 AL049884 AW022228 AW022284	Hs. 291005 Hs. 138411 Hs. 8074 Hs. 52620 Hs. 85195 Hs. 169849 Hs. 230157 Hs. 165541 Hs. 78748 Hs. 19574 Hs. 19574 Hs. 122593 Hs. 235873 Hs. 2422 Hs. 13245 Hs. 13245 Hs. 13245 Hs. 139226 Hs. 185701 Hs. 300717 Hs. 133029	KIAA0918 protein ESTs Homo sapiens mRNA; cDNA DKFZp586J1922 (f brain-specific angiogenesis inhibitor 3 integrin, beta 8 myeloid leukemia factor 1 myosin-binding protein C, slow-type ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	7.2 7.2 7.2 7.2 7.2 7.2 7.1 7.1 7.1 7.0 7.0 7.0 7.0 7.0 6.9 6.9 6.9 6.9 6.9 6.9
65 70 75	424051 442024 448243 436281 426428 407182 415293 427764 451592 429469 415734 434149 436726 417632 422421 435267 437117 445523 446900 445742 44695 4208	AB020725 AW969742 AL110203 AL243749 AW369771 AW411194 X73114 AA312551 R49462 AI767727 AI805416 M64590 NM_014747 X3829 AA324975 R20855 AA325138 N23797 AL049256 Z30118 AF070628 AB007924 NM_002914 F12101 AA620400 A199268 AI049884 AW022168 AI049884 AW022228 AW294631	Hs. 291005 Hs. 138411 Hs. 8074 Hs. 52620 Hs. 85195 Hs. 169849 Hs. 230157 Hs. 169849 Hs. 23157 Hs. 169849 Hs. 213897 Hs. 78748 Hs. 19574 Hs. 19574 Hs. 122593 Hs. 13429 Hs. 13429 Hs. 13429 Hs. 13429 Hs. 13429 Hs. 13429 Hs. 13922 Hs. 133029 Hs. 133029 Hs. 133029 Hs. 133029 Hs. 132292	KIAA0918 protein ESTs Homo sapiens mRNA; cDNA DKFZp586J1922 (f brain-specific angiogenesis inhibitor 3 integrin, beta 8 myeloid leukemia factor 1 myosin-binding protein C, slow-type ESTs ESTs ESTs ESTs glycine dehydrogenase (decarboxylating; KIAA0237 gene product hypothetical protein MGC\$469 ESTs, Wealdy similar to T00079 hypotheti glycoprotein M5B hypothetical protein FLJ22672 ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	7.2 7.2 7.2 7.2 7.2 7.2 7.2 7.1 7.1 7.1 7.0 7.0 7.0 7.0 8.9 8.9 8.9 6.9 6.9 6.9

	420000	45500010			
	429609 435056	AF002248	Hs.210863	cell adhesion molacule with homology to	6.6
	453431	AW023337 AF094754	Hs.5422	glycoprotein M6B	6.5
	444190	AI878918	Hs.32973 Hs.10526	glycine receptor, beta	6.5
5	418110	R43523	Hs.217754	cysteine and glycine-rich protein 2	6.5
_	413988	M81883	Hs.324784	hypothetical protein FLJ22202 glutamate decarboxylase 1 (brain, 67kD)	6.5
	420805	L10333	Hs.99947 -	relicution 1	6.5
	429125	AA446854	Hs.271004	ESTs, Wealdy similar to 138022 hypotheti	6.4 6.4
10	435256	AF193766	Hs.13872	cytokine-like protein C17	6.4
10	407866	AW088232	Hs.89506	paired box gene 6 (aniridia, keratitis)	6.3
	440700	AW952281	Hs.296184	guarrine nucleotide binding protein (G pr	6.3
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	6.3
	422949	AA319435		gb:EST21657 Adrenal gland turnor Homo sep	6.2
15	445102 452401	AW204610	Hs.22270	ESTs	6.2
13	435538	NM_007115 AB011540	Hs.29352 Hs.4930	tumor necrosis factor, alpha-induced pro	6.2
	410102	AW248508	Hs.279727	low density lipoprotein receptor-related	6.2
	416871	H98716	143.27 37 27	Homo sapiens cDNA FLJ14035 fis, clone HE gb:yx13d08.s1 Sozres melanocyte 2NbHM Ho	6.2
	416702	AA186428	Hs.85591	ESTS	6.1
20	419347	C15944	Hs.90005	superiorcervical ganglia, neural specifi	6.1
	424997	AL138167	Hs.96920	ESTs	6.1 6.1
	438660	U95740	Hs.6349	Homo saptens, clone IMAGE:3010666, mRNA,	6.1
	453649	Y07494	Hs.34114	ATPase, Na+/K+ transporting, atpha 2 (+)	6.1
25	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	6.1
23	414117 425517	W88559	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	6.0
	427457	AF121179	N= 404000	gb:AF121179 Homo sapiens liver (Chang L-	6.0
	437034	AW779105 AA742643	Hs.164682	ESTS	6.0
	444170	AW613879	Hs.102408	gb:my91c01.s1 NCI_CGAP_GC81 Homo sapiens ESTs	6.0
30	457183	H91882	Hs.118569	DVI-binding protein IDAX (inhibition of	6.0
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	6.0
	454048	H05626	Hs.6921	EST8	6.0 6.0
	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDN	5.9
25	448944	AB014605	Hs.22599	strophin-1 Interacting protein 1; activi	5.9
35	410011	AB020541	Hs.57856	* PFTAIRE protein kinase 1	5.9
	415486	H12214	Hs.13284	ESTs, Wealty similar to 2109260A B cell	5.9
	438993 447350	AA828995	11- 470004	gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	5.9
	451783	Al375572 R42554	Hs.172634 Hs.210852	ESTs	5.9
40	447101	N72185	Hs.44189	T-box, brain, 1 ESTs	5.9
	440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	5.9
	440274	R24595	Hs.7122	scraple responsive protein 1	5.9
	438461	AW075485	Hs.286049	phosphoseine aminotransferase	5.9
4.5	418064	BE387287	Hs.83384	\$100 calcium-binding protein, beta (neur	5.9 5.8
45	437036	Al571514	Hs.133022	ESTS	5.7
	412225	AW902042		gb:QV0-NN1022-170400-193-c02 NN1022 Homo	5.7
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.7
	444218 445828	AF070841	Hs.10684	Homo saplens clone 24421 mRNA sequence	5.7
50	447198	F05802 D61523	Hs.81907	ESTS	5.7
-	427897	NM_017413	Hs.283435 Hs.303084	ESTs	5.7
	448499	BE613280	Hs.77550	spelin; peptids ligand for APJ receptor hypothetical protein MGC1780	5.7
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	5.7
	412155	R38167	Hs.12449	Homo saplens transmembrane protein HTMP1	5.6
55	435718	R06569	Hs.269534'	ESTs	5.6 5.6
	449340	AW235786	Hs.195359	hypothetical protein MGC10954	5.6
	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	5.6
	451996	AW514021	Hs.245510	ESTs	5.6
60	422411 438328	AW749443 AI492281	Hs.22511	ESTS	5.6
	433244	AB040943	Hs.32450 Hs.271285	ESTs KIAA1510 protein	5.6
	435191	R15912	Hs.4817	Homo saplens clone 24461 mRNA sequence	5.6
	418677	\$83308	Hs.87224	SRY (sex determining region Y)-box 5	5.5
CE	400859			arri fam agreement toffert 1 Look 2	5.5 5.5
65	413625	AW451103	Hs.71371	EST8	5.5 5.5
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.5
	434933	R91095	Hs.4276	KIAA1701 protein	5.5
	438702	A1879064	Hs.54618	ESTs	5.5
70	452055 430979	A1377431 A1479755	Hs.141693	hypothetical protein MGC10858	5.5
	412709	AL022327	Hs.129010 Hs.74518	ESTs KIAA0027 protein	5.5
	439920	H05430	Hs.288433	neurotrinin	5.5
	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	5.5
76	407846	AA426202	Hs.40403	Cop/p300-interacting transactivator, wit	5.4 5.4
75	419235	AW470411	Hs.288433	neurotrimin	5.4 5.4
	418030	BE207573	Hs.83321	neuromedin B	5.4
	410330	AW023630	Hs.46786	ESTs	5.4
	410781	Al375672	Hs.165028	ESTs	5.4
80	420858 421308	AW965215 AA687322	Hs.336656	ESTs	5.4
	443740	R\$6434	Hs.192843 Hs.21062	leucine zipper protein FKSG14	5.4
	426457	AW894687	Hs.169965	ESTs chimerin (chimaerin) 1	5.4
	450375	AAD09647	Hs.8850	a disintegrin and metalloproteinase doma	5.4 5.4
				2	3.4

	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	5.4
	426600	NM_003378	Hs.171014 Hs.146858	VGF nerve growth factor inducible	5.4
	424432 429250	AB037821 H56585	Hs.198308	protocadherin 10 tryptophan rich basic protein	5.4 5.4
5	443785	AW449952	Hs.190125	basic-helix-loop-helix-PAS protein	5.4
	436282 404584	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	5.4
	430091	AB032958	Hs.233023	KIAA1132 protein	5.3 5.3
10	439845	AL355743	Hs.56663	Homo sapiens EST from clone 41214, full	5.3
10	424001 425073	W67883 W39609	Hs.137476 Hs.22003	paternally expressed 10 solute carrier family 8 (neurotransmitte	5.3 5.3
	426625	178300	Hs.300642	serologically defined colon cancer antig	. 5.3
	428137	AA421792	Hs.170999	ESTs .	5.3
15	428879 438176	AA431765 AW138970	Hs.122113	gb:zw80c03.s1 Soares_testis_NHT Homo sap ESTs	5.3 5.3
1.5	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	5.3
	451018	AW965599	Hs.247324	mitochondrial ribosomal protein S14	5.3
	416340 435244	N31772 N77221	Hs.79226 Hs.187824	fasciculation and elongation protein zet ESTs	5.3 5.3
20	446035	NM_006558	Hs.13585	Sam68-like phosphotyrosine protein, T-ST	5.3
	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for sec	5.3
	407748 430437	AL079409 Al768801	Hs.38176 Hs.169943	KIAA0606 protein; SCN Circadian Oscillat Homo sapiens cDNA FLJ13569 fis, clone PL	5.3 5.3
0.5	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	5.2
25	453941 424998	U39817 U58515	Hs.36820 Hs.154138	Bloom syndrome chitinase 3-like 2	5.2 5.2
	423419	R55336	Hs.23539	EST8	5.2
	424922	BE386547	Hs.217112	hypothetical protein MGC10825	5.2
30	447359 408206	NM_012093 AF041853	Hs.18268 Hs.43670	adenylata kinase 5 kinesin family member 3A	5.2 5.2
30	421013	M62397	Hs.1345	mutated in colorectal cancers	5.2
	429443	AB028967	Hs.202687	potassium voltage-gated channel, Shal-re	5.2
	434367 444861	AB020700 R46789	Hs.3830 Hs.76118	KIAA0893 protein ubiquitin carboxyl-terminal esterase L1	5.2 5.2
35	446142	A1754693	Hs.145968	ESTs	5.2
	448816	AB033052	Hs.22151	KIAA1226 protein	5.2
	451050 451106	AW937420 BE382701	Hs.69662 Hs.25960	ESTs v-myc avian myelocytomatosis viral relat	5.2 5.2
40	439285	AL133916	Hs.172572	hypothetical protein FLJ20093	5.2
40	416737 424800	AF154335	Hs.79691 Hs.153203	UM domain protein	5.2
	443695	AL035588 AW204099	Hs.337720	MyoD family inhibitor ESTs, Weakly similar to AF126780 1 retin	5.2 5.2
	415257	F03016	Hs.27513	ESTs	5.2
45	433929 415651	Al375499 Al207162	Hs.27379 Hs.3815	ESTs	5.1 5.1
43	451027	AW519204	Hs.40808	stathmin-tike-protein RB3 ESTs	5.1 5.1
	409172	Z99399	Hs.118145	ESTs	5.1
	423343 429172	AA324843 AA447417	Hs.246106 Hs.285491	ESTs ESTs	5.1 5.1
50	437268	AI754847	Hs.227571	regulator of G-protein signalling 4	5.1
	451270	AW341392	Hs.235795	ESTs	5.1
	452904 420560	AL157581 AW207748	Hs.30957 Hs.59115	Homo saplens mRNA; cDNA DKFZp434E0826 (f ESTs	5.1 5.1
E E	418097	R45137	Hs.21868	ESTs	5.1
55	442910 434849	Al365130 AW292765	Hs.11307 Hs.6053	ESTs, Weakly similar to T19326 hypotheti ESTs	5.1
	413554	AA319146	Hs.75426	secretogranin (I (chromogranin C)	5.1 5.1
	414217	A1309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	5.1
60	412068 413627	872043 BE182082	Hs.73133 Hs.246973	metallothlonetn 3 (growth inhibitory fac ESTs	5.0 5.0
••	418661	NM_001949	Hs.1189	E2F transcription factor 3	5.0
	422438 423728	AA445925	Hs.270898	ESTs, Moderately similar to Z195_HUMAN Z	5.0
	431431	AW891294 AL096711	Hs.132136 Hs.252953	solute cerrier family 4, sodium bloarbon Human DNA sequence from clone RP3-403A15	5.0 5.0
65	435087	AW975241	Hs.23567	ESTs	5.0
	452097 410434	AB002364 AF051152	Hs.27916 Hs.63668	a disintegrin-like and metalloprotease (toil-like receptor 2	5.0 4.9
	408692	AL040127	Hs.34074	dipeplidylpeplidase VI	4.9
70	407808	AA663559	Hs.279789		4.9
70	418940 425977	H17739 R15138	Hs.288513 Hs.165570		4.9 4.9
	425814	AF036943	Hs.172619	myelin transcription factor 1-like	4.9
	447112 449574	H17800 F05048	Hs.7154	ESTs ESTs	4.9
75	453652	AW009640	Hs.175373 Hs.28368	ESTs, Moderately similar to \$65657 alpha	4.9 4.9
-	423869	BE409301	Hs.134012	C1q-related factor	4.9
	413248 449176	T64858 A1633545	Hs.21433 Hs.198072	hypothelical protein DKFZp547J036 PESTs	4.9 4.9
	448451	AW015994	113.100012	gb:UI-H-Bi0p-abh-g-09-0-UI.s1 NCI_CGAP_S	4.8
80	402604	ALAMOSSON	11- 1010-		4.8
	436039 448769		Hs.121070 Hs.38173	ESTs ESTs	4.8 4.8
	423678		Hs.7847	ESTs	4.8

	439451	AF088270	Hs.278554	halomehmentija Eko aminin 1	4.8
	425870	R13408		heterochromatin-tike protein 1 ESTs	4.8
	408777	U71204	Hs.47626	Ric (Drosophila)-like, expressed in neur	4.8
-	413409	AI638418	Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	4.8
5	413623	AA825721	Hs.246973	ESTs	4.8
	417246 420900	A1760098 ALD45633	Hs.21411 Hs.44269	ESTs ESTs	4.8 4.8
	424153	AA451737	Hs.141496	MAGE-fike 2	4.8
	443539	AI076182	Hs.134074	ESTs, Moderately similar to ALU6_HUMAN A	4.8
10	448750	U95020	Hs.21903	calcium channel, voltage-dependent, beta	4.8
	454030	AW021429	Hs.231980	ESTs	4.8
	424458 444119	M29273 R41231	Hs.1780 Hs.184261	myetin associated glycoprotein ESTs, Wealdy similar to T26686 hypotheti	4.8 4.8
	407792	A1077715	Hs.39384	putative secreted figand homologous to f	4.8
15	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	4.7
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	4.7
	429956 435060	AJ374651 AJ422719	Hs.22542 Hs.233349	ESTS	4.7 4.7
	438203	BE384982	Hs.5076	ESTs, Wealdy similar to fork head like p Homo sapiens cDNA: FLJ22128 fls, clone H	4.7
20	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	4.7
	422222	A1699372	Hs.193247	hypothetical protein DKFZp434A171	4.7
	431733	AW298410	Hs.21475	ESTs	4.7
	449353 452022	AA001220 AW072330	Hs.271369 Hs.293875	ESTs ESTs	4.7 4.7
25	454269	AI961060	Hs.129908	KIAA0591 protein	4.7
	404541			Tara to the protection	4.7
	428189	AA424030	Hs.46627	ESTs	4.7
	409125	R17268	Hs.259873	exonal transport of synaptic vesicles	4.7
30	458435 425745	A1418718 U44060	Hs.144121 Hs.14427	ESTs, Weakly similar to T46916 hypotheti	4.6 4.6
50	413492	D87470	Hs.75400	Homo saplens cDNA: FLJ21800 fis, clone H KIAA0280 protein	4.6
	419629	AB020695	Hs.91662	KIAA0888 protein	4.6
	407638	AJ404672	Hs.334483	hypothetical protein FLJ23571	4.6
35	436140	W87355	Hs.269587	ESTs	4.6
33	439169 443150	AJ912122 AID34467	Hs.41095 Hs.34650	ESTs ESTs	4.6 4.6
	451073	AI758905	Hs.205053	ESTS	4.6
	451659	BE379761	Hs.14248	ESTs	4.6
40	452106	Al141031	Hs.21342	ESTs	4.6
40	451407	AA131376	Hs.326401	fibroblast growth factor 12B	4.6
	448765 430147	R15337 R60704	Hs.21958 Hs.234434	Homo saptens mRNA; cDNA DKFZp547D088 (fr hairy/enhancer-of-split related with YRP	4.6 4.6
	437204	AL110218	Hs.12285	ESTs, Weakly similar to 155214 salivary	4.6
4.5	431117	AF003522	Hs.250500	delta (Orosophila)-like 1	4.5
45	422175	N79885	Hs.6382	ESTs, Highly similar to T00391 hypotheti	4.5
	407889	R34556	Hs.30800	ESTs, Wealdy similar to S65657 alpha-1C-	4.5
	419343 421790	AA456245 AW896201	Hs.85603 Hs.22654	down-regulated by Ctnnb1, a sodium channel, voltage-gated, type I, a	4.5 4.5
	429399	AA452244	Hs.16727	ESTs	4.5
50	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	4.5
	453118	AW195849	Hs.252757	ESTs	4.5
	443455 442613	AB001025 Al004002	Hs.9349 Hs.130522	ryanodine receptor 3 Kv channal-interacting protein 1	4,4 4.4
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	4.4
55	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.4
	418845	AAB52985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	4.4
	435202 437496	AI971313 AA452378	Hs.170204 Hs.170144		4.4 4.4
	451254	AI571018	Hs.172967		4.4
60	439039	AI656707	Hs.48713	ESTS	4.4
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.4
	441507 424983	NM_005010 AJ742434	Hs.7912 Hs.169911	reuronal cell adhesion malecula ESTs	4.4 4.4
	410611	AW954134	Hs.20924	KIAA 1628 protein	4.4
65	402605			7.55	4.4
	409248	AB033035	Hs.51965	KIAA1209 protein	4.4
	442222	AI061301	Hs.164773		4.4
	454027 454293	R40192 H49739	Hs.21527 Hs.134013	Human DNA sequence from clone GS1-115M3 ESTs, Moderately similar to HK61_HUMAN H	4.4 4.4
70	442832	AW206560	Hs.253569		4.4
	407304	AA565832		gb:nj32b03.s1 NCI_CGAP_AA1 Homo saplens	4.4
	423279	AW959861	Hs.290943	ESTS	4.3
	427194	AA399018	Hs.250835		4.3
75	419723 445810	AL120193 AW265700	Hs.92614 Hs.155660		4.3 4.3
, ,	409734		Hs.56155		4.3
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	4.3
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	4.3
80	433024 453202		Hs.26549 Hs.26270	KIAA1708 protein hypothetical protein FLJ11588	4.3
50	425264		Hs.20369		4.3 4.3
	416427		Hs.79307		4.3
	431789		Hs.26922		4.3

	444600	R41398	Hs.6996	ESTs ·	40
	454042	H22570	Hs.172572	hypothetical protein FLJ20093	4.3 4.3
	441899	Al372588	Hs.8022	TU3A protein .	4.3
5	425256	BE297611	Hs.155392	collapsin response mediator protein 1	4.3
,	410358 430291	AW975168 AV660345	Hs.13337 Hs.238126	ESTs, Weakly similar to unnamed protein	4.2
	433597	AA708205	Hs.100343	CGI-49 protein ESTs	4.2 4.2
	444127	N63620	Hs.13281	ESTs	4.2
10	448507	AL133109	Hs.21333	Homo saplens mRNA; cDNA DKFZp566N1047 (f	4.2
10	413589	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 nonci	4.2
	408577 409719	H50572 AI769160	Hs.19515 Hs.108681	ESTs, Highly similar to NRG3_HUMAN PRO-N Homo sapiens brain tumor associated prot	4.2 4.2
	428538	AI143139	Hs.2288	visinin-like 1	4.2
1.0	429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein	4.2
15	432865	AI753709	Hs.152484	ESTs, Weakly similar to 138022 hypotheti	4.2
	447138 450648	AI439112	Hs.93828	ESTs, Wealdy similar to 2109260A B cell	4.2
	451459	A1703368 A1797515	Hs.26766 Hs.270560	ESTs, Moderately similar to ALU7_HUMAN A	4.2 4.2
	421686	AB011156	Hs.106794	KIAA0584 protein	4.2
20	452776	AA194540	Hs.13522	ESTs, Weakly similar to 138022 hypotheti	4.2
	436421	A1678031	Hs.122813	ESTs, Weakly similar to ZN22_HUMAN ZINC	4.2
	423858 434001	AL137326 AW950905	Hs.133483 Hs.3697	Homo sepiens mRNA; cDNA DKFZp43480650 (f serine (or cysteine) proteinase inhibito	4.2
	437380	AL359577	Hs.112198	Homo sepiens mRNA; cDNA DKFZp547M073 (fr	4.2 4.2
25	432328	A1572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	4.1
	439607	BE540565	Hs.159460	ESTs	4.1
	424028 446936	AF055084 H10207	Hs.153692	Homo saplens cDNA FUJ14354 fis, clone Y7	4.1
	424240	AB023185	Hs.47314 Hs.143535	ESTs calcium/calmodulin-dependent protein kin	4.1 4.1
30	412448	A1768015	Hs.92127	ESTs	4.1
	409953	AA332277	Hs.57691	cadherin 18, type 2	4.1
	416220	N49776	Hs.170994	hypothelical protein MGC10946	4.1
	419683 426071	AA248897 AW138057	Hs.48784 Hs.163835	ESTs ESTs	4.1
35	428743	AL080060	Hs.301549	Homo sepiens mRNA; cDNA DKFZp584H172 (fr	4.1 4.1
	432809	AA565509	Hs.131703	ESTs	4.1
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	4.1
	452039 425905	AI922988 AB032959	Hs.172510 Hs.318584	ESTs	4.1
40	457561	AA331517	Hs.286055	novel C3HC4 type Zinc finger (ring finge chimerin (chimaerin) 2	4.1 4.1
	429038	AL023513	Hs.194766	setzure related gene 6 (mouse)-like	4.1
	433932	AW954599	Hs.169330	neuronal protein	4.1
	436637 439231	AI783629 AW581935	Hs.26766	ESTS	4.1
45	450530	NM_006668	Hs.141480 Hs.25121	Homo sapiens mRNA; cDNA DKFZp434N079 (fr cytochrome P450, subfamily 46 (cholester	4.1 4.1
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	4.1
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-0-sulfot	4.1
	410486	AW235094	Hs.69233	zinc finger protein	4.0
50	413916 438703	N49813 AI803373	Hs.75615 Hs.31599	apolipoprotein C-II ESTs	4.0 4.0
	424726	AK001007	Hs.138760	Homo sapiens cDNA FLJ10145 fls, clone HE	4.0
	405771				4.0
	418841 421764	NM_002332 Al681535	Hs.89137	low density lipoprotein-related protein	4.0
55	424176	AL137273	Hs.148135 Hs.142307	serine/threonine kinase 33 hypothetical protein	4.0 4.0
	425773	N21279	Hs.237749	ESTs	4.0
	427304	AA761526	Hs.163853	ESTs	4.0
	428882 452834	AA436915 AI838827	Hs.131748	ESTs, Moderately similar to ALU7_HUMAN A	4.0
60	453745	AA952989	Hs.105685 Hs.63908	KIAA1688 protein hypothetical protein MGC14726	4.0 4.0
	405239	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	4.0
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	4.0
	429698	AI685086	Hs.26339	ESTs, Weakly similar to S21348 probable	4.0
65	435854 439199	AJ278120 R40373	Hs.4996 Hs.26299	putative ankyrin-repeat containing prote ESTs	4.0
-	439450	R51613	Hs.125304		4.0 4.0
	446782	AI653048	Hs.144006	ESTs	4.0
	419687	AI638859	Hs.227699	ESTs, Weakly similar to T2D3_HUMAN TRANS	3.9
70	402408 453362	H14988	Un 107275	ECT.	3.9
	414219	W20010	Hs.107375 Hs.75823	ESTs ALL1-fused gene from chromosome 1q	3.9 3.9
	420578	AA813546	Hs.99034	GTP-binding protein Rho7	3.9 3.9
	425010	T16837	Hs.4241	ESTs	3.9
75	444230	H95537	Hs.146067		3.9
, 5	441738 418951	AW292779 F07809	Hs.169799 Hs.89506	ESTs paired box gene 6 (aniridia, keratitis)	3.9
	406311			beared new Resid o fermined vestalit?)	3.9 3.9
	408480	AA054726	Hs.285574		3.9
80	410658	AW105231	Hs.192035		3.9
30	414699 418849	AI815523 AW474547	Hs.76930 Hs.53565	synuclein, alpha (non A4 component of am	3.9
	429477	Al275514	Hs.6658	Homo saplens PIG-M mRNA for mannosyltran ESTs	3.9 3.9
	433768	AA609234	Hs.112669		3.9 3.9
				162	

				7	
	435190 447891	AK001059 · R41754	Hs.6496	gb:Homo sapiens cDNA FLJ10197 fis, clone ESTs	3.9
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	3.9 3.9
-	404283			•	3.9
5	453919	AW959912	Hs.7076	KIAA1705 protein	3.9
	429656 412754	X05608 AW160375	Hs.211584 Hs.74565	neurofilement, light polypeptide (68kD) amyloid beta (A4) precursor-like protein	3.9 3.9
	445314	AI689948	Hs.65489	Homo saplens cDNA: FLJ21517 fis, clone C	3.9
10	435652	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	3.9
10	407378	AA299264	Hs.57776	ESTs, Moderately similar to 138022 hypot	3.9
	438054 436420	AA776826 AA443966	Hs.62183 Hs.31595	ESTs ESTs	3.9 3.9
	445133	AW157646	Hs.153506	ESTs	3.9
	432590	Al609273	Hs.110783	ESTs	3.9
15	453331	AI240665	Hs.8895	ESTs	3.9
	410227 424635	AB009284 AA420887	Hs.61152	exostoses (multiple)-like 2 Homo sapiens cDNA FLJ14259 fis, clone PL	3.8
	424033 451489	NM_005503	Hs.115455 Hs.26468	amyloid bets (AA) precursor protein-bind	3.8 3.8
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	3.8
20	448302	Al480208	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	3.8
	415669 417355	NM_005025 D13168	Hs.78589 Hs.82002	serine (or cysteine) proteinase inhibito	3.8
	446727	AB011095	Hs.16032	endothelin receptor type B KIAA0523 protein	3.8 3.8
0.5	424340	AA339038	Hs.7033	ESTs	3.8
25	423346	AI267677	Hs.127416	synaptojanin 1	3.8
	412788 404593	AA120960	Hs.198416	ESTs	3.8
	416856	N27B33	Hs.269028	ESTs, Weakly similar to I38022 hypotheti	3.8 3.8
~ ^	429896	AA460367	Hs.224223	ESTs, Moderately similar to 138022 hypot	3.8
30	439619	AW975998	Hs.58595	ESTs, Weakly similar to 138022 hypotheti	3.8
	439634	W79377	Hs.167	microtubule-associated protein 2	3.8
	440322 447761	AA879430 AF061573	Hs.19492	gb:oj91d08.s1 Soares_NFL_T_GBC_S1 Homo s protocadherin 8	3.8 3.8
	452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sepien	3.8
35	439671	AW162B40	Hs.6641	kinesin family member 5C	3.8
	447937	AL109716	Hs.20034	Homo saplens mRNA full length insert cDN	3.8
	459278 447028	AW294659 AI973128	Hs.34054 Hs.167257	Homo septens cDNA: FLJ22488 fls, ctone H brain link protein-1	3.8 3.8
4.0	449458	AI805078	Hs.208261	ESTs	3.8
40	445888	AF070564	Hs.13415	Homo saplens clone 24571 mRNA sequence	3.8
	407385	AA610150	Hs.272072	ESTs, Weakly similar to 138022 hypotheti	3.8
	428841 430643	AI418430 AW970065	Hs.104935 Hs.287425	ESTs MEGF10 protein	3.8 3.8
	422263	AA307839	Hs.129908	KIAA0591 protein	3.8
45	451625	R56793	Hs.106576	alanine-glyoxytate aminotransferase 2-li	3.8
	439238	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN!	3.8
	441928 441797	Al370188 Al936933	Hs.211454 Hs.214635	ESTs ESTs	3.8 3.7
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.7
50	425588	F07396	Hs.46751	ESTs .	3.7
	437007	AA741300	Hs.202599	ESTs, Weakly similar to 138022 hypotheti	3.7
	435793 443682	AB037734 Al383061	Hs.4993 Hs.47248	KIAA1313 protein ESTs, Highly similar to similar to Cdc14	3.7 3.7
	425741	AF052152	Hs.159412	Homo saplans clone 24628 mRNA sequence	3.7
55	418211	BE244748	Hs.247474	hypothetical protein FLJ21032	3.7
	440080 452898	AW051597 AA814497	Hs.143707	ESTs ESTs	3.7
	435575	AF213457	Hs.78792 Hs.44234	triggering receptor expressed on myeloid	3.7 3.7
	409234	AI879419	Hs.27206	ESTs	3.7
60	420489	AA815089	Hs.193513		3.7
	426890 438849	AA393167 W28948	Hs.41294 Hs.10762	ESTs ESTs	3.7
	441869	NM_003947	Hs.8004	hunlingtin-associated protein interactin	3.7 3.7
~-	448796	AA147829	Hs.301431	endothelial zinc finger protein induced	3.7
65	459318	NM_000038	11. 00.4000	gb:Homo sepiens edenomatosis polyposis c	3.7
	434444	A1937419 A1765276	Hs.294069 Hs.101257		3.7
	421183	AL135740	Hs.102447		3.7 3.7
70	410555	U92849	Hs.64311	a disintegrin and metalloproteinase doma	3.7
70	421637	AF035290	Hs.106300	Homo saplens clone 23556 mRNA sequence	3.7
	418522 420807	AA605038 AA280627	Hs.7149 Hs.57846	Homo sapiens cDNA: FLJ21950 fis, clone H ESTs	3.7
	449961	AW265634	Hs.133100		3.7 3.7
	422634	NM_016010		CGI-62 protein	3.7
75	421030	AW161357	Hs.101174	microtubule-associated protein tau	3.7
	427099 452355		Hs.173560 Hs.29202		3.7
	452355 440483		Hs.150386	G protein-coupled receptor 34	3.7 3.7
64	429597	NM_003816		a disintegrin and metalloproteinase doma	3.7
80	423756		11- 44-64	gb:od71a09.s1 NCI_CGAP_Ov2 Homo sapiens	3.6
	425187 434859		Hs.22509 Hs.299315	ESTs collapsin response mediator protein-5; C	3.8
	413199		Hs.75236	ELAV (embryonic tethal, abnormal vision,	3.6 3.6
					0

	445729		Hs.13223	Homo sapjens mRNA full length insert cON	3.6
	416120 429239	H46739 AA448419	Hs.45209	gb:yo14h02.s1 Soares adult brain N2b5HB5 ESTs	3.6 3.6
	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	3.6
5	446659	A1335361	Hs.226376	ESTs	3.6
	426757	AW205640	Hs.158206	ESTs	3.6
	418819	AA228776	Hs.191721	ESTs	3.6
	458332 408826	AI000341 AF216077	Hs.220491 Hs.48376	ESTs Homo sapiens clone HB-2 mRNA sequence	3.6 3.6
10	410343	AA084273	Hs.76581	ESTs, Weakly similar to \$47072 finger pr	3.6
	410507	AA355288	Hs.40834	transitional epithelia response protein	3.6
	422977	AA631498		gb:np83h04.s1 NCI_CGAP_Thy1 Homo sapiens	3.6
	425305	AA363025	Hs.155572	Human clone 23801 mRNA sequence	3.6
15	428002 428505	AA418703 AL035461	Hs.2281	gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi ctrromogranin B (secretogranin 1)	3.6
13	430530	AA480870	Hs.47660	ESTs	3.6 3.6
	436425	AI913146	Hs.318725	CG1-72 protein	3.6
	438078	Al016377	Hs.131693	ESTs	3.6
20	442927	AI024347	Hs.131519	ESTs	3.6
20	446242	N66336 Al.080123	Hs.7360 Hs.22182	ESTS	3.6
	448831 450474	AW872844	Hs.201919	zinc finger protein 23 (KOX 16) ESTs	3.8 3.6
	452198	AI097560	Hs.61210	ESTs, Weakly similar to 138022 hypotheti	3.6
0.0	455800	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	3.6
25	436443	AW138211	Hs.128746	ESTs	3.6
	426514 456038	BE616833 AA203285	Hs.170195 Hs.294141	bone morphogenetic protein 7 (osteogenic	3.6
	408902	AW014869	Hs.5510	ESTs, Weakly similar to alternatively sp ESTs	3.6 3.6
	442950	Al500417	Hs.46764	ESTs	3.6
30	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	3.6
	425478	AB007953	Hs.268840	ESTs	3.6
	453884 404721	AA355925	Hs.36232	KIAA0186 gene product	3.6 3.6
	408453	AI369838	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	3.6
35	440553	AA889416	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	3.5
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	3.5
	413999	N48124	Hs.34460	ESTs	3.5
	421458 425017	NM_003654 AL119305	Hs.104576 Hs.288405	carbohydrate (keretan sulfate Gal-6) sul ESTs	3.5 3.5
40	435958	H98180	Hs.117975	ESTs	3.5
. •	415101	R45531	Hs.144534	ESTs	3.5
	451320	AW118072	Hs.B9981	diacylglycerol kinase, zeta (104kD)	3.5
	430290	A1734110	Hs.135355	EST8	3.5
45	416836 414821	D54745 M63835	Hs.80247 Hs.77424	cholecystokinin Fc fragment of IgG, high effinity ta, re	3.5 3.5
	419412	AW161058	Hs.90297	synudeln, bela	3.5
	437860	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	3.5
	452689	F33868	Hs.284176	transferrin	3.5
50	416661 427491	AA634543 R43279	Hs.79440 Hs.22574	IGF-II mRNA-binding protein 3 ESTs, Wealdy similar to 138022 hypotheti	· 3.5 3.5
20	428037	N47474	Hs.89230	potassium Intermediate/smail conductance	3.5 3.5
	444584	AI168422		gb:ok30e11.x1 Soares_NSF_F8_9W_OT_PA_P_S	3.5
	408296	AL117452	Hs.44155	OKFZP586G1517 protein	3.5
55	453775	NM_002916		replication factor C (activator 1) 4 (37	3.5
55	412659 429077	AW753865 AB028983	Hs.74376 Hs.2352	olfactomedin related ER localized protei adenylate cyclase 2 (brain)	3.5 3.5
	436887	AW953157	Hs.193235		3.5
	450784	AW246803	Hs.47289	ESTs	3.5
60	446827	AW451243	Hs.157069		3.5
VV	436434 412777	N50465 Al335773	Hs.92927 Hs.270123	putative 47 kDa protein ESTs	3.5 3.5
	436476	AA326108	Hs.33829	bHLH protein DEC2	3.5
	408601	U47928	Hs.86122	protein A	3.4
65	429401	AW296102	Hs.99272	ESTs, Weakly similar to S32567 A4 protei	3.4
65	448425	AI500359 AA227609	Hs.233401 Hs.94834		3.4
	418727 451729	AW160725	Hs.312469	ESTS ESTS	3.4 3.4
	435910	AI084152	Hs.21782	ESTs, Wealdy similar to ALU7_HUMAN ALU S	3.4
70	434577	R37316	Hs.179769	Homo sapians cDNA: FLJ22487 fis, clone H	3.4
70	414598	AI094221	Hs.135150		3.4
	439627	BE621702	Hs.29076		3.4
	413293 423992	AL047483 AW898292	Hs.302498 Hs.137208		3.4 3.4
~-	426249	F05422	Hs.168352		3.4
75	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	3.4
	430388		Hs.240770		3.4
	435061 452291	AI651474 AF015592	Hs.16394 Hs.28853		3.4 3.4
	449714		Hs.23941	KIAA1189 protein	3.4
80	443392	A1055821	Hs.29342	D ESTs	3.4
	410082		Hs.15831		3.4
	445337 408493				3.4
	400433	DE200034	Hs.46039	phosphoglycerate mutase 2 (muscle)	3.4

	432731	R31178	Hs.287820	fibronectin 1	3.4
	448758 432613	AB018311	Hs.21917	KIAA0768 protein	3.4
	434164	AW081698 AW207019	Hs.80712 Hs.148135	KIAA0202 protein serine/threonine kinase 33	3.4
5	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	3.4
_	410108	AA081659	Hs.318775	OSBP-related protein 6	3.4 3.4
	406815	AAB33930	Hs.288036	IRNA isopentanylpyrophosphate transferas	3.4
	402855				3.3
10	422170	AJ791949	Hs.112432	anti-Mullerian hormone	3.3
10	445034	AW293376	Hs.143659	ESTs .	3.3
	424378	W2B020	Hs.167988	neural cell adhesion molecule 1	3.3
	423611	AB011163	Hs.129908	KIAA0591 protein	3.3
	435593 404819	R88872	Hs.4964	DKFZP586J1624 protein	3.3
15	436607	AW661783	Hs.211061	ESTs	3.3
	427315	AA179949	Hs.175563	Homo saplens mRNA; cDNA DXFZp564N0763 (f	3.3
	452693	179153	Hs.48589	zinc finger protein 228	3.3 3.3
	454998	AW850180		gb:lL3-CT0219-271099-022-C09 CT0219 Homo	3.3
~~	406927	M26460		gb:Homo saplens (clone 104) retinoblasto	3.3
20	409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp43400515 (f	3.3
	415238	R37780	Hs.21422	ESTs	3.3
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	3.3
	421192 426695	AA833718 AW118191	Hs.204529 Hs.112729	KIAA1806 protein	3.3
25	438885	A1886558	Hs.184987	ESTS ESTS	3.3
	451762	AF222980	Hs.26985	disrupted in schizophrenia 1	3.3
	452103	R42764	Hs.339654	ESTs, Weakly similar to I38022 hypotheti	3.3 3.3
	453590	AF150278	Hs.33578	KIAA0820 protein	3.3
20	453616	NM_003462	Hs.33846	dynein, exonemal, light intermediate pol	3.3
30	457285	AI038858	Hs.130522	Kv channel-interacting protein 1	3.3
	436045	AB037723	Hs.5028	DKFZP564O0423 protein	3.3
	437470 448520	AL390147	Hs.134742	hypothetical protein DKFZp5470065	3.3
	436480	AB002367 AJ271643	Hs.21355	doublecortin and CaM kinase-like 1	3.3
35	432656	NM_000246	Hs.87469 Hs.3076	putative acid-sensing ion channel MHC class II transactivator	3.3
	443898	AWB04286	Hs.9950	Sec61 gamma	3.3
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	3.3 3.3
	445953	AI612775	Hs.145710	ESTs	3.3
40	427940	AA417812	Hs.38775	ESTs	3.3
40	414683	S78296	Hs.76888	hypothetical protein MGC12702	3.3
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.3
	420649	A1866964	Hs.124704	ESTs, Moderately similar to S65657 alpha	3.3
	419498 457579	AL036591 AB030816	Hs.20887	hypothetical protein FLJ10392	3.3
45	436556	Al364997	Hs.38761 Hs.7572	HRAS-like suppressor ESTs	3.3
	424369	R87622	Hs.26714	KIAA1831 protein	3.2
	457065	AI476318	Hs.192480	ESTs	· 3.2 3.2
	440210	AW874562	Hs.125298	ESTs	3.2
50	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	3.2
50	434353	AA630863	Hs.131375	ESTs, Moderately similar to ALUB_HUMAN !	3.2
	414430	Al346201	Hs.76118	ubiquilin carboxyl-terminal esterase L1	3.2
	439924 411505	AJ985897 AF155659	Hs.125293 Hs.70565	ESTs	3.2
	423175	W27595	Hs.18653	molybdenum cofactor synthesis 2 hypothetical protein FLJ14627	3.2
55	415115	AA214228	Hs.127751	hypothetical protein	3.2
	407878	D87468	Hs.40888	activity-regulated cytoskeleton-associat	3.2 3.2
	410274	AA381807	Hs.61762	hypoxla-inducible protein 2	3.2
	437762	178028	Hs.154679	synaptotagmin I	3.2
60	438944	AA302517	Hs.92732	KIAA1444 protein	3.2
00	450313 409459	AI038989	Hs.332633	Bardet-Biedi syndrome 2	3.2
	410953	D86407 AW811766	Hs.54481 Hs.334858	low density lipoprotein receptor-related	3.2
	418527	AA450386	Hs.7149	hypothetical protein MGC12250 Homo sepiens cDNA: FLJ21950 fis, clone H	3.2
	420081	AW510776	Hs.94958	tubufin tyrosine ligase-like 1	3.2 3.2
65	429498	AA453800	Hs.192793	ESTs	3.2
	430099	AW194988	Hs.20537	hypothetical protein FLJ13942	3.2
	434928	AW015595	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA	3.2
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	3.2
70	438306 439274	AW188266	Hs.163645	ESTs	3.2
, 5	440847	AF086092 AA907511	Hs.48372 Hs.130178	ESTs Sets	3.2
	447750	AJ422234	Hs.143434	ESTs contactin 1	3.2
	455350	AW901809		gb:QV0-NN1020-170400-195-h02 NN1020 Homo	3.2
76	430890	X54232	Hs.2699	glypican 1	3.2 3.2
75	420568	F09247	Hs.247735	protocadherin alpha 10	3.2
	410768	AF038185	Hs.66187	Homo sapiens clone 23700 mRNA sequence	3.2
	427450	AB014526	Hs.178121	KIAA0828 gene product	3.2
	430456	AA314998	Hs.241503	hypothetical protein	3.2
80	430181 418512	AF065314	Hs.234785	cyclic nucleotide gated channel alpha 3	3.2
-	419912	AW498974 AF249745	Hs.89981 Hs.6066	diacytglycerol kinase, zeta (104kD)	3.2
	450689	Al389275	Hs.243010	Rho guantne nucleotide exchange factor (Homo saplens cONA FLJ14445 fis, clone HE	3.2
	424899	AL119387	Hs.119062	ESTs	3.2 3.2
					ω 2

	40CDT	מספינת ו	ds.120917 E	STa	3.2
				epcidin antimicroblai peptida	3.2
	445078			inctophilin 3	3.2
_	447746	AW015920		STS	3.2 3.2
5	435458			Iomo sapiens cione 24841 mRNA sequence	3.2
	427729 417417		Hs.300646 H Hs.89512 /	(IAA protein (similar to mouse paladin) NTPase, Ca⊶ transporting, plasma membra	3.1
	438810			ypothetical protein DKFZp761N09121	3.1
	439570		Hs.269165	STs, Weakly similar to ALU1_HUMAN ALU S	3.1
10	432527			ESTs	3.1 3.1
	416801			sal (Drosophila)-like 2 ESTs	3.1
	421988 426509	AW450481 M31166		pentaxin-related gene, rapidly induced b	3.1
	408786	AA773187	Hs.294027	ESTs	3.1
15	433494	AB029396		beta-1,3-gtucuronyltransferasa 1 (ghucur	3.1 3.1
	412723	AA648459		hypothetical protein AF301222	3.1
	418329 439456	AW247430 AI752409		cystathlonine-bela-synthase hypothetical protein FLJ20980	3.1
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	3.1
20	452780	BE171598	Hs.13522	ESTs, Weakly similar to 138022 hypotheti	3.1
	438192	A1859065		Homo sapiens AFG3L1 isoform 1 mRNA, part	3.1 3.1
	424939	AK000059	Hs.153881	Homo saplens NY-REN-62 antigen mRNA, par eukaryotic translation elongation factor	31
	403053 404299	R58624	Hs.2186	edital your translation exorgation raction	3.1
25	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	3.1
	410181	A1468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	31
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	3.1 3.1
	449101	AA205847	Hs.23016 Hs.166254	G protein-coupled receptor hypothetical protein DKFZp5681133	3.1
30	453240 440486	AI969564 BE243513	Hs.7212	hypothetical protein PP1044	3.1
20	408096	BE250162	Hs.83765	dihydrofolate reductase	3.1
	439864	AI720078	Hs.291997	ESTs, Wealdy similar to A47582 B-cell gr	3.1
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.1 3.1
35	438315	BE390513	Hs.27935	hypothetical protein MGC4837 Homo saplens mRNA; cDNA DKFZp566P013 (fr	3.1
33	426855 425683	AL117427 AB037813	Hs.172778 Hs.159200	hypothetical protein DKFZp762K222	3.1
	410126	BE169274	Hs.169387	KIAA0036 gene product	3.1
	435312	AJ243396	Hs.4865	voltage-gated sodium channel beta-3 subu	· 3.1 3.1
40	425491	AA883316	Hs.255221	ESTS	3.1
40	456273	AF154846 AA219691	Hs.1148 Hs.73625	zinc finger protein RAB8 Interacting, kinesin-like (rabkines	3.1
	412140 445255	NM 014841	Hs.12477	synaptosomal-associated protein, 91 kDa	3.1
	432154	AJ701523	Hs.112577	ESTs	3.1
4.5	453128	AW026516	Hs.31791	acylphosphalase 2, muscle type	3.1
45	438458	AW975186	04044	gb:EST387294 MAGE resequences, MAGN Homo	3.1 3.0
	448616 429281	AF035621 AA830856	Hs.21611 Hs.29808	kinesin family member 3C Homo sapiens cDNA: FLJ21122 fis, clone C	. 3.0
	443906	AA348031	Hs.7913	ESTs	3.0
	417318	AW953937	Hs.12891	ESTs	3.0
50	452619		Hs.61884	Homo sepiens, clone IMAGE:4298026, mRNA,	3.0 3.0
	444153		Hs.10414 Hs.47860	hypothetical protein FLJ10748 neurotrophic tyrosine kinase, receptor,	3.0
	408790 426327		Hs.44898	Homo sepiens clone TCCCTA00151 mRNA sequ	3.0
	451468		Hs.293663		3.0
55	422758		Hs.284180		3.0 3.0
	421633		Hs.106260		3.0
	428361 418932		5 Hs.183858 Hs.89484	cadherin 4, type 1, R-cadherin (refinal)	3.0
	416805		Hs.79981	Human clone 23560 mRNA sequence	3.0
60	419518	U79289	Hs.90798	Human clone 23695 mRNA sequence	3.0
	422709		Hs.153484		3.0 3.0
	423135		Hs.26411 Hs.18250	ESTs 5 PQU domain, class 3, transcription facto	3.0
	424901 426611		Hs.26625		3.0
65	42738		Hs.33771	7 ESTs	3.0
	42985		io Hs.22595	2 protein tyrosine phosphatase, receptor t	3.0 3.0
	43507		Hs.35495	ESTs Homo saptans mRNA; cDNA DKFZp761E13121 (3.0
	43509 43621				3.0
70	43693				3.0
	44585	5 BE247129	Hs.14556	9 ESTs	3.0
	45229				3.0 3.0
	43398 43022			9 phosphoserine aminotransferase ESTs, Highly similar to T00391 hypotheti	3.0
75	45102				3.0
, .	43523			cyclin-dependent kinase Inhibitor 2C (p1	3.0
	43956	65 AF08638	7	gb:Homo sepiens full length Insert cDNA	3.0
	42578		Hs.1595		3.0 3.0
80	4165 4168		Hs.1414 Hs.4256		3.0
Q.C	4103		Hs.3327	Homo septens cONA: FLJ22219 fis, clone H	3.0
	4114	11 AA34524	1 Hs.5595	D ESTs, Weakly similar to KIAA1330 protein	3.0
	4240		Hs.1124		3.0

	101010				3.0
	404048 429163	AA884766	9	b:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.0
	454117			daptor-related protein complex 1, sigma	3.0 3.0
5				(IAA1708 protein ESTs	3.0
J	434131 441255		Hs.171635 F	STs	2.9
	453900	AW003582 I	Hs.226414	STs, Weakly similar to ALU8_HUMAN ALU S	29 29
	453905			LIM domain kinase 1	29
10	416602			net (chicken)-like 2 ESTs	29
IO	431173 425599		Hs.214140	ESTs, Weakly similar to ALU1_HUMAN ALU S	29
	436401	A108785B	Hs.29088	ESTs	29 29
	422960			cadherin 13, H-cadherin (hearl)	29
15	451558		Hs.26630 Hs.288850	ATP-binding cassette, sub-family A (ABC1 Homo sapiens cDNA: FLJ22528 fis, clone H	29
13	412490 433149	AW803564 BE257872		hypothetical protein HES6	29
	434811	AW971205	Hs.114280	ESTs	29 29
	425897	AA935315	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	2.9
20	452092	BE245374	Hs.27842	hypothetical protein FLJ11210 solute center family 2 (facilitated glu	29
20	453496 411124	AA442103 AW196937	Hs.33084 Hs.53929	ESTs, Weekly similar to ALUB_HUMAN []]	2.9
	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.9
	427651	AW405731	Hs.18498	Homo saplens cDNA FLJ12277 fls. clone MA	2.9 2.9
25	441707	R42637	Hs.21963	hypothetical protein DKFZp761B0514 ESTs	29
25	435741 437273	Al240668 Al137451	Hs.113099 Hs.120873	ESTs. Highly similar to T48266 hypotheti	2.9
	422939	AW394055	Hs.98427	ESTs, Wealty similar to 138022 hypotheti	2.9
	439376	AA883521	Hs.222064	ESTs	2.9 2.9
20	439935	875105	Hs.301676	glutamate receptor, ionotropic, kainate	2.9
30	437267 453740	AW511443 AL120295	Hs.258110 Hs.311809	ESTs. Moderately similar to PC4259 ferri	2.9
	400250	ALIZE233	10.011010		2.9
	400992			n on the second of the second	2.9 2.9
25	408814	N62499	Hs.176227	hypothetical protein FLJ11155 ESTs, Moderately similar to KIAA1276 pro	29
35	411849 414853	AW984970 U31116	Hs.18861 Hs.77501	sarcoglycan, bela (43kD dystrophin-assoc	29
•	423751	AW235633	Hs.46525	ESTS	29
	426910	AA470023	Hs.190089	ESTs, Moderately similar to ALU1_HUMAN A	2.9 2.9
40	450203	AF097994	Hs.301528 Hs.21527	L-kynurenine/alpha-aminoadipale aminotra Human DNA sequence from clone GS1-115M3	29
40	459311 425304	R40192 AA463844	Hs.31339	fibroblast growth factor 11	2.9
	428500	AIB15395	Hs.184641	fatty acid desaturese 2	29
	421641	A1638184	Hs.106334		29 29
AE	421141	AW117261	Hs.125914	EST8 hypothetical protein KIAA1164	2.9
45	407870 456723		Hs.40719 Hs.4748	adenylate cyclase activating polypeptide	2.9
	436456		Hs.248122		2.9
	421483	NM_003388			2.9 2.9
50	412190	R16180	Hs.274481	ESTs phospholipase A2, group V	2.9
50	446131 441668		Hs.290 Hs.127525		2.9
	437387		Hs.28847	AD026 protein	29
	423420) Al571364	Hs.12838	Homo sapiens mRNA: cDNA DKFZp76111224 (f	2.9 2.9
55	427958		Hs.98280	potassium intermediate/small conductance splicing factor 3b, subunit 3, 130kD	2.9
55	429084 447063		Hs.19561- Hs.21964		2.9
	43088		Hs.26028	7 KIAA1841 protein	2.9
	44182		Hs.7977	KIAA0411 gene product	2.9 2.9
60	42412		Hs.96917 Hs.23879		29
W	40873 44742		Hs.98258		2.9
	43561		Hs.4975	potassium voltage-gated channel, KQT-lik	29
	44699	7 AA383439		Spir-1 protein	2.9 2.9
65	43357		Hs.57652 Hs.45080		2.9
03	40844 41958		Hs.1447		2.8
	4170			5 Res association (RaiGDS/AF-6) domain fam	2.8
	40843	32 AW19526	2	gb:xm67b05.x1 NCI_CGAP_CML1 Homo septens	28 28
70	4203				2.8
70					2.8
	4286 4244			80 enotase 2, (gamma, neuronal)	2.8
	4091		1 Hs.2524	06 hypothetical protein FLJ 12298 similar to	2.8 2.8
7.	4115				2.8
75			Hs.2986 2 Hs.2098		2.8
	4588 4200			6 ATP-binding cassette, sub-family A (ABC1	2.8
	4245		Hs.1507	741 2,3'-cyclic nucleotide 3' phosphodiaste	2.8
0/	4448	570 H58373	Hs.332		2.8 2.8
80					2.8
	416° 4401			9 Homo sepiens clone 23741 mRNA sequence	2.8
	408				2.8
				160	

			U. 2406		otic translation elongation factor	2.8
	403056 423449	R58624 Al497900	Hs.2186 Hs.33067	ESTs	OBS BOLDONAL GOLDON POPE.	2.8
	424188	AW954552	Hs.142634	zinc fir	nger protein	28 28
_	429006	AA443143	Hs.50929		netical protein FLJ13842	2.8
5	434981	AW182577	Hs.293077 Hs.27027	ESTs	netical protein DKFZp762H1311	2.8
	437435 442748	AA249439 Al016713	Hs.135787	ESTS		28
	443312	N52025	Hs.46616	ESTa	and the state of t	2.8 2.8
	450940	A1744943	Hs.143209	ESTs	, Weakly similar to 138022 hypotheti	2.8
10	452738	AL133800	Hs.7088	ESTa	hetical protein MGC12435	2.8
	409182	AA064970 AA018825	Hs.118145 Hs.7934		pel-like factor 4 (gul)	2.8
	439793 432683	AW995441	Hs.10475	EST		2.8 2.8
	434269	AK001991	Hs.3781		er to murine leucine-rich repeat pr	2.8
15	429500	X78565	Hs.289114	hexa	brachion (lenascin C, cytolactin) o sapians clone 23618 mRNA sequence	2.8
	433290	R20077 AF123659	Hs.302185 Hs.93605	leuri	ne zioner, putative tumor suppresso	2.8
	434276 435977	AL138079	Hs.5012	brair	-specific membrane-anchored protein	2.8 2.8
	430294	AI538226	Hs.32976	CILL DE	vine gudeolide binding protein 4	2.8
20	425168	R96366		gb:y	q37d04.s1 Soares tetal liver spleen	28
	428180	A1129767	Hs.182874	\ ECT	nine nucleatide binding protein (G pr	2.8
	409348	AJ401535 AL137534	Hs.14609 Hs.56876	Hor	no saolens mRNA: cDNA DKFZp434H1419 (1	2.8
	409887 457211	AW972565		E 91	to Weekly similar to S51797 vasodilat	28 28
25	430039	BE253012	Hs.15340		is, Wealdy similar to ALU1_HUMAN ALU S	2.8
_	417642	BE302665			othetical protein FLJ20357 Ts, Weakly similar to S72482 hypotheti	2.8
	419169	AW851980 AA740878				2.8
	43400B 446776	AW293417				2.8 2.8
30	408838	A1669535	Hs.40369	ES.	Ts	2.8
20	422565				ged (Drosophila)-like (sea urchin fas	2.8
	447397			5 E	1 enzyme pothelical protein FLJ13346	2.8
	412530			73 Hg	omo sapiens cDNA FLI13596 fis, clone PL	2.8
35	424330 446377			53 ES	STs	2.8 2.8
55	458924		B Hs.2442	7 DI	KFZP56601646 protein	2.8
	447710		Hs.3282	41 E	STs	2.8
	404049			e)	:RC1-DT0001-031299-011-a11 DT0001 Homo	2.8
40	416913		14 Hs.1697	43 H	omo sapiens cione 25121 neuronal olfact	2.8
40	42640 41326		Hs.1347		ypothetical protein FLJ20033	2.8 2.7
	45899		20 Hs.696	32 E	STS	2.7
	42286	4 AA31832		403 6	b:EST20390 Retina II Homo saptens cDNA Sprotein-coupled receptor, family C, gr	2.7
45	43052			ce v	7 A A 1173 postein	2.7
45	45202 43202			348 F	iomo sapiens mRNA; cDNA DKFZp761L1212 (f	2.7 2.7
	45243			95 J	IM4 protein	27
	43540	08 H07897	Hs.430		STs. Weakly similar to T29299 hypotheti	2.7
	41879				ESTS ESTS	2.7
50				1858 f	CSR1 orotein	2.7
	4234 4420			974	musnine nucleotide binding protein (G pr	2.7 2.7
	4422			124	Homo saplens cDNA: FLJ23285 fis, clone H	2.7
~ ~	4124				gb:nu78d01.s1 NCI_CGAP_Alv1 Homo septens solute carrier family 21 (organic anion	2.7
55					CCTe	2.7
	4164 4413				ESTe Wealdy similar to YD38 YEAST HYPOT	2.7 2.7
	4502		756 Hs.34		ESTs, Weakly similar to B49647 GTP-bindi	27
	426				Homo sepiens cDNA FLJ11477 fls, clone HE fissure inhibitor of metalioproteinase 4	2.7
60				10787 29908	MAAGEG amfaig	27
	449 420			3660	Homo seniens, clone IMAGE:3535476, mRNA,	2.7 2.7
		318 AA084	1050 Hs.2	39259	EGTe Weakly similar to S23650 (600Vkg	2.7
_	414	603 R5839		5119	ESTs, Westdy similar to YEX0_YEAST HYPOT cytochrome b-245, beta polypeptide (chro	2.7
6		096 H185		8974 4444	Homo spolens cDNA: FLJ22165 lts, clons H	2.7
	,	1896 AW14 1856 AA34			ESTs, Wealty similar to ZN43_HUMAN ZINC	2.7
		304 AA33		08887	ESTs	2.7 2.7
_	44	1027 Al911		26444	ESTS	2.7
7		2545 N319		4434	ESTs, Weakly similar to 138022 hypotheti KIAA0974 protein	2.7
				14131 23213	EST8	2.7
				156682	ESTS	2.7 2.7
	42	5825 Al92	9508 Hs.	159590	tymphocyte antigen 6 complex, locus H	27
7	75 44	10351 AFC		7179 455144	RAD1 (S. pombe) homolog protein tyrosine phosphatase, non-recept	2.7 2.7
				166114 24895	ESTe	2.7
			177823		gb:EST90805 Synovial sarcoma Homo saplen	2.7 2.7
	4		38548 Hs	117548	neuronatin	2.7
		24560 AA1	58727 Hs	150555	protein predicted by clone 23733	2.7
	4	32415 T16		.289014		2.7
				.274414 .23079	ESTS	2.7
	4	11000				

			Lin OCDTAA	MAAT	796 protein	2.7
			Hs.268744 Hs.239706		associated binding protein 1	27
	428862	NM_000346	Hs.2316		sex determining region Y)-box 9 (ca	2.7 2.7
_	447959	A1452784	Hs.270270		Wealdy similar to 2109260A B cell	27
5	426420	8E383808 AA764852	Hs.322430 Hs.291567	ESTS	family, member 4	2.7
	436899 444100	AA383343	Hs.22116		4 (cell division cycle 14, S. cerevi	27 27
	426501	AW043782	Hs.293616	ESTS	The state throughout the state of the state	27 27
• •	449092	U91641	Hs.22985		2,8-sialyltransferase 0865 protein	27
10	427311	AB020672	Hs.175411 Hs.153746		helical protein FLJ22490	2.7
	453313 404029	8E005771	115.155740	1.760		27
	416289	W26333	Hs.337438	EST		2.7 2.6
	439108	AW163034	Hs.6467		ologydn 3	26
15	418746	A1955289	Hs.300759		omai protein L36 related on chromsome 22	2.6
	412046 435040	Y07847 A1932350	Hs.73088 Hs.152825	EST		26
	453083	U87223	Hs.31622		actin associated protein 1	26 26
	428167	AA770021	Hs.16332	EST	S	26
20	420028	AB014680	Hs.8786		ohydrate (N-acetylglucosamine-6-0) s n E1	2.6
	443715	AI583187 BE391727	Hs.9700 Hs.102910		aral transcription factor IIH, polype	2.6
	421247 424687	J05070	Hs.151738	mat	ix metalloproteinase 9 (gelatinase B	2.6 2.6
	415056	AB004662	Hs.77867	orte	nosine A1 receptor	26
25	451697	AW449774	Hs.296380		M (POM121 rat homolog) and ZP3 fusion	2.6
	433701	AW445023 AI479755	Hs.15155 Hs.129010	EST EST		2.6
	45735B 430347	NM_002039	Hs.239708		B2-associated binding protein 1	2.6 2.6
	418027	AB037807	Hs.83293	hvn	othetical protein	2.6 2.6
30	440491	R35252	Hs.24944		Ts, Weakly similar to 2109260A B cell	2.6
	425171	AW732240	Hs.16365 Hs.25072	ES ES	T	2.6
	459335 425402	AW298545 Al215881	Hs.24970	ĒS	Te, Wealdy similar to B34323 GTP-bindi	2.6
	453169	AB037815	Hs.32156	KI/	AA1394 protein	2.6 2.6
35	433647	AA603367	Hs.22229		iTs	26
	450414	A1907735	Hs.21446 Hs.25205		AA1716 protein STs	2.6
	446233 415446		Hs.66076	F 5	aTs.	2.6
	445873		Hs.25194	6 pc	ly(A)-binding protein, cytoplasmic 1-I	2.6 2.6
40	413012	D83777	Hs.7513		AA0193 gene product	26
	428671		Hs.1894 Hs.1662		nc finger protein 179 STs	2.6
	427158 408988		Hs.4947	6 H	omo saptens cione TUA8 Cri-du-chat regi	2.6
	459516		Hs.2468		ST	26 26
45	402693	3			·	26
	40803				STs STs	2.6
	42289 42313				STs	26
	43879		Hs.1095	90 g	enethonin 1	26 26
50	43987	1 R88518	Hs.4673		nypothetical protein FLJ23476	26
	44019				ESTs hypothetical protein	2.6
	41970 44943				hypothetical protein DKFZp434l2117	2.6 2.6
	43687	70 AW20421	9 Hs.155	560	calnexin	2.6
55			2 Hs.319	24	ESTS	2.6
	4013		4 Hs.119	023	SMC2 (structural maintenance of chromoso	2.6
	4141 4339			65	lymphoid enhancer-binding factor 1	2.6 2.6
	4280		Hs.219		ESTs, Moderately similar to Transforming	26
60			Hs.660		ESTs MAD (mothers against decapentaplegic, Dr	2.6
	4230				phospholnositol 3-phosphate-binding prot	2.6
	4489 4440				ESTs, Moderately similar to S65657 aipna	2.6 2.6
_	4120		Hs.18		adenylate kinase 5	26
6:	5 4417				Homo saplens clone 25012 mRNA sequence peanut (Drosophila)-like 2	2.6
		287 R88249 149 AW614			ESTs, Weakly similar to T34549 probable	2.6
	432 452				ESTs, Weakly similar to 138022 hypotheti	2.6
	453		98 Hs.33	3021	neuro-oncological ventral antigen 2	26 26
7	O 418	982 AA7148	35 Hs.27	1883	ESTs hypothetical protein RG083M05.2	26
		858 AW961			HSPC065 protein	2.6
		1257 A13340 1748 AW593			Ksp37 protein	26
	444	1984 H1547	4 Hs.1	32898	falty acid desaturase 1	2.6 \ 2.6
7	5 433	3404 T3298	2 Hs.1	02720	ESTs	2.6
	434	4779 AF153		0151 9093	potessium inwardly-rectifying channel, s Homo sapians chromosome 19, cosmid R2837	2.6
		0582 BE047 2856 AF034		0881	novelo tyrosine obosobalase, receptor t	20
	43	5440 AJ4711	362 Hs.1	96008	Homo segiens cDNA FLJ11723 fis, clone HE	2.6 2.6
8	30 43	8527 AI969	251 Hs.1	15325	RAB7, member RAS oncogene family-like 1	26
		3216 AF217		17320 192221	neuroligin 3 ESTs	2.6
		5380 AA679 18966 AF059		94687		2.0
	74					

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Pkey CAT Number Accession 408432 1058667_1 AW195262 R27858 AW811262 412225 4W802042 N77591

			11- 5554	h-mathatian	I protein FLJ20373	26
	439653	AW021103 AJ271326	Hs.6631 Hs.146101	ESTA WAS	kiv similar to T45070 protein k	26
	419304 422991	H10940	Hs.48965	Homo sapir	ens cDNA: FLJ21693 fis, clone C	2.6 2.6
	448548	R13209	Hs.21413		er family 12, (potassium-chi	2.6
5	435370	A1964074	Hs.225838	ESTS DVEZDARA	B168 protein	2.5
	408875	NM_015434 AJ007421	Hs.48604 Hs.172597	sal (Droso		2.5
	457005 430154	AW583058	Hs.234726	serine (or	cysteine) proteinase inhibito	2.5 2.5
	438549	BE386801	Hs.21858	trinucieotic	le repeat containing 3	2.5
10	427951	AI826125	Hs.43546	ESTs		2.5
	411800	N39342	Hs.103042	MICROUDU	e-essociated protein 18 derately similar to ALU7_HUMAN A	2.5
	457683	AI821877	Hs.140002 Hs.26395	erythrocyt	e membrane protein band 4.1-li	2.5
	451422 430713	AB002336 AA351647	Hs.2642	eukaryotta	translation elongation factor	2.5 2.5
15	428826	AL048842	Hs.194019	attractin		2.5
	428963	AW382682	Hs.258208	Homo sat	niens, clone MGC:15606, mRNA, com nier family 11 (proton-coupled	2.5
	428141	D50402	Hs.182611 Hs.119357	ESTs	High Istima 11 (hoosy-coches	2.5
	429550	AW293055 AA223599	Hs.6351	deavage	and polyadenylation specific fa	2.5
20	438662 435760	AF231922	Hs.213004	chromos	ome 21 open reading frame 62	2.5 2.5
20	427513	AI476318	Hs.192480	ESTS		2.5
	430061	AB037817	Hs.230188	KIAA139	6 protein piens clone 24672 mRNA sequence	2.5
	435923	BE301930	Hs.5010		piens cione 240/2 minutes sequence	2.5
25	417123	BE326521	Hs.159456 Hs.18756	FSTs. M	oderately similar to ALU1_HUMAN A	25
25	439699 412980	AF086534 AI815750	Hs.20977	hypolhe	lical protein MGC3129 similar to	2.5 2.5
	427209	H06509	Hs.92423	KIAA15	56 protein	2.5 2.5
	424327	AA431707	Hs.31209	ESTs		2.5
	436340	R42246	Hs.21605	ESTs	lical protein MGC3295	2.5
30	450650		Hs.10125 Hs.54578	FSTs V	Veakly similar to I38022 hypotheti	2.5
	439444		FIS.D-101 G			2.5 2.5
	400777 439478		Hs.6574	deform	ed epidermal autoregulatory factor	2.5
	450407		10 Hs.2496	gamma	-aminobutyric scid (GABA) A recepto	2.5
35	450385	AI631024	Hs.2494		in, alpha interacting protein (sy	2.5
	432558		Hs.1772			2.5
	400860		4 Hs.6266	guanyi	ate binding protein 1, interferon-	2.5 2.5
	41606			I FSTs		2.5
40	41499		543 Hs.7772		ed low density lipoprotein (lectin	2.5
. •	45282	3 AB01212			ription factor-like 5 (basic helix	2.5
	41779		39 Hs.1114 Hs.691	71 ESTs ESTs		2.5
	41807			31 ESTa		2.5
45	40849 44210		Hs.188	ahora	hodiesterase 4B, cAMP-specific (dun	2.5 2.5
75	43737		67 Hs.161		saplens mRNA; cDNA DKFZp547D023 (fr	2.5
	42980			25 RAB	11, member RAS oncogene family ited p21cdc42Hs kinase	2.5
	4249			781 hvno	hetical protein MGC5618	2.5
50	4274 ⁻ 4089				5 protein	2.5 2.5
50	4152			6 ESTS		2.5
	4157	16 N59294	4 Hs.179		osome essembly protein 1-like 1	2.5
	4178			659 Hom	o sapiens, Similar to RIKEN cONA A430 o sapiens cONA FLJ11364 fis, clone HE	2.5
	4183			022 trans	eriolion factor 17	2.5
55	4210 4232			POS EST	Weekly similar to uniquitous TPR III	2.5 2.5
	423		635 Hs.98	54 EST	s, Weakly similar to DYLX_HUMAN CYTOP	2.5 2.5
	427		3165 Hs.14	134 EST	S	2.5
	428	301 AW62			s, Weakly similar to I38022 hypotheti	2.5
60				4668 SB1	3131 protein cv67d11.r1 Soares_total_fetus_Nb2HF8_	2.5
	428			ese ES.	re Weakly stratter to KIAA1392 protein	2.5
		943 AW08 1427 AL037		38 Ho	no sapiens cDNA FLJ11602 fis, clone HE	2.5 2.5
		347 AW01		2022 EC	Te	25
6:	5 437	1785	19 Hs.4		Ts, Wealdy similar to A46010 X-linked	2.5
	436	3208 AL04	1224 Hs.6	379 ES	T8 dinergic receptor, muscarinic 3	2.5
		0286 U 295	89 Hs./	11774 ES	Te Wealdy similar to ALUF_HUMAN IIII	2.5
				n401A no	umnal enecific transcription factor U	2.5
7		2337 Al37	1029 Hs.	20257 ES	To Weekly similar to TC17 HUMAN TRANS	25 25
•			04361 Hs.	31191 ES	Ts, Wealdy similar to ALU7 HUMAN ALU S	2.5
	44	5556 Al91			In-related protein 3-beta	2.5
				08037 E	STs b;IL-BT152-080399-004 BT152 Homo sapien	2.5
-	75 ⁴⁵	9583 A190)7673	9,		
,		ABLE 8B:				
		key:	Unique Ed	s probeset i	fentifier number	
	C	AT number:	Gene clus	er number		
	۰ A	ccession:	Genbank	eccession na	ilianera ,	
ì	30					

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AA665089 AA135130 AA484059 AA102419 AW877765
H46739 H51513 H19779
                     412436
                                              1571266_1
1626761_1
                     416120
416871
                                                                             H89716 N90792 N24283
AW934714 BE181007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
AA318223 H11145 R15289 AA451945 AA476690 AA436954 Z43802 F11753 T65491 D81821
AA319435 N56456 AA319377 AW961532 T48452 AA694424
AA631498 AID17191 AA491211 AA761823 AA714555 AA768099 AA688286 AI934069 AA570223 AA574389 AA582438 AI745346 AW964510 AA319842
                                              163001_1
222336_1
                       416913
   5
                       422864
                       422949
                                               223184_1
                                               223410_1
                       422977
                                                                               AW853758 H56414
AA828125 AA834883 AA330555
R98368 AJ 133929 AA351636 H78818 AA477094 Z28957 H80194
AF121179 BE162736 AA358827
                       423756
425168
                                               231725 1
10
                                                247552_1
                       425517
426413
                                               252729_1
266650_1
                                                                              AF121178 BE162736 AA358827

AA377823 AW954494 AI022688

AA418703 AA418711 BE071915 BE071920 BE071912

AA431765 AA432015

AA436760 AW237453 BE327498 N47347 N56967

D80842 AA43145 AL119015 AW904500

AA884766 AW974271 AA592975 AA447312

AW975387 AA598057 AA742735

AW9197387 AA598057
                                                285602_1
284049_1
296453_1
                        428002
                        428679
 15
                        428858
                         429007
                                                 298301_1
                                                 300543_1
                         429163
                                                 368950_1
41555_1
431713_1
457837_1
                                                                                AW975367 AA598607 AA742735

AK001069 AA633055

AA742843 AA608575 AW976668

AW975186 AA807807 D29548

AA828995 AA834879 AI926361

AF086387 W77884 W72711

AA879430 BE070262 BE070493 BE070272 BE070484 BE070397 BE070395 BE070201 BE070198 BE070404 BE070270 BE070400

AI568422 D80113 T59074
                          436190
 20
                          437034
                          438458
                                                  467651_1
47387_1
491966_1
                          438993
                          439566
440322
   25
                                                  611496_1
711623_1
                          444584
                           447197
                                                                                  R36075 Al366546 R36167
AW015994 R39898 AW000978 Al598202 Al521706
                           448451
450625
                                                   764066_1
84032_1
                                                                                   AW970107 AA513951 AA010406
AI902519 AI902518 AI902516
                            452453
                                                   918300_1
                                                                                   AW850180 AW850326
AW901809 AW901787 AW901795 AW901792 AW901744 AW901753 AW901807 AW901798
   30
                           454996
                                                     1248640 1
                            455350
                                                     1283853 1
                           TABLE 8C:
                                                                      Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
                            Pkey:
Ref:
     35
                                                                      Indicates DNA strand from which exons were predicted. 
Indicates nucleotide positions of predicted exons.
                             Strand:
                             Nt_position:
                                                                                                                  Nt position
      40
                                                         Ref
8131663
                                                                                      Strand
                                                                                                                 70745-71121
118372-118619
                                                                                     Plus
                              400777
                                                         8131663
9757499
                              400780
                                                                                     Minus
                                                                                                                  91888-92018,98131-98294,99474-99570
151830-152104,152649-152744
                                                                                      Minus
                              400859
                                                          9757499
                                                                                      Minus
                              400860
                                                                                                                   140390-140822
       45
                                                          8096828
                               400992
                                                                                      Plus
                                                                                                                  234057-234174
110326-110491
                               401324
                                                          9863791
                               402408
                                                          9798239
                                                                                      Minus
                                                                                                                   20393-20767
47680-47973
                                                           9909420
                               402604
                                                          9909420
8569863
                               402605
                                                                                       Minus
                                                                                                                   82366-82515
59763-59909
        50
                                                                                        Minus
                                402693
                                 402855
                                                            9662953
                                                                                        Minus
                                                            7671252
                                                                                                                     108716-111112
                                404029
                                                                                        Plus
                                                            3688074
3688074
                                                                                                                     54421-56808
                                 404048
                                                                                        Minus
                                                                                                                     75765-78155
                                404049
404283
                                                                                        Minus
         55
                                                                                        Minus
                                                                                                                     99460-99564
                                                             2276311
                                                                                                                     3826-4025
                                 404299
                                                            5738652
                                                                                        Minus
                                                                                                                      103458-103664
                                 404541
                                                             8318559
                                                                                         Plus
                                                                                                                      138651-139153
                                 404584
404593
                                                                                          Phis
                                                             9857511
                                                             9944086
9856648
                                                                                                                      74922-75788
173763-174294
                                                                                          Minus
                                                                                                                     16223-16319,16427-16513,16738-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578 51728-51838
          60
                                 404721
404819
                                                                                         Minus
                                                              4878240
                                                              7249119
                                                                                          Minus
                                                                                                                      91191-91254,91510-91589
2830-2967
                                                                                          Plus
                                  405771
                                                              7018349
                                                               4007557
                                                                                           Phia
                                   405819
                                                                                                                       137114-139033
          65
                                   406311
                                                              9211559
                                                                                          Minus
                                 TABLE 9A:ABOUT 1202 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CENTRAL NERVOUS SYSTEM (CNS)
Table 9A lists about 1202 genes up-regulated in glioblastoma compared to normal adult central nervous system (CNS). These were selected from 59680 probesets on the Adymetrizace Hu03 GeneChip array such that the ratio of "everage" glioblastoma to "everage" normal adult CNS tissues was greater than or equal to 2.0. The "everage" glioblastoma tumors. The "everage" normal adult CNS tissue level was set to the 75th percentile amongst various glioblastoma tumors. The "everage" normal adult CNS tissue level was set to the 95th percentile amongst various glioblastoma tumors. The "everage" normal adult CNS tissue level was set to the 95th percentile amongst various glioblastoma tumors. The "everage" normal adult CNS tissue level was set to the 95th percentile amongst various glioblastoma tumors. The "everage" normal adult CNS tissue level was set to the 95th percentile amongst various glioblastoma tumors. The "everage" normal adult CNS tissue level was set to the 95th percentile amongst various glioblastoma tumors. The "everage" normal adult CNS tissue level was set to the 95th percentile amongst various glioblastoma tumors. The "everage" normal adult CNS tissue level was set to the 95th percentile amongst various glioblastoma tumors. The "everage" normal adult CNS tissue level was set to the 95th percentile amongst various glioblastoma tumors. The "everage" normal adult CNS tissue level was set to the 95th percentile amongst various glioblastoma tumors. The "everage" normal adult CNS tissue level was set to the 95th percentile amongst various glioblastoma tumors. The "everage" normal adult CNS tissue was greater than or equal to 2.0. The "everage" normal adult CNS tissue was greater than or equal to 2.0. The "everage" normal adult CNS tissue was greater than or equal to 2.0. The "everage" normal adult CNS tissue was greater than or equal to 2.0. The "everage" normal adult CNS tissue was greater than or equal to 
            70
                                   Pkey:
ExAccn:
                                                                               Exemplar Accession number, Genbank accession number
              75
                                     UnigenelD:
                                                                               Unigene number
                                     Unigene Tille:
                                                                               Ratio of 75th percentile tumor to 95th percentile normal adult nervous system tissue
                                                                                              UnigenelO Unigene Title
              80
                                                              ExAccn
N78223
                                                                                                                        transcription factor
carbonic anhydrase XII
                                                                                              Hs.108106
                                      452461
                                                                                                                                                                                                                                                                      15.2
                                                               AF037335
                                                                                              Hs 6338
                                                                                              Hs.36820
                                                                                                                          Bloom syndrome
                                      453941
                                                              U39817
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	443247	BE614387	Hs.333893		target JPO1	12.4 12.0
	428330	L22524	Hs.2256	matrix	metalloproteinase 7 (matrilysin,	11.7
	447342	AJ199268 AF027208	Hs.19322 Hs.112360		sapiens, Similar to RIKEN cDNA 2010 nin (mouse)-like 1	11.4
5	422163 439451	AF086270	Hs.278554	heter	ochromatin-like protein 1	11.2 10.2
	424800	AL035588	Hs.153203	MyoD	family inhibitor natin assembly factor 1, subunit A (10.0
	416111	AA033813 Al878918	Hs.79018 Hs.10526	cvste	ine and glycine-rich protein 2	9.9
	444190 412140	AA219691	Hs.73625	RAB	interacting, kinesin-like (rabkines	9.9 9.8
10	449340	AW235786	Hs.195359	hypo	thetical protein MGC10954	9.4
	409731	AA125985 BE139460	Hs.56145 Hs.124673	thym Hom	osin, beta, Identified in neuroblast o saptens cDNA FLJ11477 fis, clone HE	8.9
	439978 411411	AA345241	Hs.55950	EST	s, Wealdy similar to KIAA1330 protein	8.9 8.2
	456516	BE172704	Hs.222746		1610 protein	7.9
15	420092	AA814043	Hs.88045 Hs.118793	EST	s Nhelical protein FLJ10688	7.9
	422631 453392	BE218919 U23752	Hs.32964	SRY	(sex determining region Y)-box 11	7.9
	438527	Al969251	Hs.115325	RAE	7, member RAS oncogene family-like 1	7.9 7.8
20	427581	NM_014788	Hs.179703 Hs.1189		AD129 gene product transcription factor 3	7.8
20	418661 440684	NM_001949 Al253123	Hs.127356	ES1	a, Highly similar to \$21424 nestin (H	7.8
	429643	AA455889	Hs.167279	FY\	/E-finger-containing Rab5 effector pro	7.7 7.5
	409638	AW450420	Hs.21335	ES	s ogressive lymphoma gene	7.5
25	444665 456759	BE613126 BE259150	Hs,47783 Hs.127797		a (Drosophila)-like 3	7.5
23	412777	Al335773	Hs.27012	ES		7.4 7.3
	436607	AW661783	Hs.21106 Hs.13072	ES	Ts, Wealdy similar to ALU1_HUMAN ALU S	7.3
	432058 417061	AW665996 Al675944	Hs.18869	l Ho	mo sapiens cONA FLJ12033 fis, clone HE	7.3
30	428976	AL037824	Hs.19469	5 res	homolog gene family, member t	7.2 7.1
	433244	AB040943	Hs.27128		AA1510 protein ITs, Wealdy similar to T00079 hypotheti	7.1
	436726 408432	AA324975 AW195262	Hs.12899	ab	on67b05.x1 NCL_CGAP_CML1 Homo sapiens	7.1
	434164	AW207019	Hs.14813	5 se	rine/threonine kinase 33	7.0 7.0
35	445873	AA250970	Hs.25194 Hs.29370		ty(A)-binding protein, cytoplasmic 1-i 37s, Weakly similar to 138598 zinc fing	7.0
•	439726 432656				HC class II transactivator	6.8
	431117		Hs.2505		ata (Drosophila)-like 1	6.8 6.8
40	453387		Hs.2528	24 E	STs STs	6.6
40	41B821 437034			ם וכ	b:ny91c01.s1 NCI_CGAP_GCB1 Homo sapiens	6.6
	411252		Hs.6932	8 N	tD-2 protein	6.5 6.4
	424687		Hs.1517	38 n	natrix metalloproteinase 9 (gelatinase B STs, Weakly similar to A46010 X-linked	6.3
45	452953 433533		Hs.2717 7	•	b:EST387475 MAGE resequences, MAGN Homo	6.3
43	42031		4 Hs.3820	7	tuman DNA sequence from clone RP4-530(15	6.3 6.2
	41809		Hs.2186	i8 [ESTs p::nj32b03.s1 NCI_CGAP_AA1 Homo saplens	6.2
	40730- 43525				cytokine-like protein C17	6.1
50	44944		Hs.574		E8Ts	6.1 6.0
	40379		•		gb:AF121179 Homo sapiens liver (Chang L-	6.0
	42551 42067			7	butyrylcholinesterase	6.0
	43554	2 AA68737	6 Hs.269	533	ESTS	5.9 5.8
55				099	AF15q14 protein gb:Homo sapiens full length insert cDNA	5.B
	43908 40803			233	hynothetical protein FLJ 10300	5.7
	4122	25 AW9020	42		gb:QV0-NN1022-170400-193-c02 NN1022 Homo	5.7 5.7
40	4361				hypothetical protein MGC15729 trinucleotide repeat containing 12	5.7
60) 4350 4291				ESTs, Weakly similar to 138022 hypotheti	5.7
	4181			484	SRY (sex determining region Y)-box 4	5.6 5.6
	4055		89.2H e8	17B	hypothetical protein FLJ23468	5.6
6:	5 4424 5 4425				ESTS, Wealdy similar to ALU1_HUMAN ALU S	5.6
0.	4130		37 Hs.75	184	chitinase 3-tike 1 (cartilage glycoprote	5.5 5.5
	420				ESTs dihydrofolate reductase	5.5
	408			34074	ESTs, Moderately similar to ALUS_HUMAN A	5.4
7	0 426		125 Hs.1	17112	Homo sapiens cDNA: FLJ22322 fis, clone H	5.4 5.3
	429	115 AA446		39020	Homo saplens cDNA FLJ14098 fis, clone MA ESTs, Weakly similar to ALUS_HUMAN ALU S	5.3
		900 AW000 168 AW37		26414	gb:RC1-HT0256-081199-011-f01 HT0256 Homo	5.3
_	432	789 D2638	1 Hs.3		KIAA0042 gene product	5.3 5.2
7	5 437	036 AI571		33022 n2010	ESTs general transcription factor IIH, polype	5.2
		247 BE391 1523 AW51		02910 01771	ESTs, Weakly similar to ALUF_HUMAN IIII	5.2
		106 BE38	2701 Hs.2	5960	v-myc avian myelocytomatosis viral relat	5.1 5.1
c	45	7211 AW97		12399 112481	ESTs, Wealdy similar to \$51797 vasodilat ESTs, Wealdy similar to \$66668 hydrogen	5.1
c		4157 AW16 3343 AA 3 2		312481 246106	ESTs	5.1
		5292 NM_0	05824 Hs.	55545	37 kDa leucine-rich repeat (LRR) protein	5.1 5.1
		6679 AA07	0786		gb:zm66b07.r1 Stratagene neuroepithelium	J.1
					173	

	442671	A1005668 H	is.134779 E	ST	5.1
				tone HQ0310 PRO0310p1	5.0
	418819			STs	5.0 4.9
5	432946			nannosidase, alpha, class 2B, member 1 polymerase (DNA directed), della 1, cata	4.9
3	420730 441217			ESTs	4.9
	453385			ESTS	4.8
	418203	X54942	Hs.83758	CDC28 protein kinase 2	4.7
10	450813			ESTS	4.7 4.7
10	444008			type I transmembrane protein Fn14 hypothetical protein FLJ13346	4.7
	412530 431070		Hs.249184	transcription factor 19 (SC1)	4.7
	429788		Hs.220696	Homo saplens mRNA; cDNA DKFZp586A061 (fr	4.7
1.5	405771				4.6 4.6
15	457065			ESTs gb:Homo sepiens cDNA FLJ10197 fis, clone	4.6
	436190 400859	AK001059		gorronia sapiens control to 10101 inc conto	4.6
	435267	N23797	Hs.110114	ESTs	4.6
	443454	AI057494	Hs.133421	EST8	4.5
20	452811	AA937079	Hs.118983	hypothetical protein FLJ12150	4.5 4.5
	437267 435020	AW511443 AW505076	Hs.258110 Hs.301855	ESTs DiGeorge syndrome critical region gene 8	4.5
	454269	A1961060	Hs.129908	KIAA0591 protein	4.5
	422106	D84239	Hs.111732	Fc fragment of IgG binding protein	4.5
25	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	4.5 4.5
	456534 423758	X91195 AA828125	Hs.100623	phospholipase C, bela 3, neighbor pseudo gb:od71a09.s1 NCL_CGAP_Ov2 Homo saplens	4.5
	417308	H80720	Hs.81892	KIAA0101 gene product	4.5
	422170	A1791949	Hs.112432	anti-Mullerian hormone	4.4
30	· 429500	X78565	Hs.289114	hexabrachion (tenescin C, cytotactin)	4.4 4.4
	406568	AF088886	Hs.11590 Hs.172613	cathepsin F solute carrier family 12 (potassium/chlo	4.4
	426812 402516	AF105365	113.112013	South Carrier terms 12 (possessions)	4.4
	432865	AJ753709	Hs.152484	ESTs, Wealdy similar to 138022 hypotheti	4.4
35	413625	AW451103	Hs.71371	ESTs	4.4 4.4
	436098	R20597	Hs.9739	glycerol-3-phosphate dehydrogenase 1 (so	4.4
	418333	W92113 BE561850	Hs.80506	gb:zh48e01.r1 Soares_fetal_liver_spleen_ small nuclear ribonucleaprotein polypept	4.4
	416933 438192	AI859065	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	4.3
40	457374	AA493662		gbmh05d12s1 NCI_CGAP_Thy1 Homo saplens	4.3
	433159	AB035898	Hs.150587	kinesin-like protein 2	4.3 4.3
	444386	BE065183	11- 20270	gb:RC1-BT0314-020200-012-c04 BT0314 Homo	4.3
	453202 441020	AW085781 W79283	Hs.26270 Hs.35962	hypothetical protein FU11588 ESTs	4.3
45	414733	BE514535	Hs.77171	minichromosome maintenance deficient (S.	4.3
. •	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	4.3 4.3
	405701	05070704	11-14940	ECT-	4.3
	451659 418845	BE379761 AA852985	Hs.14248 Hs.89232	ESTs chromobox homotog 5 (Drosophila HP1 alph	4.2
50	433323	AAB05132	Hs.30701	ESTS	4.2
•	439811	AA135332	Hs.71608	ESTs	4.2
	415406			gb:AB282F8R Infant brain, LLNL array of	4.2 4.1
	436282		Hs.272104 Hs.178784		4.1
55	441269 418727		Hs.94834	ESTS	4.1
	433006		Hs.190223		4.1
	436480		Hs.87469	putative ecid-sensing ion channel	4.1 4.1
	430788		Hs.31293 Hs.144928	ESTS 3 ESTs	41
60	445372 410555		Hs.64311		4.0
•	457465		Hs.12290	B DNA replication factor	4.0
	422094		Hs.27202		4.0 4.0
	442029				4.0
65	459321 421308		Hs.29953 Hs.19284		4.0
03	42056		Hs.98874		4.0
	44700		Hs.15753	9 ESTs	4.0
	44829		Hs.33485		3.9 3.9
70	43969		Hs.18756	in ESTs, Moderately similar to ALU1_HUMAN A insulin-like growth factor binding prote	3.9
70	44070 45309		Hs.162 Hs.11325		3.9
	45702				3.9
	40464	2			3.9
70	45037	5 AA009647		a disintegrin and metalloproteinase doma	3.9 3.9
75					3.9
	43771 43849		Hs.1967 2 Hs.3012		3.9
	42991			45 hypothetical protein FLJ23024	3.9
	41360	04 R51767		gb:yg73g11.r1 Soares Infant brain 1NIB H	39
80					3.9 3.9
	44879				3.8
	4493 4522		Hs.1581		3.8
				-	

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					and a constant of PNA complete	3.8
	425769 404295	U72513	Hs.159486		RPL13-2 pseudogena mRNA, complete	3.8 3.8
	410361	BE391804	Hs.62661 Hs.191381	hypothe	la binding protein 1, interferon- fical protein	3.8
5	428728 409142	NM_016625 AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	3.8 3.8
	430172 447499	AA468591 AW262580	Hs.161889 Hs.147674	ESTs protoca	dherin beta 16	3.8 3.8
	405884		Hs. 244353			3.7
10	437236 418883	AW137817 BE387036	Hs.1211	acid ph	osphatase 5, tertrate resistent Moderately similar to A56194 throm	3.7 3.7
	444143 425529	AW747996 NM_014656	Hs.160999 Hs.158282		Moderately situal to Account	3.7 3.7
	425502	R98895	Hs.12582	ESTs	in carrier protein E2-C	3.7
15	419741 402424	NM_007019				3.7 3.7
	429469	M64590 H70854	Hs.27 Hs.28305	∩ Unmo	e dehydrogenase (decarboxylating; saptens PRO1082 mRNA, complete cds	3.7 3.7
	434072 414872	U82010	Hs.77513	COXI	0 (yeast) homolog, cytochrome c oxto	3.7
20	426071 419078	AW138057 M93119	Hs.16383 Hs.89584	land the	nomal secondated 1	3.7 3.7
20	428037	N47474	Hs.89230 Hs.2689) potes	stum intermediate/small conductance i, Weakly similar to PC4259 ferritin	3.7
	416547 436899	H62914 AA764852	Hs.2915	~ COTa		3.6 3.6
25	436722 440652	AW975977 AJ216751	Hs.1439	77 EST		3.6 3.6
23	428450	NM_01479	1 Hs.1843	AAIN AC	.0175 gene product s, Weakly similar to 138022 hypotheti	3.6
	452103 409046		Hs.3398 Hs.3769	M ECT		3.6 3.6
20	439546	AF088056		A COT	iomo saplens full length insert cDNA	3.6
30	44354 41847		Hs.117	t cycl	in-dependent kinase inhibitor 2A (ma	3.6 3.6
	43588 42030			901 EST 30 pair	ed box gene 5 (B-cell lineage specif	3.6 3.6
2.5	43807	8 AI016377	Hs.131	ce with	elite elementosa 2 (X-linked recessi	3.6
35	40842 41687	1 1198716		ah	yx13d08.s1 Soares melanocyte 2NbHM Ho ilication factor C (activator 1) 2 (40	3.5 3.5
	42408 44629			323 inte	arteron, gamma-inducible protein 30	3.5 3.5
40	4322	1 AK0012	9 Hs.27	1263 hy	pothetical protein FLJ10377 Te Highly similar to unnamed protein	3.5
40	4361 4112		39	a h	:CV0-TT0010-091199-053-e09 TT0010 Homo imo sapiens cDNA: FLJ23241 fis, clone C	3.5 3.5
	4192 4350			ah.	PC4_RY0310_110300-015-008 B10310 HQ110	3.5 3.5
	4355	32 AW291	188 Hs.11	7305 H	omo sapiens, clone IMAGE:3682908, mRNA STs	3.5
45	4471 4105			1473 A	TOOGO H+ transporting, tysosomai (vacu	3.5 3.5
	422° 453	156 N34524		2010	b:yy56d10.s1 Soares_multiple_sclerosis_ ynein, exonemal, light intermediate pol	3.5 3.5
-	439	743 AL3899	356 Hs.2	83858 H	lomo sapiens mRNA full length trisen cum NA AN186 dene product	3.5
5(884 AA355 954 NM_00	0546 Ha.1	846 b	umor protein p53 (U-Fraumeni syndroma)	3.5 3.5
	420	721 AA927		C4/64 E	AP3 protein ESTs, Weakly similar to ALUC_HUMAN !!!!	3.4 3.4
_	420	649 A18669	164 Hs.1	24704 E	STs, Moderately similar to S65657 alpha zinc finger protein 23 (KOX 15)	3.4
5		1831 AL080 1371 BE540			forkhead box M1	3.4 3.4
	40	2604 2407 AW45	OSRA He	32353	mitogen-activated protein kinase kinase	3.4 3.4
	41	4300 Al304	870 Hs.	188680	ESTs	3.4
6		4670 H583° 4550 BE37		332938	gb:601159567T1 NIH_MGC_53 Homo sapiens c	3.4 3.4
	45	2211 AI985		.233420 .76084	ESTs hypothetical protein MGC2721	3.4 3.4
	A	19961 AW2	65834 Hs	133100	ESTs gb:PM3-BT0584-260300-002-g05 BT0584 Homo	3.4
•		1000		.35861	DKF7PSR6E1621 protein	3.4 3.4
	4	17404 NM		.82101 .1583	pleckstrin homology-like domain, family neutrophil cytosolic factor 1 (47kD, chr	3.4 3.4
	4	46189 H85	224 H	.214013	ESTs ESTs	3.4
-				s.164050 s.28368	COTo Moderately similar to \$65657 alpha	3.4 3.4
	4	108298 A174	15325 H 188746	s.271923	Homo saplens cDNA: FLJ22785 fis, clons K gb:CM2-BT0693-210300-123-d09 BT0693 Homo	3.3 3.3
		17548 H55	5569 H	s.18845	ESTs	3.3
			811324	s.73946	qb:IL3-ST0141-131099-017-A02 S10141 Piorito	3.3 3.3
		454294 AB	000734 H	ts.50640 ts.301463	JAK binding protein Human Chromosome 18 BAC clone CIT987SK-A	3.3 3.3
		410102 AV	/248508	ls.279727	Homo sapiens cONA FLJ14035 fis, clone HE	3.3
	80			ts.209657 ts.334828	hypothetical protein FLJ10719; KIAA1794	3.3 3.3
		453746 AL	120611	Hs.213786	gb:DKFZp761H119_r1 761 (synonym: hamy2) ESTs	3.3
		452799 Al			100	

175

3.3

	435380	AA879001	Hs.192221	EST8	e monophosphale synthetase (crotal	3.3 3.3
	426746	J03626 H14988	Hs.2057 Hs.107375	ESTs		3.3
	453362 456473	AI202788	Hs.25682	Homo	saptens mRNA for KIAA 1863 protein,	3.3 3.3
5	416426	AA180256	Hs.210473		sapiens cDNA FLJ14872 fis, clone PL	3.3
	445777	AI580371	Hs.145384 Hs.132571	ESTs	seplens mRNA; cDNA DKFZp564P016 (fr	3.3
	423757 431941	AL049337 AK000106	Hs.272227	Home	sapiens cDNA FLJ20099 fis, clone CO	3.3
	404299	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,				3.3 3.3
10	404108			aban	n26c07.r1 Soares Infant brain 1NIB H	3.3
	425189 449318	H16622 AW236021	Hs.78531	Hom	o santens, Similar to RIKEN CONA 5730	3.3
	450193	AI916071	Hs.15607	Hom	o saplens Fenconi enemia complementat	3.2 3.2
	427725	U56839	Hs.180533	milo	gen-activated protein kinase kinase io sapiens mRNA; cDNA DKFZp586J1922 (f	3.2
15	424051	AL110203	Hs.138411 Hs.89538	chok	esteryl ester transfer protein, plas	3.2
	418968 449248	NM_000078 M33782	Hs.23391	Horr	no saplens, Similar to transcription f	3.2
	439416	W58294	Hs.56254	EST	8	3.2 3.2
20	401598	AA172108	Hs.110950		C protein . iquitin	3.2
20	408380 450325	AF123050 AI935962	Hs.44532 Hs.26289	EST		3.2
	428730	AA625947	Hs.25750	EST	ís .	3.2 3.2
	457536	AA305233	Hs.278712		aryotic translation initiation factor Icle-associated membrane protein 8 (e	3.2
25	426836	N41720 AI015631	Hs.172684 Hs.23210	ES	Ta	3.2
25	442710 435232	NM_001262	Hs.4854	cyc	fin-dependent kinase inhibitor 2C (p1	3.2 3.2
	430970	AI018210	Hs.144083	ES	Ts oxisome proliferative activated recep	3.2
	416192	NM_005036 H09380	Hs.998 Hs.30096	: FR	Ts	3.2
30	446676 451459	AI797515	Hs.27056) FS	Ts. Moderately similar to ALU7_HUMAN A	3.2 3.2
50	407603	AW955705	Hs.62604	Ho	mo seplens, done IMAGE:4299322, mRNA,	3.2
	413840	AI301558 BE551203	Hs.14638 Hs.20179		IA binding molif protein, X chromosome	3.2
	448751 432593	AW301003	Hs.51483		Ts, Weakly similar to hypothetical pro	3.2 3.2
35	458786	A1457098	Hs.28084		STs .	3.2
	455909	BE156417	Hs.27879	8 E	STs cmv66a12.s1 NCI_CGAP_GCB1 Homo saplens	3.2
	419311 439710	AA689591 AF086543		at	·Homo saniens full length insert cDNA	3.2 3.1
4.0	434559	AF147315		gt	o:Horno sapians full length insert cDNA omo sapians cDNA FLJ13047 fis, clone NT	3.1
40	455800		Hs.16707 Hs.14638		NA binding motif protein, X chromosome	3.1
	436703 414799		Hs.7732	B in	sulin-like growth factor binding prote	3.1 3.1
	437860	AA333063	Hs.2798	98 H	omo septens cDNA: FLJ23165 fis, clone L	3.1
15	434182		Hs.1185 Hs.8290	r c	-protein gamma-12 subunit DC20 (cell division cycle 20, S. carevi	3.1
45	417900 434769			78 F	lomo saciens cDNA FLJ12676 fis, clone NT	3.1 3.1
	41482	5 X06370	Hs.7743	2 €	pidermal growth factor receptor (avian b:EST90805 Synovial sercoma Homo sapien	3.1
	42641			70 5	ESTs, Weakly similar to 2109260A B cell	3.1
50	44795 40458		1 20.21 02			3.1 3.1
50	42176	4 AI681535			serine/lhreonine Idnase 33 GA-binding protein transcription factor,	3.1
	41998			7Q .	ofhan omteln	3.1
	41694 41476				enhancer of zesta (Drosophila) homolog 2	3.1 3.1
55	44961	1 AI970394	Hs.197	075	ESTs	3.1
	43474			ანნ 252	ESTs ESTs, Moderately similar to ALU1_HUMAN A	3.1
	43427 42789				serum amyloid A1	3.1 3.1
	4176	42 BE30266	5 Hs.105		hypothetical protein FLJ20357	3.1 3.1
60					ESTs, Weakly similar to C55663 oligodend phospholipase A2, group V	3.1
	4461 4400				ESTs. Weakly similar to 138022 hypotheti	3.1
	4265	31 AA3810	71		ab:EST94100 Activated 1-ceus XII Homo s	3.1 3.1
	4221		Hs.11	2341	protesse inhibitor 3, skin-derived (SKAL	3.1
65	4082 4470		98 Hs.28	2915	ESTs	3.1
	4048	100			A Long 40 th antiquities	3.1 3.1
	4069			200	gb:Homo saplens (clone 104) retinoblasto ESTs	3.0
70	0 4190 0 4350				ESTs	3.0
,,	432			2688	hypothetical protein FLJ20397	3.0 3.0
	443	426 AF0981			chromosome 20 open reading frame 1 ESTs, Weakly similar to 138022 hypotheti	3.0
		202 AW962 047 X6596		52049	gb:H.sapiens SOD-2 gene for manganese su	3.0
7	5 418	1241 M2668		149	LIM domain only 1 (rhombolin 1)	3.0 3.0
•	446	599 Z9783	2 Hs.1	5476	differentially expressed in FDCP (mouse	3.0
		2950 BE018 3870 AA431		45342 34832	hypothetical protein FLJ14842 ESTs	3.0
	440	3670 AAA31 3975 BE246		6695	ublquitin-activating enzyme E1-like	3.0 3.0
8	0 43	7756 AA767	'537 Hs.1	97098	ESTS	3.0 3.0
		6084 L1699 2374 AL135		'9006 101865	deoxythymidylate kinase (thymidylate kin dopachrome tautomerase (dopachrome delta	3.0
		2374 AL135 3885 H9180		5284	ESTs	3.0
	• • • • • • • • • • • • • • • • • • • •				176	

						3.0
	434008	AA740878	Hs.112982	ESTS	olens mRNA; cDNA DKFZp547M072 (fr	3.0
	452568	AAB05634 A1288330	Hs.300870 Hs.182330	ESTs		3.0 3.0
	414239 421013	M62397	Hs.1345	mutated it	n colorectal cancers piens cDNA FL114259 fis, clone PL	3.0
5	424635	AA420687 A1554545	Hs.115455 Hs.68301	ESTs	DEIB CONT FEB 14255 III, CONT. C	3.0 3.0
	410276 433865	N29862	Hs.44104	ESTs		3.0
	406028					3.0 3.0
10	401626 415949	H10562	Hs.21691	ESTs	I al analogo	3.0
	418583	AA604379 X02308	Hs.86211 Hs.82962	District of the	ical protein ate synthetase	3.0 3.0
	417933 434577	R37316	Hs.17976	9 Homo s	apians cDNA: FLJ22487 fis, clone H apiens cDNA FLJ13569 fis, clone PL	3.0
1.5	430437	A1768801 AA417812	Hs.16994 Hs.38775	ECTo		2.9 2.9
15	427940 456060	C14904	Hs.45184	Homo s	apiens cDNA FLJ12284 fis, clone MA	29
	421988	AW450481 AB025237	Hs.16133 Hs.388	nurily (r	nucleoside diphosphate linked moi	29 29
	448775 438598	AI805943	Hs.3260	37 hypothe	etical protein MGC5178	2.9
20	429612	AF062649 AA016019	Hs.2525 Hs.4090		y tumor-transforming 1	2.9 2.9
	451189 401558				100 - minin	2.9
	426207	BE390657	Hs.3002	6 HSPC	182 protein	29 29
25	404721 401384				netical protein FLJ22004	2.9
	417288	A1984792		312 nypou 362 orotes	isome (prosome, macropain) subunit,	29 29
	427648 435928		Hs.183	nes EETe	Moderately similar to AF116721 67	2.9
20	43174		Hs.183 Hs.225	412 E515 0 leuke	mila inhibitory factor (cholinergic	2.9 2. 9
30	42824 43997	2 Al348100) Hs.124	cen ESTA		29
	43311					29 29
	42375 40674	8 AW3391	06 Hs.217	7493 anne	otin A2	2.9
35	42215 4055		Hs.120	3927 EST:		2.9 2.9
	4409	11 AA9095			s e morphogenetic protein 2	2.9
	4124 4450					29 29
40		14 AW590	540 Hs.27		is 3360e12:r1 NCI_CGAP_GCB1 Homo sapiens	2.9
	4192 4158			ina EST	TR .	2.9 2.9
	448	40 AF146	761 Hs.20)450 BC	M-like membrane protein precursor	2.9
45	453 432			000 000	tain abasahatase 4 (formerly X), cata	2.9 2.9
7-	438	380 T0843	o Hs.6	194 cho	ondroilin sulfate proteoglycan BEHAB/b 17803C12 Chromosome 7 Fetal Brain cDNA	2.9
	454 421	377 AA076 491 H9999	19 Hs.4	2736 ES	Te	2.9 2.8
-	452	291 AF015		CATE CO	OC7 (cell division cycle 7, S. ceravisi GTs	2.8 2.8
5	U 415	5445 F0889 9518 W763	~.	ab	zd60d04_r1 Soares_fetal_heart_NbHH19W	2.8
	42	7221 L1540)9 Hs.	174007 vo 250173 hy	n Hippel-Lindau syndrome pothetical protein FLJ13158	2.8 2.8
		2493 AVV47 9451 Al907	1117 Hs.	90535 sy	mterdo bindino protein 2	28 28
5	5 44	8789 BE53		00047 E	pothetical protein MGC15548 STs	2.8 2.8
			0159 Hs	282284 E	STs, Weakly similar to 138022 hypotheti	2.6 2.8
	4	18973 AAZ	33058 Hs	.191518 E	STS STS	2.8 2.8
6			04583 Hs	.101047 t	ranscription factor 3 (E2A Immunoglobul	2.8
	4			70007	ESTs protein tyrosine phosphatase, receptor-1	2.8 2.8
		21723 AA6	20400 H	.300717	sodium channel, voltage-gated, type III,	2.8
	15			s.130746 s.272348	ESTs Homo sapiens mRNA; cDNA DKFZp761L1212 (f	2.8 2.8
,	05	100517 AF	242388 H	s.14958 5	tengsin	2.8
				s.87409 ls.326416	thrombospondin 1 Homo saplens mRNA; cDNA DKFZp564H1916 (f	2.8 2.8
	•	406736 Ala	54733 H	ls.182426	ribosomal protein S2 BANP homolog, SMAR1 homolog	2.8
	70			ts.194537 ts.125221	EST8	28 28
		403961			ESTs	2.8
				Hs.22509 Hs.180059	Homo saplens cDNA FLJ 20653 fis, clone KA	2.8 2.8
	75	440483 A	200836	Hs.150386	ESTs gb:RC0-MT0004-130300-011-e07 MT0004 Homo	2.8
		412391 A	W947710 66037	Hs.38173	ESTA	2.8 2.8
		411632 A	W854829		gb:CVZ-CT0261-201099-011-01 CT0261 Homo	2.8
	80		1798853 A578027	Hs_122224	nhm120h01.s1 NCI_CGAP_HSC1 Homo sapans	2.8 2.8
	55	455510 A	A422029	Hs.143640	ESTs, Weakly similar to hyperpolarizatio Homo sapiens cDNA FLJ14597 fis, clone NT	2.8
		447769	\W873704 \A411101	Hs.320831 Hs.243888		2.8
		421101			17	7

		41004204	He 135160	king No	e-I cell membrane-associated gly	2.8
	433800 439662	A1034361 H97552	Hs.135150 Hs.269060	EST8		28 28
	425694	U51333	Hs.159237	hexoldn	ase 3 (white cell)	28
_	414747	U30872	Hs.77204	CSULLOU	nere protein F (350/400kD, mitosin ne-I cell membrane-associated gly	2.8
5	414598	AJ094221 M73700	Hs.135150 Hs.105938	tortritra	esterin	28 28
	447752 408761	AA057264	Hs.238936	ESTA V	Weakly similar to (defline not ava	27
	453350	AI917771	Hs.61790	hypoth	efical protein FLJ23338	27
• •	456629	AW891965	Hs.279789 Hs.164047	CCTo	deacetylase 3	27
10	439538 458814	AA837323 A1498957	Hs.170861	ESTs.	Wealdy similar to Z195_HUMAN ZINC	2.7 2.7
	456029	BE255990	Hs.218329	1	allani modain	27
	451129	BE072881		gb:RC	2-810548-200300-012-e09 BT0548 Homo asa, TRF1-interacting enkyrin-rela	2.7
15	456412	AW749617	Hs.280776 Hs.62578	ESTs		2.7
15	453536 438378	AA137000 AW970529	Hs.86434	hunnil	hotical nutain FLJ21816	2.7 2.7
	425745	U44060	Hs.14427	Homo	saptens cONA: FLJ21800 fis, clone H	2.7
	448322	N23033	Hs.155814			2.7
20	451592	AI805416	Hs.213897 Hs.12827	EST		. 2.7
20	429456 429747	M85835 M87507	Hs.2490		and a considered ated cysteins of	2.7 2.7
	455514	AW983871		ah-D	C1_LINGGG3_77G3GG-021-RU/ RNUVUS MUNU	2.7
	414732	AW410976	Hs.77152	mink	chromosome maintenance deficient (S. epsin D (tysosomal asparty) protease	. 27
25	444207	AI565004 AA402414	Hs.79572 Hs.3059	caul	orner protein complex, subunit beta	2.7
25	427421 449655	AM21987	Hs.59970	EST	5	2.7 2.7
	422648	D86983	Hs.11889	i3 Mela	anoma associated gene	27
	428494	AA233439	Hs.18463	بذمم م	othetical protein FLJ20005 pyrimidine tract binding protein (he	2.7
20	406895	X60648 AA278167	Hs.1725 Hs.1921	su puny 5 Hon	no sapiens, clone IMAGE:3605822, mRNA	2.7
30	453255 427348				00650 prolein	2.7 2.7
	435370		Hs.2258	38 ES	TS	2.7
	407862	BE548267	Hs.5072		no sapiens cDNA FLJ10934 ffs, done OV	2.7
25	411874				A1806 protein	2.7
35	421192 435899		Hs.1899	44 60	T.	2.7 2.7
	41460		Hs.251		Ts, Weakly similar to YEXO_YEAST HYPOT Ts, Moderately similar to ALU4_HUMAN A	2.7
	45346				STS, MODERALERY SITELLE ID ACCO-2 1011041	2.7
40	43655			173 ES 565 Mi	nichromosome maintenance deficient (S.	2.7 2.7
40	42752 40388	-				2.7
	43177		78 Hs.268	571 BÇ	odipoprotein C-I	2.7
	40498		34 Hs.200	20 14	nesin-like 2	2.7
45	4482 4468			MA m	litatic soindle coiled-coil related prot	2.7 2.7
43	4119			2 g	lycogen synthese 1 (muscle)	27
	4047	56			rosylprotein sulfotransferase 1	2.7
	4470			(19 t)	b:yu89a11.s1 Soares fetal liver splean	2.7
50	4221 3 4396			nac h	weethelical contain FLJ21841	27 27
٥,	4365		22		b:nv54h12r1 NCI_CGAP_Ew1 Homo sapiens	27
	4128	33 AW960			ibosomal protein S19	2.7
	457		•-	14579 l 1427 l	ESTs Homo saplens cDNA: FLJ21800 fis, clone H	2.7
5	5 4461 5 4531			V200 I	EQT#	27 27
	459	385 BE380	047		gb:601159382F2 NIH_MGC_53 Homo saplens o	27
	438			36452 0432	ESTs, Wealdy similar to I38022 hypotheti	2.7
		285 A19710 853 BE549		32967	Human EST clone 122887 mariner transposo	2.7
6		853 BE549 037 BE409		27789	mitogen-activated protein kinase-activat	2.7 2.7
·		892 N7360	18 Hs.	0309	ESTS	2.7
		201 AB02		14131 31260	KIAA0974 protein hypothetical protein FLJ13164	2.7
		2279 AA28 7954 J0308		247551	metadn 1	2.7 2.7
•		0371 U807	40			2.7
•	45	2449 AW01		20943	ESTS	2.7
		1114 AA49		291015 81170	ESTs plm-1 oncogene	2.7
		7088 M549 7674 BE27		19192	cyclin-dependent kinase 2	2.7 2.7
•		3680				27
	4!	4879 AW8	13110		gb:CM4-ST0189-051099-021-705 ST0189 Homo Homo sapiens, clone IMAGE:3636299, mRNA,	2.6
				.69280 .29002	KIAA1706 protein	26
				146085	KIAA1345 prolein	2.6 2.6
		05808				26
	4	19700 AF0		.92357	galactokinase 1 ESTs	2.6
				s.114198 s.557	edemorals sinha-1D-, receptor	2.6
			245680 H	5.9701	security agreet and DNA-damage-inducible.	2.6 2.6
	80 4	144156 AW	500059 H	s.86437	ESTs, Highly similar to AF219140 1 gastr ESTs, Weakty similar to S33496 trypsin [2.6
				s.98947 s <i>.2</i> 72155		2.6
				s.64859	ESTs	2.0
						78

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						2.6
			Hs.177576 (menno	syl (alpha-1,3-)-glycoprotein bela- merese (DNA) II alpha (170kD)	2.6
			Hs.156346 1 Hs.111219	ESTs.	Moderately similar to ALU1_HUMAN A	2.6
	401324	,				26 26
5	425234	AW152225	Hs.165909	ESTs,	Weakly shrillar to 138022 hypotheti	2.6
	443210 457244	A1692649 AA581385	Hs.9451 Hs.162473	FSTs.	etical protein MGC13168 Wealdy similar to I38022 hypotheti	2.6
	417144	AA382104	Hs.81337	lectin.	galactoside-binding, soluble, 9	26
	433933	Al754389	Hs.133494	Homo	sapiens clone TCCCIA00164 mRNA sequ	2.6 2.6
10	437437	AA226869	Hs.16520	hypoti	helical protein DKFZp762L0311 , Wealdy simitar to S89890 milogen I	26
	434206 400992	AW136973	Hs.288516	E318	, weddy spinial to coops mangem	2.6
	455530	AW984744		gb:R0	C1-HN0015-040400-011-d03 HN0015 Horno	2.6
	436139	AA765788	Hs.120936	ESTS		2.6 2.6
15	448330	AL036449	Hs.207163 Hs.75074	ESTS	en-activated protein kinase-activat	2.6
	412942 432753	AL120344 NM_014075	Hs.336938	Home	seplens PRO0593 mRNA, complete cds	2.6
	433430	AI863735	Hs.186755	EST		26 26
20	435693	AW973223	Hs.303197	B-cel	l CLL/lymphoma 7C formation/transcription domain-esso	2.6
20	429482	AF076974 AA247152	Hs.203952 Hs.200483		s, Weakly similar to KIAA1074 protein	2.6
	432715 414217	Al309298	Hs.279898	Hom	o sapiens cDNA: FLJ23165 fis, clone L	2.6
	434165	AA971328	Hs.95361		sin VIIA (Usher syndrome 18 (autosoma	2.6 2.6
25	414835	AA156720	Hs.185342 Hs.149250	EST	s glec precursor,	26
25	424489 436485	T48851 AA281959	Hs.5210		maturation factor, gamma	2.6
	403797			-		2.6 2.6
	434573	AW372340	Hs.159717	EST	s density (tpoprotein-related protein	26
30	418841 415785	NM_002332 R82419	Hs.89137 Hs.23603	ES1	's, Moderately similar to ALUS_HUMAN A	2.6
50	450608	AA010365	Hs.193229			2.6
	425304	AA463844	Hs.31339	fibro	oblast growth factor 11	26 26
	432268	BE311856	Hs.274230 Hs.40834	J-p	hosphoadenosine 5-phosphosulfate sy isitional epithelia response protein	2.6
35	410507 427343	AA355288 A1880044	Hs.176977		tein kinase C binding protein 2	2.6
	420917	AW135718	Hs.117330		Ts	2.6 2.6
	414399	L47345	Hs.155202 Hs.270651	trai	scription elongation factor B (SIII) Ts, Moderately similar to A47582 B-cel	2.6
	446089 440829	A1860021 AF138407	Hs.7446	chi	omosome 6 open reading frame 5	26
40	408475	AA315514	Hs.47986	hy	pothetical protein MGC10940	2.6 2.6
	450946	AA374569	Hs.127698		i7s, Moderately similar to 2109260A B c uaporin 9	2.6
	421462 434846	AF016495 AW295389	Hs.104624 Hs.119768		iTs	2.6
	422887	A1751848	Hs.49215	ES	STs	2.6 2.6
45	417435	NM_00518		ca c	rbonic anhydrase III, muscle specific pothetical protein DKFZp762M115	2.5
	437389 408981		Hs.271589 Hs.49427		em-Interacting protein	2.5
	432180		Hs.27282	2 R	vB (E coli homolog)-like 1	2.5 2.5
50	418079		Hs.6911	. E	STs STs, Weakly similar to alternatively sp	2.5
50	437820 439585		Hs.32383 Hs.29393	7 E	STs, Weakly similar to FXD2_HUMAN FORKH	2.5
	425681			33 K	(AAO754 protein	25 25
	435177		Hs.42938		STs	2.5
55	437323 422114				iptin receptor rsenate resistance protein ARS2	2.5
"	44847		Hs.20345		STS	2.5
	42662	3 AA382826			STs	2.5 2.5
	44876- 45838		Hs.18211 Hs.2462		STs STs	2.5
60	40372		Hs.1343	4 F	tomo sapiens clone 24418 mRNA sequence	25
	44488	8 Al651039			STs	2.5 2.5
	45617 42484		Hs.2719 Hs.1534	130 l 179 4	ESTs extra spindle poles, S. cerevisiae, homo	2.5
	40627			20 1	peptidylglycine alpha-amidating monooxyg	2.5
65	41805	54 NM_0023	1B Hs.8335		ysyl oxidase-like 2	2.5 2.5
	44593	38 BE54359	4 HS.6147	78	hypothetical protein FLJ22329 gb:1L3-CT0214-150200-074-E06 CT0214 Homo	2.5
	45496 4423				ESTs	2.5
	4565	83 AF17989	7 Hs.1041	105	Mels (mouse) homolog 2	2.5 2.5
70			Hs.4464		ESTs growth arrest and DNA-damage-inducible,	2.5
	4168 4245		Hs.8040 71 Hs.2381		ESTs, Weakly similar to KIAA1204 protein	2.5
	4060	138 Y14443	Hs.882	19	zinc finger protein 200	2.5 2.5
	4134	95 Y12395	Hs.315	177	Interferon-related developmental regulat	2.5 2.5
75) 4230 4108			1052 359	ESTs protein disulfide isomerase related prot	2.5
	4398		61 Hs.671	10	mannose-P-dolichol utilization defect 1	2.5 2.5
	4538	328 AW970	960 Hs.293		ESTs ESTs	25 25
80	O · 4450				checkpoint with forkhead and ring finger	2.5
01	408				ribosomal protein L13	2.5
	412	370 AW946	614		gb:RC2-ET0021-280400-011-c05 ET0021 Homo	2.5 2.5
	423	642 AW452	650 Hs.15	/148	hypothetical protein MGC13204	20
					170	

		41AP07C700	UL 165607	ESTs		2.5
	430357 414853	AW976789 U31116	Hs.165607 Hs.77501	BETCO	glycan, beta (43kO dystrophin-assoc	2.5
	416097	BE387371	Hs.118964	hypot	hetical protein FLJ20085	2.5 2.5
_	428619	AK002140	Hs.187378	hypot	hetical protein FU11278	25
5	413976	BE295452	Hs.75655 Hs.254983	EST	itagen-prolina, 2-oxoglutarata 4-di	2.5
	445223 423926	AW291553 X03833	Hs.1722	interi	eukin 1, aipha	25
	410165	BE560228	Hs.71869	apop	tosis-associated speck-like protein	2.5 2.5
	406474			COT		25
10	433908	AW298141	Hs.157975 Hs.77873	EST:	s omalog 3	2.5
	439755 437528	AW748482 N59646	Hs.169745	CRUIT	ibs (Drosophila) homolog 1	2.5
	420734	AW972872	Hs.293738	EST	•	2.5 2.5
	415345	Z43108			ISC13E071 normalized infant brain cON	25
15	419337	AW291112	Hs.209978 Hs.18041	EST		2.5
	444606 430061	R09478 AB037817	Hs.230188	KIA	A1396 protein	2.5
	413407	A1356293	Hs.75339	tnos	itol polyphosphate phosphatase-like	2.5 2.5
	411965	BE467339	Hs.280115	EST	is phase-promoting complex subunit 7	25
20	409278	AA3466B3	Hs.52763	ana	phase-promoung complex sociality	2.5
	403142 401714					2.5
	425081	X74794	Hs.154443		ichromosome maintenance delicient (S.	2.5 2.5
	416505	H66470	Hs.16004	ES		25
25	431518	AA743462	Hs.165337 Hs.107515	ES	Ts, Weakly similar to T00329 hypotheti	2.5
	448623 428301	BE613468 AW628666	Hs.98440	ES	Ts, Weakly similar to 138022 hypotheti	2.5
	404366	,				2.5 2.5
	449733	R74546	Hs.29438	Ho	mo seplens cDNA FLJ12094 fis, clone HE :IL-BT152-080399-004 BT152 Homo sepien	2.5
30	459583	A1907873		Op Gp	:RC0-DT0076-110100-031-c09 DT0076 Homo	2.5
	402856 420751	AW939659 J03019	Hs.99913	ad	renergic, beta-1-, receptor	2.4
	436805	AA731533	Hs.27075	1 FS	STs	2.4 2.4
~-	420285	AA258124	Hs.29387		5Ts, Moderately similar to ZN91_HUMAN Z Jute cerrier family 2 (facilitated glu	2.4
35	453496	AA442103	Hs.33084 Hs.18808	3 5	STs	2.4
•	453853 407909	AL040600 AW103986		- 01	NAMES AND LOCATE OV23 Homo sapiens	2.4
	454630			gl	b:CM3-HT0137-170999-012-f02 HT0137 Homo	2.4 2.4
40	451026		Hs.15749		er-d4 (mouse) homolog opamine receptor D4	2.4
40	420779		Hs.99922 Hs.22134	io E	STe.	2.4
	438322 455908		10,2210	0	b:QV0-HT0367-150200-114-h04 HT0367 Homo	2.4 2.4
	419625	U91616	Hs.91640) n	ruclear factor of kappa light polypeptid	24
4.5	440773		Hs.3325		tomo saplens, Similar to RIKEN cDNA 2700 complement-c1q tumor necrosis factor-rel	2.4
45	450823		Hs.2201 1 Hs.2879		tomo sapiens cDNA FLJ13090 fis, clone NT	2.4
	447241 42910			52 1	neutrophil cytosolic factor 4 (40kD)	24 24
	45180	2 Al817711	Hs.2093		ESTs	2.4
50	41941		Hs.3942 Hs.2240	9	ESTs teukocyte immunoglobulin-like receptor,	24
50	40709 42356				hypothetical protein FLJ13633	24
	42750		Hs.1317	43	ESTs	2.4 2.4
	45177	3 Z42044	Hs.2699		KIAA1278 prolein	2.4
55	43684				ESTs Homo saplens cDNA FLJ14115 fis, clone MA	2.4
33	43158 44061				hypothetical protein FLJ12879	24
	4237	21 AF17691	1 Hs.132		cardiotrophin-like cytokine; neurotrophi	24 24
	4521				GDP-mannose pyrophosphorylase B ATP-binding cassette, sub-family C (CFTR	2.4
60	4195 4534			3 0	gb:600944574F1 NIH_MGC_17 Homo saplens c	2.4
50	. 4197		30 Hs.190		ESTs	2.4 2.4
	4527	86 R61362	Hs.106	642	ESTs, Weakly similar to T09052 hypotheti gb:MR3-ST0220-290100-016-e04 ST0220 Homo	24
	4104			:4	cleavage and polyadenytation specific fa	2.4
65	4386 4024		33 15.00	,,	Godfogo and porture and a	2.4
0.	4439		1425 Hs.999	39	epithelial membrane protein 3	24 24
	4146	25 AA3357	38 Hs.76	686	glutathione peroxidase 1	24
	4030		EA		gb:ni85c09.s1 NCI_CGAP_Pr20 Homo saptens	24
70	0 432 0 431			7749	unc93 (C.elegans) homolog A	2.4
,,	455		907		gb:IL3-CT0220-310100-055-H11 CT0220 Homo	24 24
	426	249 F05422	Hs.16		nucleoporin-like protein 1	24
	446				ESTs plasminogen activator, urokinase	24
7	5 414	774 X0241! 252 AA346		2/4 18191	ESTs	2.4
,		918 AA209		3754	hypothetical protein FLJ 12606	24
	427	550 BE242		9606	nuclear RNA helicase, DECD variant of DE	2.4 2.4
	404	020	202 11-44	1402	Cbo/p300-interacting transactivator, wit	24
Q		1846 AA426 1222 A15254			hypothetical protein MGC2383	24
٥		7222 A15254 3639 BE269			proteasome (prosome, macropain) subunit,	24
	45	2708 AW44		57150		2.4 2.4
	40	1676				
					190	

	428882			ESTs, Moderately similar to ALU7_HUMAN A	24
	435277			ESTS	2.4 2.4
	425271 405353	AF026547	Hs.169047	chondroilin sulfate proteoglycan 3 (neur	24
5	409193	AA131483		pb:zo08e05.r1 Stratagene neuroepithelium	2.4
	431431	AL095711		Human DNA sequence from clone RP3-403A15	2.4 2.4
	407889 453335	R34556 AW857376		ESTs, Wealdy similar to S65657 alpha-1C- fucosyltransferase 3 (galactoside 3(4)-L	24
	450621	AW297288	Hs.55918	hypothetical protein FLJ11354	24
10	419652	AL157485	Hs.91973	hypothetical protein	2.4 2.4
	421151	BE174431	Hs.63386 Hs.244569	ESTs esophagus cancer-related gene-2	24
	437848 420581	AA773866 AA847602	Hs.106510	ESTs, Moderately similar to ALU2_HUMAN A	2.4
	405288				24 24
15	453527	R49570	Hs.180236	ESTs gb:qa58b08.s1 Soares_NhHMPu_S1 Homo sepi	24
	429875 436360	Al091815 Al982798	Hs.136754	ESTs	2.4
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	2.4
20	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	2.4 2.4
20	449539 419870	W80363 AW403911	Hs.58446 Hs.266175	ESTs phosphoprotein associated with GEMs	24
	404584	A11403511	10.200110	production and a second a second and a second a second and a second a second and a second and a second and a	24
	454276	AW294996	Hs.255374	ESTs .	2.4 2.4
25	423746 415558	AW361817 AAB85143	Hs.132370 Hs.125719	NADPH oxidase 1 ESTs	2.4
23	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	24
	406953	L36847		gb:Human (clone p17/90) rearranged iduro	2.4 2.4
	444471	AB020684	Hs.11217 Hs.4254	KIAA0877 protein ESTs	24
30	451031 455302	AI360187 AW997641	F15.4204	ab:RC6-BN0052-170200-011-D06 BN0052 Homo	2.4
	449063	Al627352	Hs.236547	Homo saplens, clone IMAGE:2905978, mRNA.	24 24
	401048	A A COD-17D	Hs.194864	hypothetical protein FLJ22578	2.4
	434420 425848	AA688278 BE242709	Hs.159637	valyl-IRNA synthetase 2	2.4
35	449086	AI628357	Hs.208037	ESTs	2.4
	415238	R37780	Hs.21422	ESTS	2.4 2.4
	448337 416991	AW208453 N36389	Hs.3782 Hs.141298	ESTs KIAA0226 gene product	2.3
	412600	128824	Hs.74101	spleen tyrosine kinese	2.3
40	418385	AW590613	Hs.301040	Homo septens, clone IMAGE:3357127, mRNA, KIAA1716 protein	2.3 2.3
	440769 450437	BE581793 X13958	Hs.21446 Hs.24998	hypothetical protein MGC10471	2.3
	412035	N78559	Hs.293629	hypothetical protein MGC3121	2.3
4.5	406739	AI566709	Hs.182426		. 2.3 2.3
45	418506 410286	AA084248 AI739159	Hs.85339 Hs.61898	G protein-coupled receptor 39 DKFZP586N2124 protein	2.3
	443740	R56434	Hs.21062	ESTs	2.3
	405605			1. DOL 070004 024000 044 -14 DT0004 Vemo	2.3 2.3
50	416913 426509	AW934714 M31166	Hs.2050	gb:RC1-DT0001-031299-011-a11 DT0001 Homo pentaxin-related gene, rapidly induced b	2.3
50	445828	F05802	Hs.81907	ESTs	2.3
	457195	AB011099	Hs.196647	KIAA0527 protein	2.3 2.3
	420372 423198		Hs.293860 Hs.1634	Homo saplens, clone IMAGE:3535476, mRNA, cell division cycle 25A	2.3
55	457730			gb:RC1-CT0268-060100-013-e01 CT0268 Homo	2.3
	412014	A1820650	Hs.43761	ESTs, Weskly similar to A46010 X-linked	2.3 2.3
	447131 446288				2.3
	436954			5 ESTs	2.3
60	411658		3	gb:CM1-CT0278-031199-032-e08 CT0278 Homo	2.3 2.3
	404240 456094			gb:yw57e09.r1 Soares_placenta_8to9weeks_	2.3
	416951		Hs.19078	5 ESTs, Moderately similar to S65657 alpha	23
	40673			gb:qy15h09.x1 NCL_CGAP_Bm23 Homo saplen	2.3 2.3
65	458453 45233		Hs.13509 Hs.19197		2.3
	40852			37 ESTs	23
	45547	0 AW94799	2	gb:PM0-MT0011-240300-001-c09 MT0011 Homo	2.3 2.3
70	43632		Hs.1409 Hs.1088		2.3
70	45000 41617		Hs.1257		2.3
	41913	4 T89863	Hs.2217	71 ESTs	2.3 2.3
	44593				23
75	42208 44991				2.3
, ,	41707	r9 U65590	Hs.8113	4 Interleukin 1 receptor entagonist	2.3
	41174				2.3 2.3
	4356° 4234		Hs.4975 5 Hs.1296		2.3
80	4071		1 Hs.230	157 ESTs	23
	4114	48 AA17895	55 Hs.271		2.3 2.3
	4386 4326		2 Hs.129 Hs.308		23 23
	4020				

			ts.61210	ESTs, Weatly similar to 138022 hypotheti	2.3 2.3
		AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	2.3
	404054 430458	AA479300	Hs.225706	ESTs, Wealthy similar to 138022 hypotheti	2.3
5	440210	AW674562	Hs.125296	ESTs	2.3
•	446727		Hs.15032	KIAA0523 protein	2.3 2.3
	453775		Hs.35120 Hs.171391	replication factor C (activator 1) 4 (37 C-terminal binding protein 2	23
	438379 449919		Hs.200141	ESTs	2.3
10	415293	R49462	Hs.106541	ESTs	23
	441126		Hs.323715	methionine adenosyltransferase I, alpha	23 23
	408203	AA053137	Hs.42390 Hs.334825	nasopharyngeal carcinoma susceptibility Homo sapiens cDNA FLJ14752 fis, clone NT	2.3
	434941 450748	AW073202 AI733093	Hs.130016	ESTS	2.3
15	404185	A155555			23
	418327	U70370	Hs.84136	paired-like homeodomain transcription is	2.3 2.3
	451370	A1791929	Hs.300782	ESTs	2.3
	400034 407723	AW071161	Hs.252873	ESTs	2.3
20	431320	AW969474	Hs.183070	ESTs	2.3
	429271	AF039850	Hs.198515	dead ringer (Drosophila)-like 1	2.3 2.3
	453707	AW003879	Hs.126522	Homo saplens, clone MGC:16722, mRNA, com gb:HSU70073 Human Homo sapiens cDNA clon	2.3
	419225 444556	U70073 Al277924	Hs.145199	ESTs	2.3
25	405741	P4211364	13,143130		2.3
	400917			_4.0	23 23
	432567	AA736777	Hs.293770	ESTs ESTs, Weakly similar to A45010 X-linked	2.3
	437949 450514	U78519 AC005785	Hs.41654 Hs.25059	A kinase (PRKA) anchor protein 8	23
30	418400	BE243026	Hs.301989	KIAA0246 protein	2.3
20	444019	BE173977	Hs.10098	putative nucleolar RNA helicase	23 23
	406326		11. 42400	ESTs, Weakly similar to FLJ00004 protein	2.3
	412077 427647	N51107 W19744	Hs.47199 Hs.180059		2.3
35	414528	AA148950	Hs.188836	ESTs	2.3
	414854	BE546797	Hs.51483	ESTs, Weakly similar to hypothetical pro	2.3 . 2.3
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Home sapiens c	2.3
	439467	AW292275	Hs.158365	ESTS	2.3
40	402627 451711	AK000461	Hs.26890	cat eye syndrome chromosome region, cand	2.3
-10	424308	AW975531	Hs.154443		2.3 2.3
	423869	BE409301	Hs.134012	C1q-related factor	23
	405915 431503	NM_012129	Hs.258570	5 claudin 12	2.3
45	423306	W88562	Hs.10819	B ESTs	23
	443232	AF161521	Hs.9081	phenylalanyl-IRNA synthetase beta-subuni	2.3 2.3
	433064		Hs.30002		2.3
	434437	A1912566 BE407866	Hs.18781 Hs.17025		2.3
50	436191 420006		Hs.94300		2.3
50	447942		Hs.33478	6 hypothetical protein MGC16040	2.3 2.3
	403166			22 VIAARER anno product	2.3
	422119 403751		Hs.11188	32 KIAA0590 gene product	2.3
55	426451		Hs.16994	16 GATA-binding protein 3	2.3
	427413	BE547647	Hs.1777		2.3 2.3
	409091		Hs.2694 Hs.2494	23 ESTs 4 ESTs, Wealdy similar to 2109260A B cell	2.3
	44049 42772				23
60	40574	7			23 23
	43821	0 AA780519	Hs.3116	01 EST	23
	40465 42352		Hs.1297	38 potassium voltage-gated channel, Shaw-re	22
	42352 42679		Hs.1723	50 HIR (histone cell cycle regulation defec	2.2
65	44442		Hs.1963	77 ESTs	2.2 2.2
	43403	1 BE38416	5 Hs.2372		22
	42765 43527		5 Hs.252 Hs.104	259 ribosomal protein S3 HGF activator	2.2
	43827				22
70	4245	58 D83702	Hs.151	573 cryptochrome 1 (photolyase-like)	2.2 2.2
	4299		9 Hs.226	770 DKFZP566C0424 protein	2.2
	4420				2.2
	4151 4205		5 Hs.275	438 histone deacetylase 7A	2.2
7:	4112	63 BE29780	2 Hs.693	60 kinesin-like 6 (mitotic centromere-assoc	2.2 2.3
	4437	53 AW3675			2.2
	4232				2.3
	4465				2.3
8	4210	MD AA7150	26 Hs.13	5280 ESTs	2.
_	4262		— Hs.16	PS88 neural cell adhesion molecule 1 gb:PM3-BN0142-200300-001-c04 BN0142 Homo	2.: 2.:
	4555 4068				2
	4000	. News	. 12.10		

						2.2
	444153	AK001610	Hs.10414		etical protein FLJ10748 prnerase (DNA) III alpha	2.2
	419575	U43431 L44284	Hs.91175 Hs.159743	ESTs	Kildigge (Digg) iii ahva	2.2
	418672 456261	AA210718	Hs.104157	ESTs.	Wealty similar to KIAA0694 protein	2.2
5	415737	AA167626	Hs.118743	ESTs	AND ALL STORY AND ALL STORY AND ALL ST	2.2 2.2
_	447554	AJ391598	Hs.36119	ESTs.	Wealdy similar to ALU1_HUMAN ALU S	2.2
	405159	AW661820	Hs.211413	ESTs		2.2
	442177 446139	H77395	Hs.39749	ESTS		22
10	458339	AW976853	Hs.172843	ESTs		2.2 2.2
	401876			-4-4	amo sapiens tuli length insert cDNA	2.2
	439566	AF086387	Hs.2257	go:ru	ectin (serum spreading factor, som	2.2
	425079 441837	H09963 AA361743	Hs.179881	core	binding factor, beta subunit	2.2
15	430644	AB015419	Hs.247710		oprotactin-releasing peptide	2.2 2.2
	431474	AL133990	Hs_190642	EST	i a company and a selected to AEA	22
	407739	NM_002285	Hs.38070 Hs.143601	hunn	hold nuclear protein related to AF4 thetical protein hCLA-iso	2.2
	424244 438057	AV647184 AW294544	Hs.125785	EST	, Wealdy similar to CORB MOUSE CORNI	2.2
20	412715	NM_000947	Hs.74519	orim	ase, polypeptide 2A (58kD)	2.2 2.2
	422365	AF035537	Hs.115521	REV	3 (yeast homolog)-like, catalytic sub	2.2
	404170	1122074		ab:F	luman retinoic acid receptor gamma 2	2.2
	406902 437902	M32074 AA770599	Hs.144055		S	2.2
25	401012	70117 0000				2.2 2.2
	446502	Al302654	Hs.208024			2.2
	442554	AW467376	Hs.129640	ES1	s uperfemily protein	2.2
	443021 421141	AA368546 AW117261	Hs.8904 Hs.125914	4 ÉS	TS.	2.2
30	443070	BE388662	Hs.8984	Hor	no saniens chromosome 14 BAC 98L12	22 22
•	446566	H95741	Hs.17914		mbrane-spanning 4-domains, subfamily A	2.2
	427695	R88483	Hs.17286	2 ES	15 EST93093 Skin tumor I Homo saplens cD	2.2
	426503 431468	AA380153 AW248431	Hs.25652		clear prelamin A recognition factor	2.2
35	416185	AW975861		KV.	A1785 protein	2.2 2.2
-	437319	BE410958		i Ho	mo sapiens cDNA FLJ13549 fis, clone PL	2.2
	402064		Hs.48442	, ,	iTs	2.2
	413335 408212				pothetical protein	2.2
40	406169			•		2.2 2.2
	451099	R52795	Hs.2595	4 in	erleukin 13 receptor, alpha 2	2.2
	40733		Hs.1587 Hs.2389		omo sapiens cDNA FLJ 13054 fis, clone NT STs	2.2
	409719 43192		Hs.2363 Hs.5887		STS	2.2
45	44382			h	roothetical protein	2.2
	43245	8 A1968598	Hs.7876	n 8	alignant cell expression-enhanced gene/	2.2 2.2
	41972		Hs.1274) b	one morphogenetic protein 1 forno sapiens mRNA; cDNA DKFZp564C142 (fr	2.2
	42317 45108				lomo sapiens cDNA: FLJ23269 fis, clone C	2.2
50	41521			211 F	forno sapiens cDNA FLJ11421 fis, clone HE	2.2 2.2
• •	44224	2 AV64790		24 H	tomo sapiens cDNA: FLJ23285 fis, clone H	2.2
	441B3		4 Hs.429 Hs.172	54 F	rypothetical protein DKFZp554D0372 polypyrimidine tract binding protein (he	2.2
	40666 44337			0 1	proteasome (prosome, macropain) subunit,	2.2
55	4325		Hs.177	269 (ESTs	2.2 2.2
	4081	45 R45621	Hs.810		nypothetical protein MGC2718 U1-snRNP binding protein homolog (70kD)	22
	4198				ESTs, Weakly similar to 138022 hypotheti	2.2
	4394 4384			673	eukaprotic translation initiation factor	2.2
60	4501			7617	Homo sapiens, clone IMAGE:3447394, mRNA,	2.2 2.2
-	4091	30 BE0766			phosphorylase, glycogen; brain	2.2
	4288				hypothetical protein FLJ12671 aristaless-like homeobox 3	2.2
	4294 4330				Homo sapiens cONA FLJ11660 fis, clone HE	2.2
6:	5 4400				FSTs. Weakly similar to neuronal thread	2.2 2.2
	4083	204 AA4545			protein tyrosine phosphatase type IVA, m	2.2
	427				methyl-CpG binding domain protein 3 ESTs, Weakly similar to 138022 hypotheti	2.2
	408			3345	olycine dehydrogenase (decarboxylating:	2.2
7	0 43	703 AV654 446 AW 2 94	1929 Hs.25	55369	Homo sapiens cDNA FLJ10265 fis. clone HE	2.2
•	456	660 AA909	249 Hs.11	12282	sotute carrier family 30 (zinc transport	2.2 2.2
	433	099 NM_00			nuclear transcription factor, X-box bind Homo sapiens cDNA FLJ11381 fis, clone HE	2.2
		857 AA866 245 N5965		27797 7252	ESTs	2.2
7		3245 N5965 3657 R1497	3		gb:yl42l10.s1 Soares fetal liver spleen	2.2
•		521 AW50	1216 Hs.1	08945	KIAA0515 protein	2.2 2.2
	414	1819 BE177		56148	hypothetical protein FLJ13231	2.2
		5530 AV65		82642 2800	ESTs ESTs	2.2
9		5797 AJ291 4812 X7275		7367	monokine induced by gamma interferon	2.2
		3028 AB00		1442	RecQ protein-like 4	2.2 2.2
	41	2133 U834	50 ' Hs.7	73614	solute carrier family 31 (copper transpo	2.2
	40	7881 AW07	2003 Hs.4	10968	heparan suttate (glucos amine) 3-O-sutfot	2.6

					.hala	2.2
	437033	AW248364	Hs.5409 Hs.24937	NA polymerase i su ransformer-2 alpha (ibumii (htra-2 atoha)	2.2
	422732 416388	AA577455 AI417358	Hs.73677	ESTs		2.2 2.2
	452849	AF044924	Hs.30792	hook2 protein	_	2.2
5	446615	BE513202	Hs.15589 Hs.183858	PPAR binding protei banscriptional intern	nediary factor 1	2.2
	428361 446279	NM_015905 AA490770	Hs.182382	ESTs		2.2 2.2
	422938	NM_001809	Hs.1594	centromere protein	A (17kD)	22
• •	403969	*******	Hs.63489	omtein tymsine pho	sphatase, non-recept	2.2
10	410423 429736	AW402432 AF125304	Hs.212680	homes exercise forth	ov necesitat substitativ	2.2 2.2
	447091	AW089648	Hs.157779	ESTs. Weakly simil	St P CV11 HOWAN COLLY	2.2
	422017	NM_003877	Hs.110776	STAT induced STA	nain (PTPRF interact	22
16	426728	NM_007118 AB033103	Hs.171957 Hs.6385	KIAA1277 protein	The state of the s	22
15	438726 453315	BE544203	Hs.24831	ESTE		22 22
	423244	AL039379	Hs.209602		lar to ubiquitous TPR m	2.2
	433610	AA806822 BE409861	Hs.112547 Hs.202833	ESTs heme oxygenase (decycling) 1	2.2
20	429451 417980	R32235	10,20200	gb:yh67f08.r1 Soa	res placenta Nb2HP Homo	22 22
20	406347				NIH_MGC_17 Homo sapiens c	22
	414406	BE297904				22
	401827 446913	AA430650	Hs.16529	transmembrane 4	superfamily member (telt	2.2 2.2
25	452294	AI871925	Hs.11789	ESTs, Moderately	similar to A47582 B-cel	2.2
	404084		Hs.13285	hypothetical prote	in FLJ11222	2.2
	456786 435031		Hs.11687			2.2 2.1
	442609		Hs.8518	entoenemtein N	EUDONAACE 1709	21
30	439732	AW629604			ein from EUROIMAGE 1703	2.1
	421506			ESTs		21
	439253 409669			hypothetical prot	ein MGC13098	21 21
	42957	4 BE268321			lein MGC861 Lein DKFZp547D065	2.1
35	43747			DVEZP588.1162	4 protein	21
	40894 44768		Hs.1501	hypothetical pro	tein DKFZp566K1946	21 21
	45958	4 A1910884				2.1
40	43913			7 ESTs 4 guanine nucleo!	ide binding protein (G pr	2.1
40	42818 44202			ECTe		21 21
	43098	8 AW9728		gb:EST384925	MAGE resequences, MAGL Homo milar to A Chain A, Human	2.1
	44360			heterogeneous	nuclear ribonucleoprotein	21
45	41710 4445			ESTS		2.1 2.1
45	4383	91 Al26224				2.1
	4420				otein MGC4126	2.1
	4562 4169			o major vault pro	otein	2.1 2.1
50		10 028419	Hs.82	9 hydroxymethyl	ibilane synthase similar to ALU1_HUMAN ALU S	2.1
	4452			ob:RC5-LT005	54-140200-013-D01 LT0054 Homo	21
	4527 4349		269 Hs.50	72 mitochondrial	ribosomal protein L32	2.1 2.1
_	421	564 AB007		ISO KIAAO4O4 pro	itein Irotein C321D2.4	2.1.
5:					Total Colored	21
		742 AA564 958 H9818	0 Hs.11	975 ESTs		21 21
	421	531 AA713		769 ESTs	al adaptor 3 (ADA3, yeast h	21
6	0 410	431 BE261 1503 AI5709		EAC ECTe		21
U		1503 A15705 3127 A1478	416 Hs.2	883 ESTs, Weald	y similar to ALU1_HUMAN ALU S	2.1 2.1
	453	2897 BE066			rately similar to 178885 serin	2.1
		7112 H1784 6577	00 Hs.7			2.1 2.1
6		7162 AWO	5505 Hs.5		one receptor coactivating pr	21
•	45	1460 AJ797		9652 ESTs	protein FLJ20452	21
		7402 H545	20 Hs. 10705 Hs.	oco ESTe		21
		15828 AA70 16398 A168:	3487 Hs.	2213 wingless-lyl	ne MMTV integration site fami	2.1 2.1
7		20582 BEO4			ens chromosome 19, cosmid R2837 day similar to AT2A_HUMAN POTE	N 2.1
				5757 ESTs, Wea 05:HSC2Q	E041 normalized infant brain cDN	4.
			36504 Hs.	MOC ECTA		21 A 21
	4	57066 BE2	44613 Hs	58272 ESTs, Wes	ady similar to CA13 MOUSE COLL receptor expressed on myeloid	2.1
				83022 triggering r 91701 ESTs	Andhen ankinessa an mana	21 21
			294828 Hs	09203 ESTs		21 21
	6	40818 Al1	17060 Hs	46726 ESTs	4C245 protein	2.1
			806007 Hs	9461 DKFZP43		21 21
		100822 112760 AW		1324 ESTs	de chlantama andele bladina es	2.1
		410653 BE	383768 H		tinoblastoma protein binding pr xiens cDNA: FLJ22373 fis, clone H	2.1
		426925 NW	I_001196 H	315689 Homo sap	No	104

		4.4.227.47C	Hs.293984	hventh	etical protein MGC13102	2.1
	424242 452560	AA337476 BE077084	Hs.336432	FSTs		21
	456437	AJ924228	Hs.1151B5		Moderately similar to PC4259 ferri	2.1 2.1
-	458922	BE501B31	Hs.282053	ESTS	sapiens mRNA; cDNA DKFZp434N079 (fr	2.1
5	439231	AW581935 AA316241	Hs.141480 Hs.90691		enhasmin/nucleoniasmin 3	2.1
	419488 411829	AW865749	110.00001	ab:Q\	3-SN0021-100500-185-c03 SN0021 Homo	21 21
	457192	AL135682	Hs.22452	Homo	sapiens mRNA for KIAA1737 protein,	21
10	422128	AW881145	U= 24006	gb:CN ESTs	/0-OT0033-010400-182-e07 OT0033 Hamo	2.1
10	452571 423699	W31518 H41850	Hs.34665 Hs.131846		associated factor 65 alpha	21
	406610	N4 1030	. 4 4 . 4			21 21
	453638	AW814996		gb:M	R1-ST0206-170400-024-h09 ST0206 Horno	21
1.5	418856	AA362858	Hs.5719	gb:E	ST72900 Ovary II Homo sapiens cDNA 5 nosome condensation-related SMC-asso	2.1
15	437623 410908	D63880 AA121688	Hs.10592	EST		21
	420221	N25991	Hs.43725	EST		2.1 2.1
	424739	AA346108	Hs.22161	EST	S	2.1
20	425398	ALD49689	Hs.15636 Hs.18250	y nypo	thetical protein slmilar to tenascin I domain, class 3, transcription facto	2.1
20	424901 411096	Z11933 U80034	Hs.68583	mito	chondrial intermediate peolidase	21
	415635	F13168		ohil	ICC2 IF 101 normalized infant brain CDN	2.1 2.1
	418181	U37012	Hs.83727	clea	wage and polyadenylation specific to	21
26	407103	AA424881		n nyp	othetical protein MGC13170 L3-CT0213-170100-055-F02 CT0213 Homo	2.1
25	454389 400021	AW752571	•			2.1
	439228	N51700	in ou.		y/72d01.s1 Soares_multiple_sclerosis_	2.1 2.1
	456505	AA504595	Hs.1114	18 ES	ī s	21
20	405258	AI184564	Hs.1016	54 ES	Ts	21
30	444645 430246	A1269069			pothetical protein FLJ12552	2.1 2.1
	458687	AW02481			UT4 enhancer factor	21
	403857					2.1
35	400258	AA30664	9 Hs.1693	70 F	'N oncogene related to SRC, FGR, YES	2.1
33	422221 441054			180 FS	RTs .	2.1 2.1
	452700	A1859390) Hs.2889	940 ffy	e-span transmembrane protein M83 :MR4-ST0124-181299-020-b06 ST0124 Horno	2.1
	454606				MR4-510124-181299-020-000-510124-1-2-10 AA0664 protein	2.1
40	448954 443148			194 E	STs. Weakly similar to ALUS_HUMAN ALU S	2.1
40	453486			554 ul	alquinol-cytochrome c reductase core pr	2.1 2.1
	43769	5 AA7692		142 E	STS	2.1
	42544			441 6	pleen focus forming virus (SFFV) provir eneral transcription factor IIIC, polyp	2.1
45	44727 43567			726 E	STs, Wealdy similar to TSGA RAT TESTIS	21
7,7	43638			1191 F	STR	21 21
	43583	7 Al6892			forno sapiens cDNA FLJ11431 fis, clone HE	21
	45828				STs STs	2.1
50	42379 40804				tesmoptakin (DPI, DPII)	2.1 2.1
-	4027	25			normal sales Co., Ale Analidis hav nobres	2.1
	45199			424	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep hypothetical protein FLJ22439	21
	41754 4148			0	modulator recognition factor I	2.1 2.1
55	4357		922 Hs.21	3004	chromosome 21 open reading frame 62	2.1
_	4280			4137	hypothetical protein ESTs, Weakly similar to AFGI_YEAST AFGI	2.1
	4478 4190				hemopoietic cell kinase	2.1
	4310		05249 Hs.2	714	forthead box G1B	2.1 2.1
60) 4210	64 A1245	432 Hs.1	01382	tumor necrosis factor, alpha-induced pro	21
	4164			79703 22531	KIAA0129 gene product ESTs, Weakly similar to \$59501 interfero	2.1
	4370 4593				gb:yd40e03.r1 Soares fetal liver spleen	21
	_ 402	239				2.1 2.1
6:				72814	hypothetical protein DKFZp434E1723 pregnancy-associated plasma protein A	21
	426 438			5874 184987	ESTE	2.1
			62714		gb:EST374787 MAGE resequences, MAGG Homo	21 21
_	404	561		0000	bromodomain adjacent to zinc finger doma	2.1
7				8858 19066	hypothetical protein DKFZp667O2416	2.1
		1175 W29 1867 AA3	1686 31886	. ,,,,,,,	ob:EST35757 Embryo, 8 week I Homo sapien	21
		604 W37	944 Hs.	4007	Sarcolemmal-associated protein	2.1 2.1
_	_ 409	9650 T084	190 Hs.	288969	HSCARG protein	2.1
7		1729 2675 AVAG	977653 Hs	75319	ribonucleotide reductase M2 polypeptide	2.1
		3675 AWS 8741 W37		184492	ESTs .	21
		7037 BE0	83936 Hs	.80976	antigen identified by monoclonal antibod	21 21
				.22895 .333045	hypothetical protein FLJ23548 ESTs	2.1
ď		9262 AA8 3108	332333 Ha	· sow		21
		6718 AW		289053		2.1 2.1
		0696 AI7	62757 Hs	.187660	putative Rab5 GDP/GTP exchange factor ho	2.1

				b:7B14E12 Chromosome 7 Fetal Brein cDNA	2.1
	409745	AA077391 BE620712	Hs.33026	ypothetical protein PP2447	2.1
	453485 418177	N44967	Hs.5663	STs	21 21
	457292	AI921270		nypothetical protein FLJ14251	21
5	454434	AA083558	Hs.261286	ESTs	21
	406085 424441	X14850	Hs.147097	H2A histone family, member X	2.1
	422726	U11690	Hs.1572	laciogenital dysplasia (Aarskog-Scott sy	21 21
	424576	BE154142	Hs.96833	ESTs Homo sapiens mRNA; cDNA DKFZp434L137 (fr	2.1
10	423660	AL045228 AF231919	Hs.130831 Hs.18759	KIAA0539 gene product	2.1
	403509 441940	AW298115	Hs.128152	ESTs	21
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15	423701 427239	AA329856 BE270447	Hs.174070	ubiquitin carrier protein	21
	459642	(BE243103		qb:TCAAP2E0949 Pediatric scute myelogeno	2.1 2.1
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-00	425159	I NM_004341	Hs.154868 Hs.279727	carbamoyl-phosphate synthetase 2, aspart Homo sapiens cDNA FLJ14035 fis, clone HE	2.1
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	426369	AF134157	Hs.169487	Kreisler (mouse) mai-related leucine zip ESTs	21
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	450704	H85157	Hs.40696 Hs.97960	ESTs ESTs, Wealtly similar to T51145 ring-box	2.1
30	427539 402028	AA405205	13.37300	Coro, ricary annua - review	2.1
30	405362				2.1 2.1
	414718	H95348	Hs.107987	ESTS ESTS	2.1
	433424		Hs.163566 Hs.44737	ESTS	2.0
35	444875 449523			chemotine (C-C motif) receptor 5	2.0 2.0
55	456072	H54381		gb:yq89a03.s1 Soares tetal liver spleen	2.0
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	448418 447250		Hs.17883	protein phosphatase 1G (formerly 2C), ma	2.0
40			Hs.4958	ESTs	2.0 2.0
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	41079 43687			ah Human H1 RNA	2.0 2.0
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	44630		Hs.9094 3 Hs.12650	ESTs S ESTs	2.0
	43658 45248			Homo sapiens cDNA FLJ13329 fis, clone OV	2.0
	43042	20 AW14002	7 Hs.2637	Homo sapiens cDNA: FLJ23449 fis, clone N	2.0 2.0
5(6 Hs.2723 Hs.898	3 Interleukin 20 dystrophia myotonica-protein kinase	2.0
	4144 4335			1 ESTs	2.0
	4279		2 Hs.9828	ESTs, Weakly similar to T20655 hypotheti	2.0 2.0
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5	5 4345 4543				2.0
	4435			2 ESTs	2.0 2.0
	4497	22 BE28007			2.0
6	O 4526			52 FSTs. Wealdy similar to ALUB_HUMAN ALU S	2.0
U	O 4123 4293			phosphorylase kinase, alpha 1 (muscle)	2.0 2.0
	435	63 AF2553	46 Hs.629		2.0
	400				2.0
6	453 5 419				20
•		529 T26460	Hs.225	io ESTs	2.0 2.0
		206 AB0114			2.0
		360 AA4484 660 A16588			2.0
-		660 Al6588 9030 Al3655	82 Hs.57	00 Homo sapiens mRNA for FLJ00016 protein.	2.0 2.0
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		5624 AF052 1668 T9996			2.0
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•		7698 R6183	7 Hs.79	O ESTs, Moderately similar to 184505 catcl	2.0 2.0
	42	6607 AA382			2.0
		9246 AW41 2564 Al148			2.0
	43	2682 AI376	400 Hs.15	9588 ESTs	20 20
	80 4	2140 BE29			2.0
)8215 BE61 17129 AJ381		OCB4 calcitonin gene-related peptide-receptor	2.0
			3680 Hs.5	1 A4440 - DMA	2.0
				_	

	434928	AW015595	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA 2.0
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	430603	AA148164	Hs.247280 Hs.318584	HBV associated factor novel C3HC4 type Zinc finger (ring finge 2.0
5	425905 401125	AB032959	10.01000	20
,	412939	AW411491	Hs.2186	eukaryotic translation etongation factor 2.0
	448740	BE250632	Hs.8026	sesum 2
	454390	AB020713	Hs.56966 Hs.77793	KIAA0906 protein 2.0 esrc tyrosine kinase 2.0
10	415012 410407	NM_004383 X66839	Hs.63287	enharia mhateria iX
10	403478	A00003		2.0
	456485	A1393037	Hs.97871	HOMO Saprens, Giore Invide. John Co.
	430294	A1538226	Hs.32976 Hs.303116	gramma nucleonada unang protestara samana samana nucleonada samana nucleonada samana protestara samana samana samana samana nucleonada samana
15	411669 451944	BE612676 AW445218	Hs.210876	FSTe Liv
13	436395	AJ227900	10.210010	gb:Homo sepiens partial mRNA; ID EE2-16B 2.0
	456457	AA252905	Hs.194477	E3 chaddiniu adase swords
	449123	D50920	Hs.23106	KIAADI SU gene produce Harma sugene br>Harma sugene
20	409214	AW405967 AW351491	Hs.333388 Hs.334853	humathatical pentain FL 173544
20	437619 453348	BE272318	Hs.8595	hypothetical protein FLJ12438 2.0
	424382	AA351898	Hs.23539	ES18 20
	447079	AA280057	Hs.105280) ES18, Weakly samuar to 00000023.2 [11.60
25	449501	AI652924 X98411	Hs.231942 Hs.121555	Commein IF
25	422893 412125	Y17114	Hs.73393	eves absent (Drosophila) homolog 4
	434845	BE267057	Hs.32532	t hypothetical protein R32184 1
	410422	AL042014	Hs.33469	8 Homo sapiens, cone moc. 1200. In the sapiens
20	430255	AK000703	Hs.32382 Hs.21275	2 CCT-
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	442690	AI014727	Hs.16004	ESIS, Webby Similar to Tart Allisant Table 2.0
25	454277	AW295069		on ESTA Maderately similar to ALUT HUMAN A
35	426910 402798		ns.15000	2.0
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40	TABLE	9B:	Injuse Fos pro	beset Identifier number
40	Pkey: CAT m		Gene cluster nu	
	Access		Genbank acces	ssion numbers
		CAT Nor	iber Accessi	on
45	Pkey 40790		1 AW103	986 BE156395 BE156391 BE156190 BE156184 BE156366 BE156364
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55	4116 4118			5749 BE179419 BE179492
55	4122	25 128410		2042 N77591 6614 AW946622 AW946663 AW946667 AW946615 AW946619
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	4123 4132		3 1 RF07	5035 BE074999 BE075006 BE075005 BE075032 BE075008 BE075037
60	4138		5 1 R\$17	67 BE152515 Z44834 HZ3397
Ų.	414		13_1 BE29	7904 BE294312
	414			
	415 415		31_1	08 F06295 R13085 10 F07926 R53367
65	415		16_1 Z454	81 F12393 T74437
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		8856 1 79 64 9217 1829!		005371 AA235243 AA411737 AW969068 AA408543
7		9217 1829! 9225 1830:	274 1 177	7077
•		9311 1837	93_1 AA	89591 AW974261 AA236240 A077451 AAB31399 AW974262 258835 AW968316 AA258918 AW8A3305 R14744 A1880388 BE071923 R36280
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        55
                          TABLE 9C:
                                                         Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunharn, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunharn, et al. (1999) Nature 402:489-495.
                          Pkey:
                          Ref:
                                                          Indicates DNA strand from which exams were predicted. Indicates nucleotide positions of predicted exons.
         60
                           Strand:
                           Nuposition:
                                                                      Strand
                                                                                           Nt position
                                                                                           185223-188402,186878-187275
91888-92018,98131-98294,99474-99570
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400859
                                              7465000
                                                                      Plus
                                                                      Minus
                                              9757499
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                                                                                            173258-173631
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7232177
                                                                      Minus
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                                                                       Plus
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           70
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                             401324
401384
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Plus
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110326-110491
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			Minum	CAMPA CENTS
	****	9796344	Minus Minus	64925-65073 195342-195511
		9798099 9909420	Plus	
	402604 402627	9931216	Plus	20393-20767 12138-12272,16487-16628,17654-17798,18494-18621,18933-19089,20669-20790,21134-21298,22866-22973,23686-23820,26626-
5	402021	33312.0	:	76895, 79279-7946 9
,	402721	8969253	Minus	144428-144715
	402798	3355547	Plus	23596-23867
	402856	9801288	Minus	90119-90411
	403048	4210991	Plus	44275-44592,49658-49955
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	403142	9444521	Plus	89286-90131 67762-67940,68595-68856,70394-70507
	403166	9838127	Minus Plus	116458-116564
	403478	9958258 7331517	Minus	157184-157415
15	403680 403751	7229815	Minus	158794-160929
13	403790	8084957	Minus	87825-87947,69835-90002
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	403857	7708910	Minus	2524-3408
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	404054	3548785	Plus	66713-69175 2795-2969
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25	404108	8247074 9930793	Plus	168338-169248
	404170 404185	4572584	Minus	129171-129327
	404240	5002624	Minus	116132-116407,116653-116922
	404295	9856663	Minus	75747-75947 · · · · · · · · · · · · · · · · · · ·
30	404299	6738652	Minus	3826-4025
	404366	9964977	Plus	96589-96801
	404554	7243881	Plus	42637-42839
	404561	9795980	Minus	69039-70100
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	404652	9856648	Minus	173763-174294
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	405159		Ptus	79659-79804
	405258		Plus	129930-130076
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	40580		Plus	109758-111166 62383-62583
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	40591 40602		Minus	177459-177829
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	4064			52758-53211
	4065			11377-11509 13096-13334
65	4056	10 8312226	i Plus	1907

TABLE 10A: ABOUT 582 GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES
Table 10A first about 582 genes significantly down-regulated in glioblastoma compared to normal adult CNS fissues. These were selected from 59680 probesets on the
Allymetriz/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" stational was greater than or equal to 3. The "average" normal CNS issues. The "average" adults array to the 85th percentile amongst various tumor samples. In order to remove
gene-specific background levets of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the
gene-specific background levets of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the
gene-specific background levets of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the
gene-specific background levets of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the
gene-specific background levets of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the
gene-specific background levets of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the
gene-specific background levets of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the
gene-specific background levets of non-specific hybridization.

Unique of the 10th tissues to 10th percentile number
gene-specific background levets of non-specific hybridization.

Unique of the 10th tissues to 10th tissues t 70

75

80	Pkey	ExAcon	UnigenelO	Unigene Title	R1
	453655	AW960427	Hs.79059	transforming growth factor, beta recepto	138.7
	417275	X63578	Hs.295449	parvalbumin	29.0
	430829	AW451999	Hs.194024	ESTs	25.7

189

						22.6
	410657	AF063228	Hs.65248	dynein	cytoplasmic, intermediate polype	22.6 21.2
	419954	D14720 N46243	Hs.93883 Hs.110373	CCT-	protein zero (Charcot-Mane-Tooth Highly similar to T42626 secreted	18.5
	459247 416133	NM_001683	Hs.89512	ATPor	o Case transporting, piasma memora	15.5 15.2
5	415018	AW138239	Hs.78977		tein convertase subtilisin/kexin t	14.B
	417167	AW206437 H06129	Hs.4290 Hs.7459	ESTs cyclic	AMP-regulated phosphoprotein, 21	13.4
	433940 413324	V00571	Hs.75294	andia	emoin releasing harmone	13.1 12.6
	439830	AA846666	Hs.151489		Wealthy similar to XE7_HUMAN PROTEI	12.6
10	408068	AW148652 NM_004415	Hs.167398 Hs.74316	ESTs desm	oplakin (OPI, OPII)	. 12.5
	412636 429096	AB011106	Hs.196012		0534 protein	12.2 12.2
	412638	AA910199	Hs.203838	EST	Wealdy similar to PN0099 son3 prot	12.1
1.5	423690	AA329648 AI264155	Hs.23804 Hs.152981	COP	diacylolycerol synthase (phosphagga	11.9
15	455844 418318	U47732	Hs.84072	trans	membrana 4 superfamily member 3	10.9 10.8
	442593	R39804	Hs.31961	EST		10.4
	446353	AJ290919 AW977318	Hs.15366 Hs.19448	· cet		10.3
20	420290 414220	BE298094	152.154.15	gb:6	01118231F1 NIH_MGC_17 Homo sapiens c	10.3 10.2
20	414290	A1568801	Hs.71721	EST	s Libinding motif protein BB	10.0
	426365	AA376667 R38698	Hs.10283 Hs.12382	ES1	S	10.0
	414937 419643	F06066	Hs.91791	che	mosome 11 open reading frame 25	9.5 9.5
25	407173	T64349	11. 4072		c10d08.s1 Stratagene tung (937210) H	9.5
	412454 439366	R55745 AF100143	Hs.1673: Hs.6540	fibri	ablast growth factor 13	9.4
	415315	F12240	Hs.2506	is pro	thymosin, alpha (gene sequence 28)	9.3 9.2
••	441790	AW294909				9.1
30	448117 400661	H49129	Hs.1729			9.0
	433558	AA833757			Ts. Wealdy similar to T24435 hypotheti	9.0 9.0
	412453		Hs.1673 Hs.4899		118 ronectin leucine rich transmembrane p	8.9
35	408920 409031				Ts .	8.7 8.3
33	428106		Hs.1824	70 PI	0010 protein	8.2
	446544				STS, Wealdy similar to Unknown (H.sapie eath-associated protein kinase 2	8.2
	423479 439480			316 E	STs, Weakly similar to S33990 finger pr	8.2 8.0
40	41803		Hs.833	37 ta	tent transforming growth factor beta b	8.0
	45649		Hs.972 7 Hs.101	016 S	nall Inducible cytokine subfamily A (Cy targardt disease 3 (autosomal dominant)	8.0
	41020 41450			so H	nmo spriens mRNA: cDNA DKFZp564B1264 (1	8.0 7,9
	40842	8 NM_014	787 Hs.448	96 D	naJ (Hsp40) homolog, subfamily 6, membe	7.9
45	43707				STs ypothetical protein FLJ22344	7.9
	40843 43815)59 t	ransforming growth factor, beta recepto	7,9 7.8
	44020	9 H05049	Hs.22	269 1	eurexin 3 STs, Weakly similar to T00331 hypotheti	7.8
50	4081				nuclear receptor subfamily 4, group A, m	7.8
30	41741 4105			412	-homosome 9 open reading frame 5	7.8 7.7
	4296			1388	Homo sapiens BAC clone CTB-60N22 from 7q	7.7
	4058 4217		68 Hs.10	7872	hypothetical protein FLJ20761	7.7
55	4263	56 BE5368	36 Hs.98	682	hypothetical protein FKSG32	7.7 7.7
	4234	40 R25234			contactin 1 ESTs	7.6
	4451 4162			16304 1170	KIAA0227 protein	7.6
	4240		3 Hs.1	13434	contactin 1	7.6 7.5
60	374	479 R6186	6 Hs.1	01277	ESTs	7.5
	405 421		2154 Hs.1	25812	ESTs	7.4
		025 AW88	7434 Hs.1	1810	CDA11 protein	7.4 7.2
-	459	476 BE185		36345	gb:ILS-HT0731-110500-087-c08 HT0731 Homo ESTs	7.1
6		673 AA744 836	1000 115-1	30343	2313	7.1
		958 AB020		2653	KIAA0844 protein	7.1 7.1
	430	152 AB00		234642 155849	aquaporin 3 ESTs	7.1
7		9474 AW98 1780	10013 112.	1330-3		7.1 7.0
•		6052 AA35			gb:EST67699 Fetal lung II Home sapiens c	7.0
	42	3605 AF04		129887 151143	cadherin 19, type 2 ESTs	7.0
		3098 AW19 9511 Al438		296261	augnine auclectide binding protein (G pr	6.9 6.8
7	75 45	1285 AW1	37912 Hs	227583	Homo sapiens chromosome X map Xp11.23 L-	6.8
				.184216 .293490	DKFZP564C152 protein ESTs, Wealdy similar to I38022 hypotheti	6.8
		19273 BE27 13155 R54		.23772	ESTs	6.8 6.8
	45	50561 R496	674 Hs	.25909	ESTs	6.8
ł				.288215 .128204	FSTs	6.8
			18315 H:	.280776	tankyrase, TRF1-interacting ankyrin-rela	6.7 6.6
				.209569	ESTs	0.0
					190	

	415681	A1379882	Hs.72630	ESTs	6.5
	413510	F13044		ab:HSC3HH101 normalized infant brain cON	6.4
	427992	Y15014		UDP-Gal:betaGicNAc beta 1,3-galactosyftr	6.4 5.4
_	453344			ESTs	6.4
5	450642	R39773	Hs.7130 Hs.232165	copine IV polycythemia ruhra vera 1; cell surface	6.4
	432251 429322	AW972983 D86984	Hs.199243	KIAA0231 protein	6.4
	444927	AW016637	Hs.199425	ESTs	6.4
	447482	AB033059	Hs.18705	KIAA1233 protein	6.4
10	400332	S66407	Hs.248032	FLT4	6.3
• •	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	6.3 6.3
	448129	AW244073	Hs.145946	ESTS	6.3
	454076	AW204712	Hs.61957	ESTs gb:EST69040 Fetal lung II Homo sapiens c	6.3
15	425526 421913	AA359933 AJ934365	Hs.109439	osteoglycin (osteoinductive factor, mime	6.3
13	434273	AA913143	Hs.26303	ESTs	6.2
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	6.2 6.2
	451301	AI769514	Hs.209890	EST	6.2
30	430754	AW862610	Hs.157068	ESTS	6.2
20	438356	AA805530	Hs.48527 Hs.119598	ESTs ribosomal protein L3	6.2
	422743 453355	8E304678 AW295374	Hs.31412	Homo sapiens cDNA FLI11422 fis, clone HE	6.2
	425388	AW081394	Hs.97103	ESTs	6.2
	452502	AI904296		gb:PM-BT046-220199-286_1 BT046 Homo sapi	6.1
25	402548			•	6.1 6.1
	457534	AJ761307	Hs.232226	ESTS	6.1
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	6.1
	404958 432501	BE546532	Hs.25682	Homo sepiens mRNA for KIAA1863 protein,	6.1
30	442979	AW440782	Hs.174743	ESTs	6.1
50	422262	AL022315	Hs.113987	tectin, gatactoside-blading, soluble, 2	6.0
	408713	NM_001248	Hs.47042	ectonucleoside triphosphate diphosphohyd	6.0 6.0
	454065	BE394588		gb:601311808F1 NIH_MGC_44 Homo sepiens c	5.9
25	430004	U27768	Hs.227571	regulator of G-protein signalling 4	5.9
35	401521 425087	R62424	Hs.126059	ESTs	5.9
	446298	AF187813	Hs.14637	kidney- and liver-specific gene	5.9
	417761	R13727	Hs.21435	ESTs	5.9
4.0	424806	AA382523	Hs.105689		5.9 5.9
40	441695	T12411	Hs.183745		5.9
	457483	AB034694	Hs.272558 Hs.94002	endomucin-1 ESTs	5.8
	417175 437483	R44558 AL390174	715.54002	gb:Homo sapiens mRNA; cDNA DKFZp547J184	5.8
	436427	AI344378	Hs.143399		5.8
45	411939		Hs.146246		5.8
	459053		Hs.21036	ESTS	5.7 5.7
	411052			gb:MR1-ST0206-130400-023-d06 ST0206 Homo hypothetical protein bk125H2.1	5,7
	431063		Hs.32684 Hs.60257		5.7
50	450382 408478				5.7
50	442675		Hs.13089	7 ESTs	5.7
	445443		Hs.13422	8 ESTs	5.7 5.7
	400865			S ESTs	5.5
55	459080 407957		Hs.29085 Hs.88845		5.6
25	43198				5.6
	42570			55 kruppel-related zinc finger protein hcKr	5.6
	44223				5.6 5.6
60	42299		2 Hs.2962		5.6
60	45714				5.6
	42835 41592				5.5
	40209		113.1031		5.5
	44052		Hs.2114	71 ESTs	5.5
65	44440				5.5
	41787				5.4 5.4
	45823				5.4
	43070		Hs.2506 Hs.4494		5.4
70	45618 4274				5.4
, ,	4373			386 ESTs	5.4
	4556	17 BE07807	0	gb:CM1-BT0614-160300-149-f02 BT0614 Homo	5.4 5.3
	4292				5.3 5.3
76	4278		15 Hs.981 Hs.463		5.3
75	4085 4442				5.3
	4228		Hs.332		5.3
	4031			• •	5.3
-	4180	26 BE3797			5.3
80					5.2 5.2
	4315		Hs.277		5.2
	4319				5.2
	4374	(ATM)	- 110.16	···	

	438285	AA782845	Hs.2279	O ESTs		5.2 5.2
	439901	N73885	Hs.1241			5.2
	438507	AA809052	Hs.2112 Hs.1976	24 5014		5.2
5	449222	AW293984 AK001507	Hs.306		sapiens clone FLB6914 PRO1821 mRNA,	5.2 5.2
)	402834 419042	T81429	Hs.221	DES EST		5.2
	438777	AA731199	Hs.293			5.1
	445071	AI280245	Hs.149 Hs.256			5.1
10	408016	AW136827 AA934589		AC ECT	•	5.1 5.1
10	412047 436953	AW959074		AR HOT	o sapiens cDNA FLJ13097 fis, clone NT	5.1
	436773	AW07862	9 Hs.821		and SFRS1 interacting protein 1	5.1
	409263	AAD69573				5.1
1.5	453830	AA53429E AA02288E				5.1 5.1
15	459580 417616	R07728	Hs.26	RAAR EST	īs	5.1
	423457	F08208	Hs.28	3844 sim	ilar to rat tricarboxylate carrier-6	5.0
	441535	AL13573		240	sphalidylinositol binding clathrin as ulator of G-protein signaling 7	5.0
30	416490		8 Hs.79 He 10	7010 He	ma conjuga cOMA FL 112965 fis, clone N1	5.0 5.0
20	417284 447135			ah.	who and a stratagene lung (93/210) in	5.0
	448505		8 Hs.21	1597 Ho	mo septens mRNA full length insert con-	4.9
	442240	A179188		92719 ES	iTs atine kinase, mitochondrial 1 (ubiqui	4.9
~ ~	45939			53998 cm 81304 pu	tative gene product	4.9
25	42797			0040 F	77.	4.9 4.9
	43294 44019		93	gt	:601345159F1 NIH_MGC_B Homo sapiens cD	4.9
	44404	7 AI09745	2 Hs.1	35095 E	omo sapiens cDNA FLJ12048 fis, clone HE	4.9
	41604	0 AW819		89044 H	omo sapiens cono FLJ 13752 fis, cione PL	4.8
30	44492				STs	4.8
	43667				STs	4.8 4.8
	44807 40897			293549 E	STS	4.8
	4126	22 AW664	708 Hs.		STs	4.8
35	4149	43 D8064		124193 8	S7s ypothetical protein DKFZp761C121	4.8
	4292					. 4.8 4.8
	4535 4079			*****	James estricate talends CINA UKF 20009U 1204 \	47
	4410			.17558	Homo sapiens cONA FLJ 14446 fis, clone HE	4.7
40		30			gb:QV3-BN0046-150400-151-g09-BN0046 Homo	4.7
, -	455				ALAVESTICO CI C Homo sabiens CUNA Cione	4.7
	446			3.133244	melanoma-derived leucine zipper, extra-n	4.7 4.7
	443	347 MUSZ 176				4.7
45		577 BE06		s.79381	grancalcin Homo sapiens cDNA FL/10919 fis, clone OV	4.7
•		221 AK00		s.296543	hypothetical protein	4.7
		480 AL13		ls.98173 ls.46925	eyes absent (Drosophila) homolog 3	4.5
		800 Y102		ls.272091	ESTs	4.6 4.6
5	0 40	5161 AF12 4793				4.6
,	43	0895 U66		15.248121	G protein-coupled receptor 22	4.6
				Hs.55022	ESTs ESTs	4.6
				Hs.164166 Hs.6594	CAY-	4.6 4.6
5				Hs.311736	LL ONA companse from clone RP1-238D15	4.6
ر	41	8274 AI4	58587	Hs.128677	Human DNA sequence from clone RP 1-30024	4.6
	43	5475 W5		Hs.107057 Hs.266263	ESTs Homo sapiens cDNA FLJ14115 fis, clone MA	4.5
				Hs.46988	ESTs	4.5
-			64022	Hs.138207	ESTs TO 425 handhall	4.5 4.5
•			408145	Hs.185254	ESTs, Weakly similar to T24435 hypotheli gb:601301177F1 NIH_MGC_21 Homo sapiens c	4.5
		14630 BE	410857		gb:yu56e10.r1 Soares fetal liver spleen	4.5
			4314			4.5
		01024	815523	Hs.76930	synuclein, alpha (non A4 component of am	4.5 4.5
'			497900	Hs.33067	ESTs	4.5
		405138			gb:PM2-HT0225-031299-003-f11 HT0225 Homo	4.5
			E147225	11- 20463	CCTe Weakly similar to 138022 hypother	4.5
	70	_	1803168 56087	Hs.28462 Hs.11248		4.4
	70		A922009	Hs.15026	9 ESTs	4.4
		429876 A	8026977	Hs.22597	4 KIAA 1054 protein	4.4
		445481 A	W661846	Hs.14883	86 ESTs ISL1 transcription factor, LIM/homeodoma	4.4
	75		IM_002202	Hs.505	IOF (ROSSISSON ISSUE)	4.4
	75	404769 444331	W193342	Hs.2414	4 ESTs	4.4 4.4
		429726	W628326	Hs.2715	1 ESTs	4.4
		449093	AB035356	Hs.2299		4.4
	00		AA056203	Hs.2733 Hs.1796	co	4.4
	80		N59294 R23053	ns.1170	objyh31a05.r1 Soares placenta Nozhir homo	4.4
		417888 419656	AB002314	Hs.9207	JUDONO SOSO RIFINANIA	4.4
		425864	U56420	Hs.159		
					10	17

192

		A3A/E1000	B Hs.40	037 F	STs		4.4
	435078 413493	AW51888 BE144444			NAMP.	0-HT0168-141199-002-09 HT0168 Homo	4.3 4.3
	432712	AB016247	Hs.28	8031	terol-	C5-desaturase (fungal ERG3, delta	4.3
•	459650	R25754	Hs.30	11185	STs		4.3
5	404828 423782	AI472209	Hs.37		ESTs		4.3 4.3
	426867	AA45096			ESTS		4.3
	426802 457353	AA38518 X65633		40444	ESTs melan	ocortin 2 receptor (adrenocorticotr	4.3
10	412112	BE18034			gb:R0	3-HT0622-130400-012-807 HT0022 Holio	4.3 4.3
• •	401522	N47812		06198	CGI-3	35 protein o sapiens cDNA FLJ11570 fis, clone HE	4.3
	419055 410171	A136538- H07892		1571 2431	EST		4.3 4.3
	419564	U08989	Hs.9	1139	solut	e carrier family 1 (neuronal/epithe	4.3
15	458789	AL15746		125825	Hom	o sapiens cDNA FLJ20848 fls, clone AD NO-CT0225-100400-187-608 CT0225 Homo	4.3
	455040 438533	AW8527 AJ44026	365 6 Hs.1	170673	CCT.	a Manakha elmilar in T24K32 hyddineu	4.3 4.2
	459005	AA4476	79 Hs.	144558	CCT	e, Weakly similar to ALU1_HUMAN ALU S nosine deaminase, RNA-specific, B1 (h	4.2
20	418489	U76421		85302	atter	lomo sapiens clone 23671 mRNA sequenc	4.2
20	433389 454356	AF0381 AW390		11522	Burn.	who tival omitein from X025	4.2 4.2
	442339	BE2996	68 Hs.	227591	CCI	s, Wealdy similar to 1901303A Leu zip 1TH277 HTCDL1 Homo sapiens cDNA 5/3	4.2
	421249	AA285		296276	go:		4.2
25	443998 452197	AI6206 AW023	1595 Hs	.232048	ES.		4.2 4.2
2.7	451117	AA015	752 Ha	.205173	ES	Ts deoside phosphorylase	4.2
	404501	AW247 R2332		.75514 .41693	Dn:	aJ (Hsp40) homolog, subfamily B, membe	4.2
	410378 422528			.118087	KI/	A0610 protein	4.2 4.1
30	440323	AA970	614 H	.127992	ES	Ts romosome 1 open reading frame 7	4.1
	425767 434460			s.159483 s.3852	K	AA0368 protein	4.1
	410362		11 H	s.93164	pro	oprotein convertase subtilisin/kexin t	4.1 4.1
26	41312			s.142678 ls.6634	E	STs amo sapiens cDNA: FLJ22547 fis. clone H	4.1
35	40940 45023			s.17538	= =	eT-	4.1 4.1
	44975	4 H008	20 F	ls. 3 0977	E	STs, Weakly similar to 834087 hypotheti b:tz49b05.y1 NCI_CGAP_Bm52 Homo sapien	4.1
	42181		18255 3802 F	ts.13618		STs	4.1
40	40849 43026			ls.23722	5 h	ypothetical protein HT023	4.1 4.1
-,0	43410	1 AA5		ts.25959		JAA1822 protein	4.1
	45183 41177		157	Hs.16970		:ST8 b::QV4-HT0538-040500-193-f05 HT0536 Homo	4.1 4.1
	4376			Hs.15307		NAIAD 70 mmlain	4.0
45			69153		•	p:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	4.0
	4002 4298		37278	Hs.2258	41 1	DKFZP434D193 protein	4.0 4.0
	4531	65 574	727	Hs.3204		aspartoacylase (aminoacylase 2, Canavan	4.0
50	4180		633	Hs.4847		ESTS	4.0
30) 4053 4279		206512	Hs.1869		ESTs	4.0 4.0
	428	775 AA	434579	Hs.1436		ESTs ESTs	4.0
	449- 453		001373 /021407	Hs.5982 Hs.2106		hunothetical protein	4.0 4.0
5:		407 AV	V968614			gb:EST380690 MAGE resequences, MAGJ Homo	4.0
			A_003947	Hs.800 Hs.102		huntingtin-associated protein interactin ESTs, Moderately similar to S65657 alpha	4.0
			5158 \352026	Hs.943	19	VPS10 domain receptor protein	4.0 4.0
_	_ 429	628 H	19604	Hs.132		ESTs ESTs	4.0
6			12079 W502122	Hs.332	3/3	gb:UI-HF-BROp-afr-c-08-0-UI-1 NIH_MGC_5	4.0 4.0
			A437061	Hs.140		orovineticin 1 precursor	4.0
			A662913	Hs.190		ESTs, Weakly similar to A45010 X-linked ESTs	4.0
6			A402713 :17758	Hs.22		Homo sepiens cDNA FLJ14323 fis, clone PL	3.9 3.9
·			A115575	Hs.11		ESTs	3.9
		5629 10299 <i>f</i>	J056871	Hs.15	276	ESTs	3.9
			25935	Hs.86		EQT.	3.9 3.9
7	70 ≪	5752	¥F230801	£1 a.e	2177	gb:Homo saplens growth hormone receptor Homo saplens mRNA; cDNA DKFZp547G133 (fr	3.9
			241305 A1307802	Hs.30 Hs.13		ESTE Weakly similar to T43458 hypotheti	3.9
		42257	AW503831	Hs.32	23370	Human EST clone 25267 mariner transposon	3.9 3.9
	4	22563	BE 299342	Hs.11	9348 23017	hypothetical protein FLJ13119 Human unproductively rearranged 1g mu-ch	3.9
			M21388 AW014723		23017 34512	ESTS	3.9 3.9
	4	12677	AW029608	Hs.1	7384	ESTS CONTRACTOR OF CASE OF	3.9 3.9
			AL117352	Hs.1	20828		3.9
		105377 114376	BE393856		6915	ESTs, Wealdy similar to 16.7Kd protein (3.9 3.9
	•	153341	AI758912	Hs.2	9634		3.9
		431960 416854	AW241821 H40164		10192 10298		3.9
						193	

	422746	NM_004484	Hs.119651	ESTs glypican 3	3.9 3.9
	452346	BE243534		gb:TC8AP1D0885 Pediatric pre-8 cell acut	3.9 3.8
-	414666			glypican 5	3.8
5	418217	A1910647 AA234223		ESTs ESTs	3.8
	419118 445017 405867	A1205493		EST6	3.8 3.8
	422760	BE409561		gb:601299865F1 NIH_MGC_21 Homo sapiens c	3.8
10	453863	X02544	Hs.572	orosomucoid 1	3.8 3.8
	457821	H47166	Hs.124322	ESTs, Weakly similar to A47582 B-cell gr	3.B
	457330	AB013818 AL047034	Hs.247220 Hs.119747	peroxisome biogenesis factor 10 ESTs	3.8
	435600 456083	U46922	Hs.77252	fragile histidine triad gene	3.8
15	413341	H78472	Hs.191325	ESTs. Wealdy similar to T18967 hypotheti	3.8
	449057	AB037784	Hs.22941	KIAA 1363 protein	3.8
	421855	F06504	Hs.27384	ESTs, Moderately similar to ALU4_HUMAN A	3.8 3.8
	414764	AW013887	Hs.72047	ESTs	3.7
20	404391 433629	R13140	Hs.13359	ESTs	3.7
20	424738	AI963740	Hs.46826	ESTs	3.7
	401315				3.7
	407706	AA191085	Hs.26612	ESTs, Moderately similar to \$23650 retro	3.7 3.7
25	440530	AA888546	Hs.174187 Hs.273781	ESTs ESTs	3.7
23	433930 409662	AA620338 AW452320	Hs.279726	ESTs	3.7
	437268	A1754847	Hs.227571	regulator of G-protein signalling 4	3.7
	445688	AJ248205	Hs.153244	EŜTS	3.7 3.7
20	408593	R19566	Hs.197617	ESTs	3.7
30	417091	AA193283 AW885606	Hs.291990 Hs.5064	ESTs ESTs	3.7
	448556 423135	N67655	Hs.26411	ESTS	3.7
	400135	1.07.000			3.7
	459150	BE155356		gb:PM1-HT0350-160300-009-d06 HT0350 Hamo	3.7 3.7
35	457221	AW383197	Hs.218260	ESTs	3.7
	451660	AIB07927 BE247275	Hs.249601 Hs.151787	ESTs U5 snRNP-specific protein, 116 kD	3.7
	401600 446818	Al342668	Hs.279765		3.7
	447795	AW295151	Hs.163612		3.7
40	427562	R56424	Hs.26534	ESTs	3.6 3.6
	412258	AA376768	Hs.324841	hypothetical protein FLJ22622 gb:QV4-HT0316-091199-028-d05 HT0316 Homo	3.6
	454339 439274	AW381980 AF086092	Hs.48372	ESTs	3.6
	452381	H23329	Hs.290880		3.6
45	422897	AA679784	Hs.4290	ESTs	3.6
	429656	X05608	Hs.211584		3.6 3.6
	421908	AW935200 AW385129	Hs.285814 Hs.41717		3.6
	407978 426452	AW814271	Hs.121647		3.6
50	400685				3.6
	417154		Hs.21388		3.6 3.6
	447178		Hs.160891 Hs.13484		3.6
	423893 449231		Hs.29857		3.6
55	411607			gb:RC1-CT0252-170200-025-h02 CT0252 Homo	3.6
	405977			A FAT.	3.6 3.6
	441470		Hs.30198 6 Hs.12981		3.6
	423568 441235		Hs.13557		3.6
60	450238		Hs.24684	KIAA1376 protein	3.6
	425384	AF052150			3.6 3.6
	426775		Hs.10882 Hs.77439		3.6
	414831 416876				3.6
65	400876				3.6
	425153	3 AW02319	3 Hs.27040		3.6
	43222			gb:an03c03.x1 Stratagene schizo brain S1	3.5 3.5
	41504			gb;HSC3JD031 normalized infant brain cDN	3.5
70	40153 44649		Hs.1534	60 ESTs	3.5
	43132			ESTs, Wealdy similar to 2109260A B cell	3.5
	44589	8 AF07062	3 Hs.1342	3 Homo sapiens clone 24458 mRNA sequence	3.5
	45590			gb:PM1-HT0350-190400-013-b08 HT0350 Homo	3.5 3.5
75	41642			6 eutraryotic translation initiation factor gb:CM0-8T0365-061299-122-g09 BT0365 Homo	3.5
13	45569 40567		•	Barausa i anna an i ran, i se Ban a i anna i mua	3.5
	41820		Hs.3477	72 ESTs	3.5
	42538	33 D83407	Hs.1560	Down syndrome critical region gene 1-lik	3.5 3.5
0.0	4170				3.5
80) 40831 41770		'8 Hs.444' Hs.191		3.5
	4456		Hs.149	297 ESTs	3.5
	4087				3.5
				104	

	413164	BE068494		ob:MF	1-BT0371-050500-009-a12 BT0371 Homo	3.5
		BE386764		იხრი	1273249F1 NIH MGC_20 Homo sapiens c	3.5 3.5
		AB033089	Hs.32452	Homo	sapiens mRNA for KIAA1263 protein.	3.5 3.5
-	415621	A)648602	Hs.55468	ESTS	hetical protein MGC12938	3.5
5	454437	AI248173 AI343931	Hs.191460 Hs.149383	ESTs		3.5
	446066 423374	AB037770	Hs.127656	KIAA	1349 protein	3.5
	419347	C15944	Hs.90005	SUDE	forcervical ganglia, neural specifi	3.5 3.5
	418516	NM_006218	Hs.85701	phos	phoinositide-3-kinase, catalytic, al	3.5
10	451776	W45679	Hs.169854	hypo	thetical protein SP192 n-like growth factor binding prote	3.5
	432305 456995	M62402 T89832	Hs.274313 Hs.170278	EST		3.5
	403323	103032	100.1702.0			3.5
	425022	M95724	Hs.154207		omere protein C 1	3.5 3.4
15	439394	AA149250	Hs.56105	EST		3.4
	433803	AIB23593 AI266484	Hs.27688 Hs.31570	EST	s. Wezkly similar to KIAA1324 protein	3.4
	450715 411474	AW848427	13,515/0	ab:II	.3.CT0214-150200-075-H10 CT0Z14 H0mb	3.4
	415076	NM_000857	Hs.77890	qua	wiata cyclasa 1, soluble, beta 3	3.4 3.4
20	423826	U20325	Hs.1707	COC	sine- and amphetamine-regulated trans	3.4
	459495	BE544158	Hs.97540	go:t	01076707F1 NIH_MGC_12 Home sapiens c	3.4
	427173 408112	BE255017 AW451982	Hs.248613	EST		3.4
	446092	N33522	Hs.145894	ES.		3.4 3.4
25	416868	A1656856	Hs.292597	ES		3.4
	458234	BE551408	Hs.127196	ES	nc07d11.s1 NCI_CGAP_Pr1 Homo sapiens	3.4
	419555	AA244416 BE312991		gb:	601150275F1 NIH_MGC_19 Homo sapiens c	3.4
	414314 400425	AY004252	Hs.287385	PR	domain containing 12	3.4
30	414366	BE549143			601076456F1 NIH_MGC_12 Homo sapiens c	3.4 3.4
	434053	AW445136	Hs.134946		iTs	3.4
	449997	A1683052 A1636047	Hs.201577 Hs.197623		AA1829 protein iTs	3.4
	433461 428006	AA41B743	Hs.98306	K	AA1862 protein	3.4
35	424695	U58331	Hs.151899) sa	rcoglycan, delta (3SkD dystrophin-asso	3.4 3.4
	443294	AI733625	Hs.13305		STs	3.4
	428212	AW444451 AA551569	Hs.13481 Hs.27203		STs rpothetical protein PRO2822	3.4
	457673 446390		Hs.14992		pothetical protein FLJ11151	3.3
40	428536		Hs.2288	٧i	sinin-like 1	3.3 3.3
	426597	AA382250	Hs.14560		ST8	3.3
	410366		Hs.30268 Hs.12797		ypothetical protein STs	3.3
	458258 401738		ns.12/3/			3.3
45	409038		Hs.50002		mall inducible cytokine subfamily A (Cy	3.3 3.3
	425785	T27017	Hs.1595	28 1	forno sapiens cione 24400 mRNA sequence	3.3
	433328				STs, Weakly similar to \$65824 reverse t aldehyde dehydrogenase 1 family, member	3.3
	414541 434998				STs	3.3
50	45635		Hs.9357	4 1	nomeo box D3	3.3 3.3
	42652			38	sodium channel, vottage-gated, type I, b cell division cycle 25C	3.3
	45426		9 Hs.656 Hs.1915		lotate hydrofase (prostate-specific memb	3.3
	40030 43407			51	Homo sapiens PRO1412 mRNA, complete cds	3.3
55	43660		Hs.1668	117	ESTs	3.3 3.3
	44920				Down syndrome critical region gene 4	3.3
	41793 42331		Hs.1700 Hs.1244		ESTs Homo sapiens cDNA FLJ14218 fis, clone NT	3.3
	43652		Hs.524		fatty acid binding protein 1, liver	3.3
60	45340	36 Al 19298			hypothetical protein FLJ14451	3.3 3.3
	42016				ESTs ESTs	3.3
	44783 4198				proenkephalin	3.3
	4445				ESTs	3.3
6:	4185		18 Hs.853		Homo sapiens mRNA; cDNA DKFZp564D1462 (f	3.2 3.2
	4152				ESTs	3.2
	4181				eSTs phosphoinositide-3-kinase, catalytic, be	3.2
	4303 4216				nh FST378726 MAGE resequences, MAGI Homo	3.2
70	0 4323		49 Hs.27		Homo sapiens cDNA FLJ10229 fis, clone HE	3.2 3.2
•	4088	306 AW847	814 Hs.28		Homo saciens cONA: FLJ21532 fis, clone C	3.2
	4004				Homo sapiens winged helix/forkhead trans hypothetical protein FU10971	3.2
	4460				ESTs, Weakly similar to similar to ankyr	3.2
7	5 403					3.2
•	452	971 AI8738		789	ESTs	3.2 3.2
	454	186 BE141	030		gb:MR0-HT0067-201099-002-h11 HT0067 Homo	3.2
	401					3.2
8	0 401 0 457	949 452 AW972	2675		gb:EST384766 MAGE resequences, MAGL Homo	3.2
		100 Al6932	231 Hs.12	26043	chromosome 21 open reading frame 51	3.2 3.2
	448	1440 AA173	467 Hs.6		p21/Cdc42/Rac1-activated kinase 1 (yeast	3.2
	421	200 AA284	1811 Hs.21	54433	ESTs	J.2

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		NIA 000427	Hs.234392	elatelel.	activating factor acetylhydrota	3.2
	430142 433197	NM_000437 AB040889	Hs.281022	MAAGA	SS protein	3.2 3.2
	443509	AV645470	11. 120120		45470 GLC Homo sapiens cDNA clone	3.2
•	440827	A1733110 NM_016161	Hs.128128 Hs.278960	ESTs alpha-1	.4-N-acetylglucosaminyltransferas	3.2 3.2
5	432799 409257	AW370362		-h-DC1	L_BT0255_1910994-012-007 B10233 NONO	3.2
	459235	BE246010	Hs.271458		sapiens mRNA for FLI00038 protein,	3.2
	416789	AA223439 AL162010	Hs.79933 Hs.223603	Cyclin (sapiens mRNA; cDNA DKFZp761D09121 (3.2
10	429809 420156	AW449258	Hs.6187	CCTA		3.2 3.2
10	455577	BE006341	11. 25050	- Alexandria	2-BN0127-240300-011-b05 BN0127 Homo netical protein	3.2
	400617	AF151064 AL049327	Hs.36069 Hs.302057	Homo	sapiens mRNA; cDNA DKFZp564E016 (fr	3.2
	437129 451820	AW058357	Hs.337353	CCT.		3.2 3.2
15	457535	AA609685	Hs.278672		arane component, chromosome 11, surfa	3.1
	419956	AL137939 AA203637	Hs.40096	ESTs	58b12r1 Soares_fetal_liver_spleen_	3.1 3.1
	456235 423930	AA332697	Hs.42721	ESTs		3.1
	403796		75745	aldah	ryde dehydrogenase 1 family, member	3.1
20	414085	AA114016 A)793176	Hs.75746 Hs.145596			3.1 3.1
	445886 414401	AJ760159	Hs.124833	EST.		3.1
	441573	BE563966	Hs.6529		s. Weathy similar to 178885 serine/th	3.1
25	450725	R71389 AJ282933	Hs.17595° Hs.23294	hypo	khetical protein FLJ14393	3.1 3.1
25	458805 417868	AI078534	Hs.12259	2 EST	S	3.1
	458391	AI792628	Hs.13327	c aum	estalanin 1	3.1
	423346 454486		Hs.12741 7	gb:F	RC1-CT0302-140300-016-f04 CT0302 Homo	3.1 3.1
30	408341		2 Hs.24995	7 EST	is .	3.1
50	410669	AW80574		IS sup	eroxide dismutase 2, mitochondrial	3.1
	404907 434910		Hs.21547	74 ES	Ts, Moderately similar to alternative	3.1 3.1
	436990		Hs.1205	57 ES	Te	3.1
35	441921			op.	othetical protein FLJ21939 similar to RC3-ST0186-070100-016-c04 ST0186 Homo	3.1
	454673 429470		Hs.2038	62 gua	enine nucleotide binding protein (G pr	3.1 3.1
	40434	5 AA73040	7 Hs.1591	SR OWN	nor protein, translationally-controlle	3.1
40	40821			eo cur	zr32f09.r1 Soares_NhHMPu_S1 Homo sapi	3.1
40	41731 42732			77 hv	pothetical protein FLJ11155	3.1 3.1
	41100	3 AA1810	18 Hs.130		pothetical protein FLI13920	3.1
	42533			113 E3 921 SE	STs ema domain, immunoglobutin domain (tg),	3.1
45	42671 44901		56 Hs.229	75 KI	IAA 1576 protein	3.1 3.1
43	4296	08 U49250	Hs.210	862 T-	-box, brain, 1 broblast growth factor 9 (glia-actival	3.1
	4423			653 E	STs	3.1 3.1
	4284 4116			146 n	eurofilament 3 (150kD medium)	3.1
50	4479	65 AW292			STs STs	3.1
	4139 4196			282	paired-like homeodomein transcription fa	3.1 3.1
	425		27 Hs.31	903 E	ESTs	3.1
-	4270	865 AA416		4005	ESTs hypothetical protein DKFZp43400320	3.1
5.		060 AW139 708 U7830		0405	alfordou recentor (SMBV 1, SUDIBITILIY	3.1 3.1
		084 AJ487	BOO Hs.27	1000	ESTs, Weakly similar to 138022 hypotheti gb:RC0-CT0205-240999-021-e01 CT0205 Homo	3.1
		1506 AW84			carboxytesterase 1 (monocyte/macrophage	3.0
6	0 47	1629 AA34 2963 M791	41 Hs.13	3234	ESTs	3.0 3.0
v	41	7696 BE24			CD69 antigen (p60, early T-cell activati hypothetical protein FLJ13102	3.0
		8175 BE29 4686 BE40		25160 3189	ESTs, Moderately similar to TBB2_HUMAN T	3.0 3.0
		8360 AI027	7207 Hs.1	32253	ESTs	3.0
6	5 45	1829 AW9		47377	ESTs ESTs	3.0
	44			24768 45362	immortalization-upregulated protein	3.0 3.0
			24447 Hs.	152377	FSTs	3.0
	. 40)7988 N47	760 Hs.	285107	hypothetical protein FLJ13397	3.0
-		05911 18808 AI82	1836 Hs.	10359	ESTs	3.0 3.0
		31900 AW	72048 Hs.	192534	ESTs ESTs, Moderately similar to KIAA1395 pro	3.0
	4	52893 H18		22869 136102	KIAA0853 protein	3.0
				15780	ATP-binding cassette; sub-family A (ABC1	3.0 3.0
	, ,	105793			MA ACCITA Orolein	3.0
	4	110711 AB	002316 Hs /884776	.65746	KIAA0318 protein gb:QV4-OT0067-010300-121-401 OT0067 Homo	3.0
			/978309 Hs	.136235	Homo sepiens cDNA FLJ13542 fis, clone PL	3.0 3.0
	80	427071 AA	397958 H	3.192719	eSTs gb:EST387061 MAGE resequences, MAGN Horno	3.0
		434961 AV	v974956		An	

TABLE 10B:

PCT/US02/29560 WO 03/025138

Unique Eos probeset identifier number Pkey: CAT number: Gene cluster number Genbank accession numbers Accession: 5 **CAT Number** Pkey 409257 1112994_1 1156071_1 AW370362 AW809101 AW502122 AW502125 AW501663 AW501720 409840 411052 AW814950 R98513 H69459 BE176242 H54583 AW884776 AW935737 AW835261 AW835247 AW835246 AW835263 AW835240 AW835258 AW848476 AW935737 AW835261 AW85247 AW835246 AW835263 AW835240 AW835258 AW848427 AW848590 AW848159 AW848118 AW848634 AW848285 AW848086 AW848485 AW848283 AW848162 AW853498 AW853442 AW853590 AW853433 AW853592 1230374_1 411279 411474 1237516_1 1247047_2 10 AW853498 AW853442 AW853590 AW853433 AW853592
BE170301 AW861539 AW904851 BE154336 BE154090 BE154275
BE180342 BE180347 AW901900 BE180222 BE180218 BE180226 BE180413 BE180416 AW901899 BE180228 AW901897 BE180224 AW901898
BE1802229 BE180249 BE180346 BE180343 BE180418 BE180225 BE180218 BE180341 AW901894 BE180217 BE180227 AW901891 BE180345
AW893614 AW893615 H85799 H83501 BE160220
BE068494 BE068414 BE068312 BE068332 BE068433 BE068766 BE068623 BE068408 BE068300 BE068295 BE068498 BE068765 BE068328
BE068778 BE068671 BE068526 BE068493 BE068433 BE0684740 BE068306 BE068631 BE068458 BE068458 BE068567 BE068528 BE068549 BE068578 BE068676 BE068676 BE068676 BE068683 BE0686839 BE0686839 BE0686839 BE0686839 BE0686849 BE068675 BE068676 BE068683 BE0686839 BE0686858 BE068839 BE0686858 BE0686858 BE0686858 BE0686858 BE0686858 BE0686858 BE0686858 BE0686858 BE0686858 BE0686578 BE068676 BE068676 BE068676 BE0686773 BE068676 BE0686839 BE068676 BE068676 BE068676 BE068676 BE0686773 BE068676 BE0686839 BE068878 BE068676 BE068676 BE068683 BE068878 BE 411607 1251251_1 411772 1257386 1 412112 1277883_1 15 413164 1351422 1 20 1373555_1 25 413493 1374377_1 1375671_1 1426940_1 F13044 T77009 BE145525 BE145493 BE147225 BE147205 BE147234 413510 413544 414220 BE298094 BE267860 BE312991 BE272945 414314 414366 1435028_1 1438636_1 BE549143 BE390613 BE277344 30 H74314 BE299593 BE386764 BE387560 BE410857 BE390605 414456 414593 1447655_1 1464909_1 1468083_1 F13142 Z42926 F06135 F06147 H08517 D51360 T75341 415047 1517450 1 35 417313 166644_1 1706092 1 AA195602 W01148 N40632 R23053 R79884 R76271 417888 185884_1 200649_1 204833_1 AA244416 AA244401 AA244416 AA244401
AA285362 AW752388 AW847156 AA285373 AW879575 AW879558
AW966653 AW7966653 AA294989 AA385977
BE048255 AA313083 AA298419
BE409561 BE162756 AW732798
AA359933 AA358889 AW955306 AW962995 AW837746 AW837755 AW837697
AA469153 AI718503 AA469225
AI204995 AW827539 AW969908 AW440776 AA528756
AF038171 Z43209 F07347
AW974956 AA781075 AA554944 419555 421249 421640 40 207654_1 221034_1 421813 422760 252776_1 314437_1 343347_1 425526 430212 432222 45 433389 36497 1 434961 435752 AW974956 AA781075 AA654944 AF230801 AF230800 AA401795 AA398260 396357_1 41050_1 43756_1 437483 AL390174 AW898817 48824_-2 57199_1 440198 443509 RE560093 AV645470 T84636 T82805 AA358760 AA158850 AW062737 AW062738 AV656291 50 65988_1 66686_1 70963_1 912206_1 446052 446218 AV657159 BE145509 BE145512 BE145505 BE145507 T58148 AW516579 AW059603 BE243534 BE243752 AI880228 L44326 AI904296 BE007223 R30687 BE394588 AW024754 BE183166 BE183167 447135 452346 55 919733_1 452502 454065 998401 1 BEJ34030 BE141078 BE143100 BE103107 BE141030 BE141474 BE141467 BE141753 BE141024 BE141761 AW177583 AW177579 AW177582 AW177585 AW177587 AW807582 AW177581 BE141477 BE141520 BE141456 BE141492 BE141028 BE141775 BE141489 BE141751 AW177599 BE141750 AW177597 BE141512 BE141460 1049791_1 454186 BE141749 AW177598 AW381980 BE152244 BE152235 BE152238 BE152232 60 454339 454486 1122972_1 1215703_1 AW857077 AW861268 AW847383 AW795787 AW847346 AW847395 AW847408 AW847385 AW847342 AW847396 AW847339 AW801718 AW801787 454506 454673 1219857_1 AW812807 AW812815 AW812802 AW852286 AW851934 AW852096 AW852274 AW895689 AW996380 AW996453 BE085550 AW868687 BE085595 1228669_1 455040 455225 1250028_1 1262318_1 65 455577 1333898_1 BE006341 BE006307 BE006311 BE078070 BE061030 BE077927 BE067952 BE067945 BE067942 BE067943 BE067949 BE067954 BE067944 BE067953 BE067956 BE067948 BE155527 BE155503 BE155188 BE155126 455617 455697 1351148_1 455901 456235 1381569 1 AA203637 AA832266 H67452 AW868614 AA243209 AA281411 70 168686_1 456407 457452 184986_1 AW972675 AASA1366 AAS23039 BE155356 BE153488 BE153461 BE155059 BE155210 BE155413 BE153577 BE153688 BE155063 BE155347 AI903640 BE155492 339381_1 459150 919196_1 75 TABLE 10C: Unique number corresponding to an Eos probesel Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Indicates ONA strand from which exons were predicted.
Indicates nucleotide positions of predicted exons. Strand: 80 Nt_position: Pkey 400661 Strand NI position

84912-85187

8118474

Plus

	400685	8118768	Minus	72969-73050,73713-73800
	400865	1945037	Minus	44482-45526
	400878	9864757	Plus	31493-32842
	401024	8117489	Plus	60551-60802
5	401315	9212516	Minus	198960-199619
•	401485	7341723	Ptus	68009-68209,68841-69077
	401521	7705251	Plus	9127-9234
	401532	7798785	Plus	124414-124950,125050-125418
	401738	2982169	Minus	41547-41757
10	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
	401836	7534063	Plus	71981-72084
	401949	3492889	Plus	160728-161660
	402092	7249154	Minus	107533-108094
	402176	7543687	Minus	10-750
15	402546	7637348	Plus	24673-25170
	403092	8954241	Plus	174720-175016,175104-175408,175508-175813
	403180	7523976	Minus	63603-63759
	403323	8348082	Minus	120366-120845
	403796	8099896	Minus	75073-77664
20	404391	3135305	Minus	26030-26173,27852-27997
	404769	B099713	Minus	175801-176823
	404793	7232206	Minus	61087-61590
	404828	6580415	Minus	26291-27253
	404907	7331453	Minus	102880-103828
25	404958	7407941	Minus	2731-4531
	405071	7708797	Minus	11115-11552
	405130	8516045	Plus	150235-150449
	405138	8576241	Plus	90303-90516
	405354	2642452	Plus	52213-53089
30	405377	5649375	Plus	216656-216848
	405629	4508116	Minus	101678-101866
	405678	4079670	Plus	151821-152027
	405793	1405887	Minus	89197-89453
	405800	2791346	Plus	19271-19813
35	405867	6758731	Minus	74553-75173
	405911	6758795	Plus	101008-101643
	405977	8247789	Minus	135548-136177

TABLE 11A: ABOUT 533 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES
Table 11A fists about 533 CNS-enriched genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on
the Affymetrix/Eos Hu03 Gene-Chip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 2. The "average" normal CNS level was
set to the 75th percentile amongst various normal CNS tissues. The "average" norm-CNS normal adult tissues was calculated to be greater than or equal to 2. The "average" CNS level was set to the 85th
percentile amongst various CNS tissues. The "average" norm-CNS adult tissue level was set to the 85th percentile amongst various non-CNS normal tissues. In order to
remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and
the denominator before the ratios were evaluated.

Pkey:

Unique Eos probeset Identifier number
ExAccn:
Exemptar Accession number, Genbank accession number
Unique elos prometers. 40 45

50

UnigenelD: Unigene Title: R1: R2: Unigene number
Unigene number
Unigene gene title
Ratio of 75th percentile normal central nervous system tissue to 85th percentile turnor
Ratio of 85th percentile central nervous system tissue to 85th percentile normal body tissue

55	Pkey	ExAccn	UnigenetD	Unigene Title	R1	R2
-	417275	X63578	Hs.295449	parvalbumin	29.0	30.0
	430829	AW451999	Hs.194024	ESTa	25.7	6.2
	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype	22.6	25.8
	419954	D14720	Hs.93883	myelin protein zero (Charcot-Marie-Tooth	21.2	30.3
60	416133	NM_001683	Hs.89512	ATPase, Ca++ transporting, plasma membra	15.5	16.8
•	416018	AW138239	Hs.78977	proprotein convertase subtitisin/kexin t	15.2	18.0
	417167	AW206437	Hs.4290	EST\$	14.8	17,7
	433940	H05129	Hs.7459	cyclic AMP-regulated phosphoprotein, 21	13.4	18.1
	413324	V00571	Hs.75294	corticotropin releasing hormone	13.1	18.0
65	439830	AA846666	Hs.151489	ESTs, Weakly similar to XE7_HUMAN PROTEI	12.6	16.5
00	408068	AW148852	Hs.167398	ESTs	12.6	16.9
	429096	AB011106	Hs.196012	KIAA0534 protein	12.2	21.1
	412638	AA910199	Hs.203838	ESTs	12.2	16.0
	442593	R39804	Hs.31961	ESTs	10.8	15.0
70	446353	AI290919	Hs.153661	ESTs	10.4	13.2
	426365	AA376667	Hs.10283	RNA binding motif protein 88	10.0	5.9
	414937	R38698	Hs.12382	ESTs	10.0	10.8
	419643	F06066	Hs.91791	chromosome 11 open reading frame 25	9.5	10.9
	412454	R55745	Hs.167330	ESTs	9.5	14.1
75	439366	AF100143	Hs.6540	fibroblast growth factor 13	9.4	12.3
	441790	AW294909	Hs.132208	ESTs	9.2	3.2
	448117	H49129	Hs.172982	ESTS	9.1	12.8
	433558	AA833757	Hs.201769		9.0	14.7
	412453	R20205	Hs.167330		9.0	13.7
80	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	8.9	17.3
-	409031	AA376836	Hs.76728	ESTA	B.7	8.6
	446544	AI531932	Hs.7047	ESTs, Wealdy similar to Unknown (H.sapla	8.2	20.0
	439480	AL038511	Hs.125316		8.2	8.3
	-JJ-00				• -	

					9.0	8.9
				targandt disease 3 (autosomal dominant) InaJ (Hsp40) homolog, subfamily B, membe	8.0 7.9	9.6
				STs	7.9	11.3
	408434	AW195317	Hs.107716 P	ypothetical protein FLJ22344	7.9 7.8	16.4 34,3
5	440209		Hs.22269 (eurexin 3 STs, Wealdy similar to T00331 hypotheti	7.8	9.0
	408119 429611	W26213 AI889077	Hs.101672 Hs.211388	tomo sapiens BAC clone CTB-60N22 from 7q	7.7	5.0
	423440	R25234	Hs.143434	contactin 1	7.7 7.6	9.9 9.1
10	445148	AI214510		ESTs	7.6 7.6	7.6
10	416294 424087	D85980 N69333		KIAA0227 protein contactin 1	7.6	10.3
	437479	R61866		ESTs	7.5	9.3 2.8
	430573	AA744550		ESTs	7.1 7.1	10.4
15	448958 419474	AB020651 AW968619	Hs.22653 Hs.155849	KIAA0844 protein ESTs	7.1	3.0
13	423605	AF047826	Hs.129887	cadherin 19, type 2	7.0	6.9 9.2
	433098	AW190593	Hs.151143	ESTs	7.0 6.9	3.1
	449511	AI436187 AL049980	Hs.296261 Hs.184216	guanine nucleotide binding protein (G pr DKFZP564C152 protein	6.8	5.0
20	428414 443155	R54485	Hs.23772	ESTs	6.8	3.5 8.1
	450561	R49674	Hs.25909	ESTs	6.8 6.8	20
	433068	NM_006456 AA328082	Hs.288215 Hs.209569	sialytransferase ESTs	6.6	10.5
	423589 415681	A1379882	Hs.72630	ESTs	6.5	9.0
25	413510	F13044		gb:HSC3HH101 normalized infant brain cDN	6.4 6.4	7.1 9.5
	427992	Y15014	Hs.191353 Hs.7130	UDP-Gal-betaGlcNAc beta 1,3-galactosyltr copine IV	6.4	5.7
	450642 429322	R39773 D86984	Hs. 199243	KIAA0231 protein	6.4	8.2
- 4	447482	AB033059	Hs.18705	KIAA1233 protein	6.4 6.3	2.3 8.3
30	446129	AW244073	Hs.145946	ESTs osteoglycin (osteoinductive factor, mime	6.3	21
	421913 434273	A1934365 AA913143	Hs.109439 Hs.26303	ESTs	6.2	10.3
	408480	A1350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	6.2 6.2	3.5 12.4
26	451301	A1769514	Hs.209890	EST	6.2	8.1
35	438356 426388	AA805530 AW081394	Hs.48527 Hs.97103	ESTs ESTs	6.2	8.6
	452502	AI904296	•	gb:PM-BT046-220199-286_1 BT046 Homo sapi	6.1 6.1	2.8 6.3
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (I	6.1	6.3
40	442979 408713	AW440782 NM_001248	Hs.174743 Hs.47042	ESTs ectonucleoside triphosphate diphosphohyd	6.0	3.8
40	430004	U27768	Hs.227571	regulator of G-protein signalling 4	5.9	21.4
	425087	R62424	Hs.126059	ESTs	5.9 5.9	8.1 3.1
	441695	T12411 R44558	Hs.183745 Hs.94002	hypothetical protein FLJ 13456 ESTs	5.8	12.5
45	417175 437483	AL390174	113.54002	gb:Homo sapiens mRNA; cDNA DKFZp547J184	5.8	2.2 13.8
	436427	A1344378	Hs.143399	ESTs	5.8 5.7	4.4
	450382 408478		Hs.60257 6 Hs.45740	Homo sapiens cDNA FLJ 13598 fis, clone PL gamma-aminobutynic acid (GABA) A recepto	5.7	12.5
	442676		Hs.130897		5.7	6.8 6.4
50	446443	AV659082	Hs.134226		5.7 5.6	15.6
	459080		Hs.290855		5.6	8.2
	431984 428356		Hs.10338	ESTs	5.6	6.2 4,9
	417877	AI025829	Hs.86320	ESTs	5.4 5.3	13.1
55	429290 408558		Hs.19876 Hs.46362	neurofilament, heavy potypeptide (200kD) 5-hydroxytryptamine (serotonin) receptor	5.3	6.6
	43193		Hs.27221	cadherin 7, type 2	5.2	6.0 7.3
	43828	5 AA782845			5.2 5.2	7.3 27
60	43990 44922		Hs.12416 4 Hs.19762		5.2	8.1
UU	40801			6 ESTs	5.1	2.5 3.0
	43695				5.1 5.1	7.3
	43677 40926				5.1	12.9
65	45383			ESTS	5.1	3.4
-	44153	5 AL13573	5 Hs.7885	phosphatidylinositol binding clathrin as	5.0 5.0	20.1
	41649 41728		6 Hs.7934 Hs.1072		5.0	3.9
	44860				5.0	6.1
70	4422	40 AJ791883	Hs.2927		4.9 4.9	6.7 5.2
	4279				4.9	2.8
	4160- 4449				4.8	3.7
	4089	36 AL13804	3 Hs.2935	49 ESTs	4.8 4.8	6.6 3.1
75			Hs.1241 Hs.9184		4.8	2.3
	4292 4079				4.8	9.1
	4165	77 BE0632	07 Hs.793	1 grancalcin	4.7 4.7	2.2 2.8
80	4204		61 Hs.981	73 hypothetical protein	4.6	2.2
0(<i>)</i> 4047 4308		Hs.248	21 G protein-coupled receptor 22	4.6	7.4
	438	571 AW0207	775 Hs.560	22 ESTs	4.6 4.6	5.4 6.0
	444	585 AW17 0 0)15 Hs.659	4 ESTs	4.0	0

							4.5	2.2
	* * * * * * * * * * * * * * * * * * * *	• • • • • • • • • • • • • • • • • •	Hs.46988	ESTS	lein, alpha (non A4 component of am		4.5 4.5	30.9
	414599 423449	AI815523 AI497900	Hs.76930 Hs.33067	ESTs	em, apria (non res component o am		4.5	20.8
	433521	T66087	Hs.112482	Homo	sepiens unknown mRNA sequence		4.4	2.0 19.2
5	429876	AB028977	Hs.225974	ESTS	1054 protein		4.4	10.2
	429726 449093	AW628326 AB035356	Hs.27151 Hs.22998	Reure			4.4	9.4
	415716	N59294	Hs.179662	nucle	osome assembly protein 1-like 1		4.4	15.1 8.2
	419656	AB002314	Hs.92025		0316 gene product bory receptor, family 5, subfamily		4.4	24
10	425864	U56420 AW518888	Hs.159903 Hs.40937	EST			4.4	5.7
	435078 432712	AB016247	Hs.288031	stero	I-C5-desaturase (fungal ERG3, delta		4.3 4.3	5.9 6.0
	426867	AA460967	Hs.22668	EST:	s C3-HT0622-130400-012-e07 HT0622 Homo		4.3	3.2
15	412112	BE180342 H07892	Hs.12431	EST:			4.3	5.3
13	410171	BE299668	Hs.227591	EST	s. Weakly similar to 1901303A Leu zip		4.2 4.2	5.0 3.5
	421249	AA285362			ITH277 HTCDL1 Homo sepiens cDNA 5/3*		4.2	3.9
	422528	AB011182 AA478488	Hs.118087 Hs.3852		AD610 protein AD368 protein		4.1	8.3
20	434460 410362	H04811	Hs.93164	proc	xotein convertase subtilisin/kexin t		4.1 4.1	7.0 3.9
	449754	H00820	Hs.30977		s, Weakly similar to B34087 hypotheti		4.1	4.7
	408496	AI683802 AA625205	Hs.136182 Hs.259599		s A1622 protein		4.1	6.3
	434101 430212	AA469153	113.233033	ap:r	1067804.51 NCI_CGAP_Pr1 Homo sepiens		4.0 4.0	2.5 7.4
25	453165	S74727	Hs.32042	asp	artoacylase (aminoacylase 2, Canavan EST380690 MAGE resequences, MAGJ Homo		4.0	5.1
	456407	AW988614 NM_003947	Hs.8004	go:	tingtin-associated protein interactin		4.0	32.3
	441869 429628	H09604	Hs.13268	ES.	Ts		4.0 4.0	4.5 6.9 .
	410087	F12079	Hs.332579	ES	Ts. Westdy similar to A45010 X-linked		4.0	2.6
30	419910 441005	AA562913 Z41305	Hs.190173		mo sapiens mRNA; cDNA DKFZp547G133 (fr		3.9	21.7
	412677	AW029608	Hs.17384	ES	Ts .		3.9 3.9	2.2 7.2
	453341	A1758912	. Hs.29634		enylyl cyclase-associated protein 2		3.9	2.2
35	416854 414666	H40164 NM_004456	Hs.80296 Hs.76828		rkinje cell protein 4 rpican 5		3.8	6.2
25	418217	AI910847	Hs.13442	È	Te .		3.8 3.8	3.2 2.2
	421855	F06504	Hs.27384		STs, Moderately similar to ALU4_HUMAN A		3.8	10.7
	414764 433629	AW013887 R13140	Hs.72047 Hs.13359		STs		3.7	2.7
40	424738		Hs.45826	3 E	STs		3.7 3.7	2.1 5.3
	407706				STs, Moderately similar to \$23650 retro equiator of G-protein signalling 4		3.7	53.7
	437268 423135		Hs.22757 Hs.2641		STs		3.7	21.7
	446818		Hs.2797	65 E	STs		3.7 3.6	2.6 3.6
45	427562		Hs.2653		STs		3.6	34.5
	439274 452381		Hs.4837 Hs.2908		STs. Wealdy similar to ALU1_HUMAN ALU \$		3.6	6.0
	422897		Hs.4290) E	STs		3.6 3.6	5.1 24.6
	429656		Hs.2115		neurofilament, light polypeptide (68kD) ESTs		3.6	5.8
50	41715		Hs.2138 Hs.1608		ESTS		3.6	6.4
	40597						3.6 3.6	3.9 2.5
	42356			318 9	growth arrest-specific 2 Homo sapiens cDNA: FLJ21268 fis, clone C		3.6	5.4
55	44123 42677			829	ESTs		3.6	3.4
33	41483		Hs.774	39	protein kinase, cAMP-dependent, regulato		3.6 3.6	2.8 4.9
	42515		93 Hs.270 Hs.153		ESTs ESTs		3.5	9.8
	44649 44589			23	Homo sapiens clone 24468 mRNA sequence		3.5	16.6
60	41642		6 Hs.793	306	eukaryotic translation initiation factor		3.5 3.5	5.0 16.0
	41821		Hs.347		ESTs Down syndrome critical region gene 1-lik		. 3.5	6.2
	4253 4170		Hs.156 06 Hs.239		triadin		3.5	2.5
	4083	67 AK0011	78 Hs.444	424	homolog of rat orphan transporter v7-3		3.5 3.5	5.3 5.5
65					ESTs. Wealdy similar to 138022 hypotheti Homo saplens mRNA for KIAA1263 protein,		3.5	23.6
	4532 4193				superiorcervical ganglia, neural specifi		3.5	42.3
	4338	03 AIB2359	3 Hs.27	688	ESTs		3.4 3.4	3.6 4.1
7/	4507	15 AI26646	34 Hs.31		ESTs, Weakly similar to KIAA1324 protein guanylate cyclase 1, soluble, beta 3		3.4	9.8
70	J 4150 4238				cocaine- and amphetamine-regulated trans		3.4	4.7
	4271	173 BE2550	17 Hs.97	540	ESTs		3.4 3.4	2.4 3.5
	4460	092 N33522			ESTs ESTs		3.4	4.5
7.	5 458				ESTS		3.4	4.5
	434	053 AW445	136 Hs.13	34946	ESTs		3.4 3.3	3.9 42.3
	428	536 AJ1431		288 02689	visinin-like 1 hypothetical protein		3.3	14.4
	425	366 Al2675 785 T2701		59528	Homo sepiens clone 24400 mRNA sequence		3.3	4.6
8	O 434	998 AW975	5157 Hs.21	6037	ESTs		3.3 3.3	4.7 4.4
		359 AI9679		3574 70238	homeo box 03 sodium channel, voltage-gated, type 1, b		3.3	5.2
		3527 NM_00 3302 N4805			totate hydrolase (prostate-specific memb		3.3	9.0
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419373 AASSAUT 143.25014 157.25014						3.3	3.6
153-12		*****			roenkephalin :ete		
10 AMPS-6552 Ho. 25905 Ho. 25905 Ho. 25905 AMPS-7814 Ho. 25905							22
AGE					b:EST378726 MAGE resequences, MAGI Homo		
### 420-95 AA3594-54 No. 79.005 ESTs, Weakly similar to smillar to entrol ### 122 29 40.005 ASSESTI No. 19.100 ASSESTI NO. 19.1	5			Hs.289005 I	tomo sapiens cDNA: FLJ21532 fis, clone C		
ASSISTANCE ASS				Hs.13531			
Sizeri Auf 1987/878 Hs.1976 Sizeri Siz			AA338454	MS./0020	1315, Wearly Strong to strong to circle		
Additional			AI873878				
40000 AA-028611 hs. 284433 ESTs	10	454100		Hs.126043	duromosome 21 open reading frame 51		
1.5 1.5							
1.5							
15 A20156 AV449236 Hs.1 187 ESTs A27877 A27827 A27							
1995	15			Hs.6187			
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417868 AU78507 Hs. 122892 ESTs yangakipain 1 3.1 12.0 4733376 Hs. 164478 Hs. 273852 yangakipain 1 3.1 12.0 4733376 Hs. 164478 Hs. 273852 yangakipain 1 3.1 12.0 4733376 Hs. 164478 Hs. 273852 yangakipain 1 42.0 47332 yangak							
August							
### 1987 He 203867 guarine mucleotide binding protein (G pr 3.1	20			Hs.127416	synaptojanin 1		
Add							
25 407322 ACCOUNT 16, 176277 hypothetical protein FL11155 3, 1, 6, 3 26 42668 U49250 H29250 H29756 H29757 StAA1578 protein 3, 1 30, 1 27 426688 U49250 H2, 111 41966 AF 106544 H2, 17136 41968 AF 106544 H2, 17136 41968 AF 106544 H2, 17136 41968 AF 106544 H2, 17136 41969 AF 106544 H2, 17136 41989 AIB21836 H2, 17808 41829 AW97681 H2, 17809 41900 AW976555 H2, 15790 41000 AW976565 H2, 15790 41000 AW976565 H2, 15790 41000 AW976565 H2, 15790 41000 AW97657 AB 10000 H2, 15790 41000 AW97657 AW9767 AB 10000 H2, 15790 41000 AW97657 AW9767 H2, 15800 H2, 15790 41000 AW97657 AW9767 H2, 15800 H2, 15790 41000 AW97657 AW9767 H2, 15800 H2, 15790 41000 AW97650 H2, 15790							
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425608 449250 4421692 4421692 4411666 4571695 4411666 4571695 4411666 4571695 441169	25						
411666 AF 10594 Ha.7136 427853 A416931 II.72605 451829 AM95C081 Ha.27377 40289 Hil8017 Ha.27377 41289 A418931 Hil8017 Ha.27377 41289 A418931 Hil8017 Ha.2865 Ha.10398 417900 AM95F655 Ha.15780 AFD Framework Ha.13805 Ha.27379 417910 A.975793 Ha.138102 Ha.2865 Ha.10393 Ha.27379 417011 A8002216 Ha.5746 Ha.30316 protein Green Framework Ha.2865 Ha.27379 417011 A8002316 Ha.30316 Ha.27379 417011 A8002316 Ha.30316 Ha.27379 417011 A8002316 Ha.27379 Ha.138102 Ha.2865 Ha.27373 Ha.273810 Ha.27389 H			U49250				
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30							
451829 AM964081 No. 247777 ESTs 3.0 6.2 409911 418080 AMS21836 No. 10359 42393 HB017 No. 122869 551s, Moderately similar to KIAA1395 pro 3.0 5.2 423952 AW977787 No. 13.0102 4107011 AB002316 No. 15.51 427001 AA397958 No. 15.76 427071 AA397958 No. 15.76 427071 AA397958 No. 15.76 435354 NN. 014795 No. 13.15 46666 U0230 No. 15.76 435354 NN. 014795 No. 13.15 43545 APROXIMATE NO. 15.15 435590 AF150278 No. 15.15 435590 AF	30						
409911	50						
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3.5 423932 AW977787 Hs. 139102 KLAA68S3 protein 412000 AW977878 Hs. 15780 AW977878 Hs. 15780 AW977878 Hs. 15780 AW97787 Hs. 15780 AW9701 Assays Hs. 157719 ESTs AW97123 AW978289 Hs. 15780 AW978287 AW982893 Hs. 15780 AW98274 Rt 17315 AW982893 AW982891 Hs. 15780 AW98289 Hs. 15780 AW2718 AW98289 Hs. 15780 AW98289 Hs. 15780 AW98289 Hs. 15780 AW2718 AW88289 Hs. 15780 AW88289 AW98289 Hs. 15780 AW88289 Hs. 15780 AW88289 Hs. 15780 AW88289 AW98289 Hs. 15780 AW88289 AW98289 Hs. 15780 AW88289 AW98289 Hs. 1		418808					
## 1,500 A12992 A1797/787 FR. 1,5780 A179-binding cassetts, sub-family A (ABC1 3.0 2.1 ## 1,5780 A179-binding cassetts, sub-family A (ABC1 3.0 2.1 ## 1,5780 A179-binding cassetts, sub-family A (ABC1 3.0 2.1 ## 1,5780 A179-binding cassetts, sub-family A (ABC1 3.0 2.1 ## 1,5780 A179-binding cassetts, sub-family A (ABC1 3.0 2.1 ## 1,5780 A179-binding cassetts, sub-family A (ABC1 3.0 2.1 ## 1,5780 A179-binding cassetts, sub-family A (ABC1 3.0 2.1 ## 1,5780 A179-binding cassetts, sub-family A (ABC1 3.0 2.1 ## 1,5780 A179-binding cassetts, sub-family A (ABC1 3.0 2.1 ## 1,5780 A179-binding cassetts, sub-family A (ABC1 3.0 3.0 3.0 3.0 ## 1,5780 A179-binding cassetts, sub-family A (ABC1 3.0 3.0 3.0 3.0 ## 1,5780 A179-binding cassetts, sub-family A (ABC1 3.0 3.0 3.0 3.0 3.0 ## 1,5780 A179-binding cassetts, sub-family A (ABC1 3.0 3.0 3.0 3.0 3.0 ## 1,5780 A179-binding cassetts, sub-family A (ABC1 3.0 3.0 3.0 3.0 3.0 3.0 ## 1,5780 A179-binding cassetts, sub-family A (ABC1 3.0	25						
AB07216	22						
A			A+13.0003	13.13.00	The same of the sa		
According to the composition of the composition o							
## 13933 AA49643 Hs. 22136 ESTs ## 22166 U02330 Hs. 172816 neuregulin 1 3.0 11.3 ## 13934 AA49643 Hs. 22136 hs. 172816 neuregulin 1 3.0 11.3 ## 14945 AB030055 Hs. 4280 ## 14003 AW961284 Hs. 295235 ESTs	40						
42866 U02300 Hs. 4280 KDA17281 protein	40						
### ### ### ### ### ### ### ### ### ##							
45.53590 AF150278 Hs.32673 ESTs							
41592 AL133721 Hs.23458 ESTs 2.9 2.3.1 41592 AL133721 Hs.23458 ESTs 2.9 2.3.1 42594 AL13390 Hs.3830 AB020700 Hs.3830 AB020700 Hs.3830 AB020700 Hs.3830 AB020700 Hs.3830 AB020700 Hs.384579 AL13390 Hs.192 ADP-thosylation factor domain protein 1 2.9 20.8 AU1213 401028 AW672312 Hs.50848 hs.205457 AL15911 AL1592 AW560848 hs.205457 Hs.304575 AW560848 hs.205457 Hs.30457 AL1592 AW560848 hs.205457 Hs.30457 AL1592 AW560848 hs.205457 Hs.304585 AW552691 Hs.30455 Horro sapiens mRNA; cDNA DKFZp761D191 (fr 2.9 35.0 AW56084 Hs.59485 Horro sapiens mRNA; cDNA DKFZp761D191 (fr 2.9 35.0 AW56084 Hs.59485 Hs.205457 AL25945 Hs.505457 Hs.50545							
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1.5540				Hs.14559	7 ESTs		
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434826 AF155661 Hs. 22285 pyruvetia dehydrogenase phosphatase 2.8 2.4	75						
415462 R52692 Hs. 12698 ESTs 2.8 3.4 416070 NM_000844 Hs. 83407 ghttamate receptor. metabotropic 7 2.8 4.5 432149 AW614326 Hs. 157022 ESTs, Weakly similar to T34549 probable 2.8 9.5 430371 D87466 Hs. 240112 kIAA0276 protein 2.8 7.0 437357 AL399559 Hs. 331666 Homo sapiens mRNA; cDNA DKF2p76202215 (I 2.7 2.5 415838 R44336 Hs. 7093 ESTs 2.7 3.6	/3						
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80 432149 AW614326 Hs.157022 ESTs, Weakly similar to T34549 probable 2.8 9.5 430371 B97466 Hs.240112 KIAA0276 protein 2.8 7.0 437357 AL339559 Hs.331666 Homo sapiens mRNA; cDNA DKFZp762O2215 (I 2.7 2.5 415838 R44336 Hs.7093 ESTs 2.7 3.6					glutamate receptor, metabotropic 7		
437357 AL359559 Hs. 331666 Horno sapiens mRNA; cDNA DKF2p762O2215 (I 2.7 2.5 415838 R44336 Hs.7093 ESTs 2.7 3.6	00	43214	9 AW61432	6 Hs.15702			
415838 R44336 Hs.7093 ESTs 2.7 3.6	80						
25							3.6
							2.5

				FORSER LA LIE CE MARGE MAGE HOME	2.7	3.1
		AW953679 AI949389		b:EST365749 MAGE resequences, MAGC Homo STs	2.7	4.1
	446318 445183	AB007877		IAA0417 gene product	2.7	5.3
	457012	R41480		STs	2.7	19.0
5	431988	AC002302	Hs.77202 g	rotein kinase C, beta 1	2.7	7.2
•	430223	NM_002514	Hs.235935	ephroblastoma overexpressed gene	2.7 2.7	2.B 3.8
	447932	AAB37474		reside-associated membrane protein 1 (s	27	6.9
	450214	BE439763		egulator of G-protein signalling 4	2.7	5.0
10	434731	AA648049 AI767756	Hs.121518 (ESTs Homo sapiens cDNA FLJ14814 fis, clone NT	2.7	5.2
10	428839 407709	AA456135		ESTs	2.7	2.5
	422420	U03398		tumor necrosis factor (ligand) superfami	2.7	3.3
	443305	AI050693		ESTs	2.7	5.9
	435648	H24347		ESTs	2.7 2.7	15.0 2.7
15	418407	AL044818		nuclear transcription factor Y, beta	2.7	6.0
	436771	AW975687		ESTs sulfortranferase (amily 4A, member 1	2.7	4.8
	428689 440503	NM_014351 NM_006539		calcium channel, voltage-dependent, gamm	2.7	4.4
	441006	AW605267		CGI-60 protein	2.7	3.1
20	410330	AW023630	Hs.46788	ESTs	2.6	29.5
	434398	AA121098	Hs.3838	serum-inducible kinase	26 26	26 7.8
	438831	BE263273	Hs.6439	synapsin II	26	3.4
	419066	298492	Hs.6975	PRO1073 protein	2.6	2.2
25	412643	AW971239	Hs.293982 Hs.241503	ESTs hypothetical protein	2.6	17.9
23	430456 416498	AA314998 U33632	Hs.79351	potassium channel, subfamily K, member 1	2.6	2.9
	401421	0,0002			2.6	20
	419530	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	2.6	4.2
	441817	AW969706	Hs.293332	ESTs	2.6 2.6	3.8 4.2
30	439203	AA448930	Hs.8453	KIAA1587 protein	2.6	5.1
	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision, hypothetical protein FLJ14600	2.6	3.7
	444583 417919	AW994403 AI928203	Hs.100861 Hs.86379	ESTS .	2.6	3.0
	434293	NM_004445		EphB6	2.6	3.2
35	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	2.6	6.4
	443037	AW500305	Hs.299166	syntaxin 7	2.6	2.2 7.1
	440736	D\$6919	Hs.265848	myomegalin	26 26	3.0
	404648			gb:zx72e09.r1 Soares_total_fetus_Nb2HF8_	. 26	3.5
40	429995	AA463571 AW504381	Hs.121121	ESTs, Weakly similar to S00755 plackstri	26	3.9
40	436508 441190	H09073	Hs.25045	ESTs	2.6	3.1
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	2.6	2.9
	442731	AI868167	Hs.131044	ESTs	2.6	4.1 14.9
4.5	416836	D54745	Hs.80247	cholecystokinin	2.6 2.5	2.4
45	449071	NM_005872		breast carcinoma amplified sequence 2	2.5	2.8
	436321	AA709133	Hs.180144 Hs.125897	ESTs ESTs	2.5	3.6
	439693 443212	AI741816 AW269515		hypothetical orotein FLJ20481	2.5	2.8
	423981	AL122104	Hs.136664		2.5	3.8
50	407868			profine-rich Gla (G-carboxyglutamic acid	2.5	3.1
	443992		Hs.322922		2.5 2.5	27.9 5.3
	444124		Hs.6818	ESTS	25	38.0
	411379		Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE gamma-eminobutyric acid (GABA) A recepto	2.5	3.8
55	440474		Hs.7195 Hs.159204		2.5	2.2
"	446277 410111		Hs.189647		2.5	3.5
	445162		Hs. 12376	piccolo (presynaptic cytomatrix protein)	2.5	4.8
	410718		Hs.19143		2.5 2.5	4.5 2.9
	417201		Hs.26908	ESTs, Moderately similar to AF097994 1 L	2.5 2.5	2.8
60	420274				2.5	4.7
	43349			VLCS-H1 protein hypothetical protein DKFZp781G0313	2.5	3.3
	43733 43735				2.5	3.0
	44198				2.5	3.6
65	41002				2.5	9.2
-	41468	D AA74333			2.5	3.6 23 .9
	42995				2.5 2.5	2.8
	42902				2.5	3.1
70	43810			db:Homo sapiens mRNA full length insert	2.5	2.3
70	43978 44088		Hs_32681		25	3.9
	44524				2.5	2.6
	4401			KIAA0378 protein	2.4	23.6
	43274	40 AF06103	4 Hs.2788		2.4	2.1 3.9
75			Hs.2224		2.4 2.4	9.8
	4322			93 Homo sapiens mRNA; cDNA DKFZp761G1111 (f 27 ESTs	24	9.8
	4379				2.4	2.8
	4213 4271				2.4	2.2
80	4520			7 G protein-coupled receptor 37 (endotheli	24	10.0
	4366	39 D14838	Hs.111	fibroblast growth factor 9 (glia-actival	24	3.5 3.1
	4345	20 AA2052	73 Hs.1770		2.4 2.4	3.0
	4115	29 AA4303	48 Hs.3175	96 Homo sapiens cDNA FLJ12927 fis, clone NT	4. 7	~~

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					2.4	21
				STs alchum binding protein 1 (calbrein)	2.4	27
	422927 444647			luman ctone 23589 mRNA sequence	2.4	2.8
	415827	H17462	Hs.23079 E	STs	2.4	15.0
5	451397	AA017432		STs, Weatly similar to Z202_HUMAN ZINC	2.4 2.4	3.9 3.7
	445200	AA084460		omatostatin Iomo sapiens mRNA; cDNA DKFZp564C1416 (I	2.4	2.4
	451062 420328	AL110125 Y19062		taufen (Drosophila, RNA-binding protein	2.4	4.3
	432122	AA526514		timi60f02.s1 NOI_CGAP_Ov2 Homo septens	2.4	4.3
10	444125	AI124882		ST8	2.4 2.4	3.5 10.8
	430538	AB032435		ifferentiation-associated Na-dependent early growth response 4	2.4	2.4
	457519 409371	X69438 R51736		ESTs	2.4	2.1
	456303	AA224872	Hs.115088	ESTa	24	3.2
15	440105	AA694010	Hs.6932	Homo sepiens clone 23809 mRNA sequence	24 24	23.4 4.1
	400979	DAGGE	Hs.24980	ESTs	24	6.5
	435296 408950	R49685 AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	24	18.5
	452032	BE244005	Hs.27610	retinoic acid- and interferon-inducible	2.4	22
20	432098	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	2.4	2.7
	408974	AW015458	Hs.297017	ESTs	2.4 2.4	2.5 2.8
	412177 413153	Z23091 N94205	Hs.73734	glycoprotein V (platelet) gb:za27a08.r1 Soares fetal liver spleen	2.4	25
	417583	AA668782	Hs,191284	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4	2.6
25	452034	F12234	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.3	3.0
	424940	AA985308	Hs.194327	ESTs	2.3 2.3	6.3 4.1
	431706	AI816086	Hs.296341 Hs.130881	adenylyl cyclase-associated protein 2 B-cell CLL/lymphorna 11A (zinc finger pro	2.3	2.9
	419125 423641	AA642452 AL137256	Hs.130489	ATPase, aminophospholipid transporter-li	2.3	8.7
30	436407	T88803	Hs.271507	ESTs, Wealty similar to TIM_HUMAN PROBAB	2.3	3.2
	448681	AL109781	Hs.21754	Homo sepiens mRNA full length insert cON	2.3 2.3	5.2 54.7
	415669	NM_005025	Hs.78589 Hs.66180	serine (or cysteine) proteinase inhibito nucleosome assembly protein 1-like 2	2.3	9.1
	410765 422386	Al 69 4972 AF 105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	2.3	5.0
35	414828	AA156651		gb:zi05h05.r1 Soares_pregnant_uterus_NbH	23	2.4
	445556	AI910241	Hs.12887	actin-related protein 3-beta	2.3 2.3	8.5 26.3
	426968	U07616	Hs.173034 Hs.335429	amphiphysin (Stiff-Mann syndrome with br RIKEN cDNA 9130422N19 gene	2.3	2.5
	444562 423420	AA186715 AI571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp76111224 (f	23	7.6
40	439450	R51813	Hs.125304	ESTs	23	26.3
	427127	AW802282	Hs.22265	pyruvate dehydrogenase phosphatase	2.3 2.3	2.2 3.8
	447179	AW015633	Hs.157299	ESTs Homo sapiens cDNA FLJ13522 fis, clone PL	2.3	2.3
	414711 433449	AJ310440 AW772282	Hs.288735	gb:hn71b05.x1 NCI_CGAP_Kid11 Horno sapien	2.3	3.8
45	414320	U13616	Hs.75893	ankyrin 3, node of Ranvler (ankyrin G)	2.3	2.5
	416778	M16505	Hs.79876	steroid sulfatase (microsomal), arytsulf	23 23	7.8 4.1
	425130	AA44B208	Hs.99163	ESTs metallothionein 1G	2.3	2.5
	456664 438283	AW963354 AI458931	Hs.334409 Hs.37282	ESTs	2.3	4.2
50	417455	AW007068		ESTs, Wealthy similar to CA2B_HUMAN COLLA	2.3	3.0
	412100	AW892731		gb:CM0-NN0005-100300-279-c02 NN0005 Homo	2.3 2.3	3.7 3.2
	448981	AI968719 R24854	Hs.195387 Hs.268806		2.3	6.5
	416101 439731	A1953135	Hs.45140	hypothetical protein FLJ14084	2.3	17.8
55	415734			KIAA0237 gene product	2.3	40.1
	424596	AB020639	Hs.151017		2.3 2.3	2.9 2.4
	420230		Hs.284186 Hs.20935	forkhead box C1 hypothetical protein DKFZp761D221	2.3	5.7
	451559 404835		115.20333	Hypotheses protest ord Epitational	2.3	2.1
60	456765		Hs.33067	ESTs	23	4.1
	455517			gb:RC0-HN0006-160300-011-e06 HN0006 Homo	2.3 2.2	2.4 18.5
	408206			kinesin family member 3A heat shock protein (hsp110 family)	2.2	3.9
	411770 430109		Hs.2540	chotinergic receptor, nicotinic, etpha p	2.2	2.6
65	458694		Hs.13298	ESTs	2.2	4.9
	41509			3-hydraxy-3-methylglutaryt-Coenzyme A sy	2.2 2.2	4.4 2.4
	43964		Hs.15396		2.2	4.9
	45013 45422			9 ESTs • ESTs, Weakly similar to A46010 X-linked	2.2	3.7
70	40532		112.1503	20.3, 113237 2	2.2	2.7
. •	43134	2 AW97101			2.2	5.2
	45310			ESTS	2.2 2.2	3.3 2.8
	40889		Hs.28370 Hs.14447		2.2	4.6
75	45139 43820				2.2	10.4
, ,	40844			51 dynamin 1	2.2	6.1
	41413	O A1570831	Hs.7159	Homo sapiens cDNA: FLJ21893 fis, clone H	2.2	3.1 3.0
	44501		Hs.1224		2.2 2.2	3.9 2.3
80	42437 42464				2.2	11.7
50	40972		Hs.1062		2.2	4.9
	43280)9 AA56550	9 Hs.1317	03 ESTa	2.2	19.9
	4228	30 Z43784	Hs.7589	ankyrin 3, node of Ranvier (ankyrin G)	2.2	10.4

		AE4E3336	LL 104700 1	BP-Interacting protein	2.2	6.5
				ypothetical protein DKFZp761M0423	2.2	3.4
			Hs.32501 (STs	22	3.2 2.0
_	452768	AW069459		STs	2.2 2.2	3.2
5	450440	AB024334		rrosine 3-monooxygenase/byptophan 5-mo xidalion resistance 1	2.2	23
	426281 428411	AK000987 AW291464		ESTs	2.2	2.3
	413787	AI352558	Hs.75544	yrosina 3-monooxygenase/tryptophan 5-mo	5.2	31
	451734	NM_006176	Hs.26944	neurogranin (protein kinase C substrate.	2.2 2.2	8.5 7.9
10	439108	AW163034	Hs.6467	synaptogyrin 3	2.2	2.4
	405385	AJ371849	Hs.200696	ATPase, Class VI, type 11C	2.2	2.2
	447285 452667	T87219		ESTs	2.2	3.1
	422234	AF119818	Hs.113287	discs, læge (Drosophila) homolog-associ	21	8.3 3.2
15	410339	AI916499	Hs.298258	ESTs .	21 21	4.5
	413231	D87461	Hs.75244 Hs.210706	BCL2-like 2 Homo sapiens cONA FLJ13182 fis, clone NT	21	2.2
	447104 451952	R19085 AL120173	Hs.301663	ESTs	2.1	36.5
	415841	Z45637	Hs.7093	ESTs	21	24
20	441086	A1928489	Hs.213490	ESTs, Weakly similar to N33_HUMAN N33 PR	2.1 2.1	2.2 6.6
	450407	NM_000810	Hs.24969	gamma-aminobutyric acid (GABA) A recepto guanine nucleotida binding protein (G pr	21	5.3
	427627	R87582 R56545	Hs.179915 Hs.6100	ESTs	2.1	4.5
	449712 409660	AW452065	Hs.258905	ESTs	2.1	2.1
25	430434	AL049548	Hs.241420	Homo sapiens mRNA for KIAA1756 protein.	2.1 2.1	5.4 3.0
	434138	AA625804		gb:zu86h01.s1 Soares_testis_NHT Homo sap	2.1	4.8
	448610	NM_006157	Hs.21602	nel (chicken)-like 1 gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	21	2.9
	418948 414876	A1217097 AW950925	Hs.924	crystallin, mu	2.1	3.4
30	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13563 fis, clone PL	2.1	3.7
-	451249	AA016227	Hs.27280	ESTs	2.1 2.1	4.1 2.1
	451475	T19093	Hs.26450	KIAA0725 protein	21	29.7
	448743	AB032962	Hs.21896 Hs.247993	KIAA1136 protein NG5 protein	2.1	2.7
35	430814 426990	U89336 AL044315	Hs.173094	Homo sapiens mRNA for KtAA1750 protein,	2.1	23
22	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	2.1	4.5
	427335	AA448542	Hs.251677	Gantigen 7B	2.1 2.1	2.2 2.3
	459089	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp56401763 (f	2.1	5.9
40	435832	AA425688	Hs.41641 Hs.92511	Bruno (Drosophila) -lika 4, RNA binding ESTs	2.1	2.9
40	446383 412768	T05816 AW996044	Hs.26239	Human DNA sequence from clone RP11-438B2	2.1	2.1
	453976	BE463830	Hs.163714	ESTs	2.1	4.2
	415111	R39039	Hs.328455	EST	2.1 2.1	3.3 4.9
40	452238	F01811	Hs.187931	ESTs	2.1	9.8
45	445279	R41900	Hs.22245 Hs.179080	ESTS .	2.1	3.1
	448799 418338	AJ937094 NM_00252		neuronal pentraxin I	2.1	8.3
	445725		Hs.13209	hypothetical protein FLJ 10094	2.1	5.4
	443537	D13305	Hs.203	cholecystokinin B receptor	2.1 2.1	4,1 6.4
50	454066		Hs.37058	calcitonin/calcitonin-related polypeptid	2.1	7.2
	429954		Hs.21374 Hs.20057	ESTs ESTs	2.1	3.9
	415292 423563		Hs.75209	protein kinase (cAMP-dependent, catalyti	2.1	3.1
	424906		Hs.15371	Homo sapiens mRNA for Hmob33 protein, 3	2.1	4.7 2.2
55	459309			hypothetical protein AF 140225	2.1 2.1	4.7
	439340			brain-specific Na-dependent inorganic ph polymerase (RNA) II (DNA directed) polyp	21	5.4
	402598 435408		Hs.3128 Hs.4884	calcium/calmodulin-dependent protein kin	2.1	6.6
	44879		Hs.12826		2.1	4,1
60	44950	0 AW95634		ESTs	2.1 2.1	2.4 5.8
	44113		Hs.7678	cellular retinoic acid-binding protein 1	2.1	2.7
	43336		73 Hs.30014 Hs.31092		2.1	5.0
	45294 42618			6 RAN binding protein 6	2.0	2.2
65	45366				2.0	3.1
	42463				2.0 2.0	3.5 4.1
	44858				2.0	2.3
	43041			ESTs	2.0	2.1
70	44562 41709		75 FB.7303 Hs.1811		2.0	2.5
, 0	4536			59 ESTs	2.0	4.7
	4358	50 AF25084	17 Hs.2835	14 milochondrial ceramidase	2.0 2.0	3.7 2.1
	4350				2.0	21
75	4231		Hs.8417 01 Hs.7076		2.0	28
13	4115 4316				2.0	2.5
	4298		5 Hs.225	36 synapsin I	2.0	3.6
	4398	07 BE5405	65 Hs.159	60 ESTs	2.0	17.5 4.0
0/	ADRO	33 AW1380			2.0 2.0	2.7
80					2.0	2.6
	4196 4326				2.0	2.3
	4540				2.0	15.9

5	423246 A 415989 A 420276 A 424983 A 446296 A	L119114 H H267700 H A290938 H A742434 H A8885662 H	s.77196 spei ls.317584 ES1 ls.190561 ES1 ls.169911 ES1	's, Highly similær to SORL_HUMAN SORTI 's no sapiens cDNA FL.113155 fis, clone NT	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	3.1 2.9 4.8 5.1 15.9 2.7 3.5
10	TABLE 118: Pkey: CAT number Accession:	: Gene d	Eos probeset ide luster number it accession num			
15	408274 412100	CAT Number 104999_1 1277224_1 1277883_1	AW89273 BE18034 AW90189	43964 AA053547 1 H08502 Z45826	180418 RF18025 RF1804	16 AW901899 BE180228 AW901897 BE180224 21 BE180341 AW901894 BE180217 BE180227 AW901891
20	413153 413510 414828 418948	1350849_1 1374377_1 149563_1 180808_1	N94205 (F13044 1 AA15665	XE067565 BE067556 77009 BE145525 BE145493 1 AA155622 R14472 1 AW88690 W38035 W38792 AA232835 AW9350 79 AW9853680 AA244436 H82527 AA381046 AA24	43	
25	419558 421249 421640 429995 430212	185904_1 200649_1 204833_1 311738_1 314437_1 341756_1	AA28536 AW9666 AA4635 AA4691	22 AW752386 AW847156 AA285373 AW879575 A 52 AW966653 AA294899 AA385977 11 A1277645 AL118763 53 A4718503 AA465925 14 AW873343 AA554293	W879558	
30	432122 433449 434138 437483 439780	366532_1 380572_1 43756_1 47673_1	AW772 AA6258 AL3901 AL1096	82 AA592974 D4 AW418787 AW074833 AI675642 AI393368 74 AW98817 88 R23665 R26578 66 BE007223 R30687		
35	452502 455517 456407 TABLE 11	919733_1 1321782_1 184986_1	AW984	568 AW984072 AW984077 514 AA243209 AA281411		
40	Pkey: Ref: Strand: Nt_positio	Uniq Sequ sequ Indic	uence source. To sence of human o sates DNA strand	sponding to an Eos probeset to 7 digit numbers in this column are Genbank Ider shromosome 22" Dunham, et al. (1999) <u>Natura</u> 402: from which exons were predicted. positions of predicted exons.	itifier (Gi) numbers. "Dunha 489-495.	am, et al." refers to the publication entitled "The ONA
45	Pkey 400979 401213 401421	Ref 8072554 9858408 7452889	Strand Plus Plus Minus	Nt_position 160842-161028 98743-98380,98489-98619 142291-142461 174720-175016,175104-175406,175508-175813		·
50	403092 404648 404793 404835 405326	8954241 9796894 7232206 6970743 4375975	Plus Minus Minus Plus Plus	115334-116020 61087-61590 5462-85684,88139-88287.90338-91018,94827-9 10633-10709,30805-30893,38078-38253.55112-5	14990 15327,57718-57818,66696-	56841
55	405385 405793 405911 405977	6552772 1405887 6758795 8247789	Plus Minus Plus Minus	48332-48454 89197-89453 101008-101643 135648-136177		
60	Table 1	ZA lists about 67 metrix/Eos Hu0:	8 genes up-regul 3 Gene Chip array	such that the tano or average Loc to average	CNS tissues was greater th	CENTRAL NERVOUS SYSTEM typicer (CNS). These were selected from 59680 probesets on an or equal to 2.5. The "average" LGG level was set to the 85° typicous CNS tissues. In order to remove gene-specific ubtracted from both the numerator and the denominator before
65	the ration Pkey: ExAcor Unigen	o was evaluated Ur a: E: eID: U	nique Eos probes xemplar Accessio nigene number	et identifier number in number, Genbank accession number		
70	R1:	R	nigene gene title atio of LOWER (UnigenetD	RADE GLIOBLASTOMA to normal CNS Unigene Title	RI	
75	Pkey 412420 424800 45339: 40260 44419	0 AL035588 2 U23752 4	Hs.73853 Hs.153203 Hs.32964	bane marphogenetic protein 2	20.3 19.5 18.5 16.9 15.0	
80	40963 44373	8 AW45042 11 AI083928 19 BE25915 12 AI199268 11 AF21751	Hs.21335 Hs.145416 Hs.127793 Hs.19322 Hs.27990	ESTs ESTs delta (Drosophila)-like 3 Horno sapiens, Similar to RIKEN cDNA 2010 clone HQ0310 PR00310p1	14.6 14.6 13.0 12.0 10.0 9.5) 5 2 3
					005	

					•-
				ESTs	9.0 8.8
				ESTs ESTs	8.4
	448769 437034	AA742643	16.50115	gb:ny91c01.s1 NCI_CGAP_GCB1 Homo sepiens	8.2
5	449539	W80363	Hs.58446	ESTs	8.1 8.0
	417061		Hs.188691	Homo sapiens cDNA FLJ12033 fis, done HE DiGeorge syndrome critical region gene 8	7.8
	435020 414217		Hs.301855 Hs.279898	Homo sepiens cDNA: FLJ23165 fis, clone L	7.7
	449300	A1656959	Hs.346514	ESTs	7.6
10	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fis, clone PL	7.\$ 7.2
	452372	A1885742	Hs.228474 Hs.279727	ESTs ESTs; homologue of PEM-3 (Clona savignyi	7.2
	410102 417308	AW248508 H60720	Hs.81892	KIAA0101 gene product	7.2
	447004	AW296968	Hs.157539	ESTs	7.1
15	418113	Al272141	Hs.83484	SRY (sex determining region Y)-box 4	7.1 7.1
	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, done Pt. Target Exon	7.1
	406478 428728	NM_016625	Hs.191381	hypothetical protein	6.9
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	6.9
20	428037	N47474	Hs.89230	potassium intermediate/small conductance	6.7 6.7
	423343	AA324643 R45137	Hs.246106 Hs.21868	ESTS ESTS	6.7
	418097 431553	X78075	Hs.2799	cartilage linking protein 1	6.6
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	6.6
25	425397	J04088	Hs.156346	topoisomerase (ONA) II aipha (170kD)	6.4 6.4
	419169 431117	AW851980 AF003522	Hs.262346 Hs.250500	ESTs, Wealdy similar to S72482 hypotheti delta (Drosophila)-like 1	6.4
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	6.3
	402855			NM_001839":Homo saptens calponin 3, acid	6.2
30	424009	F11690		gb:HSC30D041 normalized Infant brain cDN	6.2 6.2
	400419 446584	AF084545 U53445	Hs.15432	Target downregulated in overian cancer 1	6.0
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	6.0
	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	5.9
35	427144	X95097	Hs.2126	vasoactive intestinal peptide receptor 2 fibrillin 2 (congenital contractural ara	5.9 5.8
	416658	U03272	Hs.79432	Target Exon	5.7
•	405238 421977	W94197	Hs.110165	ribosomal protein L26 homolog	5.7
	405348			C7001664:gi 12698081 dbj BAB21849.1 (AB	5.6 5.4
40	428795	R45503	Hs.97469	ESTs, Highly similar to A39769 N-acetyll	5.3
	422672 403349	X12784 NM_001406	Hs.119129	collagen, type IV, alpha 1 ephrin-B3	5.3
	453941	U39817	Hs.36820	Bloom syndrome	5.2
	429139	F09092	Hs.66087	ESTs	5.2 5.2
45	454860	AW835767	11- 51050	gb:CV4-LT0016-240200-110-b08 LT0016 Homo hypothetical protein FLJ13164	5.1
	452279 418030	AA286844 BE207573	Hs.61260 Hs.83321	neuromedin 8	5.1
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	5.1
60	450639		Hs.27717		5.1 5.1
50	412811	H06382 AW206560	Hs.25356	ESTS 9 ESTS	5.1
	442832 436608		FI3.23300	down syndrome critical region protein DS	5.1
	408161			3 hypothetical protein MGC3032	5.1
66	443744		Hs.27154		5.1 5.0
55	447497 450811		Hs.20572 Hs.24549		5.0
	433244		Hs.27126	IS KIAA1510 protein	4.9
	438458	AW975186		gb:EST387294 MAGE resequences, MAGN Homo	4.9 4.9
60	438456		Hs.20594 Hs.6799		4.9
OU	411048 456304		L/2/0133	gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	4.9
	44254	7 AA306997		B4 ESTs, Weakly similar to ALU1_HUMAN ALU S	4.9
	41999	1 AJ000098	Hs.9421	o eyes absent (Drosophila) homotog 1 C19000498*:gij4567179tpbjAAD23607.1jAC00	4.8 4.8
65	40227 42009		Hs.8804		4.8
0,5	43628		Hs.2721		4.8
	43080		Hs.2620	09 ESTs, Moderately similar to 138022 hypot	4.8
	45510)	gb:RC1-BT0313-110300-015-f06 BT0313 Homo	4.8 4.8
70	40396 42495		46 Hs.1846	Target Exon tumor protein p53 (U-Fraumeni syndrome)	4.8
,,	41482		Hs.774		4.8
	44789	1 R41754	Hs.6496	ESTS	4.7 4.7
	42352		Hs.1204		4.7
75	42273		Hs.1190 Hs.190		4.6
, ,	43769		Hs.799		4.6
	4034	81		Target Exon	4.6 4.6
	4260				4.6
80	4221 4163		Hs.112 Hs.203		4.6
	4064			Target Exon	4.5
	4560	52 BE31190			4.5 4.5
	4231	78 AI033140	D Hs.124	983 Homo sapiens mRNA; cDNA DKFZp564C142 (fr	4.3

	411642	NM_014932	Hs.71132	neuro	ligin 1	4.5
	428282	N34905	Hs.44653	Homo	sapiens cDNA: FLJ22669 fis. clone H	4.5 4.5
	432625	A1243596	Hs.94830	ESTS	, Moderately similar to 103094 A-kin 1547 protein	4.5
5	452994 449961	AW962597 AW265634	Hs.31305 Hs.133100	EST:		4.4
,	401454	A1120004	113.100.00	NM_	014226*:Homo sapiens renal tumor anti	4.4 4.4
	406395			Targ	et Exon	4.4
	432281	AK001239	Hs.274263		thetical protein FLJ 10377 .1678	4.4
10	453792 415131	AL134539 D61119	Hs.254129	ob H	UM158C11B Clontech human fetal brain	4.4
10	437695	AA769202	Hs.192142	EST		4.4
	422081	AW136820	Hs.196011	EST		4.4 4.3
	437748	AF234882	Hs.5814		ression of tumorigenicity 7	4.3
15	433323	AA805132 BE258835	Hs.159142	EST	01117374F1 NIH_MGC_16 Home septens c	4.3
15	420352 444218	AF070641	Hs.10684	Hon	no sapiens clone 24421 mRNA sequence	4.3
	441035	A1594309	Hs.126458	EST	\$	4.3 4.3
	443836	BE221613	Hs.140553	EST	's Da teucine-rich repeat (LRR) protein	4.3
20	425292	NM_005824 AA429504	Hs.155545	ES1		4.3
20	450166 429149	AW193360	Hs.197962	EST	To Weakly similar to U38022 hypotheti	4.2
	422798	R92347	Hs.34574	ES.	rs. Wealdy similar to ALU1_HUMAN ALU S	4.2 4.2
	451254	A1571016	Hs.172967	ES	Ts	4.2
25	409189	AA125984 AI208762	Hs.345572		zn27h06.r1 Stratagene neuroepithellum	4.2
25	445118 444326	A1208762 A1939357	Hs.270710	ES	Ts	4.2
	456060	C14904	Hs.45184	Ho	mo sagiens cONA FLJ12284 ffs, clone MA	4.2 4.2
	404120				000537::gij3298595jgbjAAC41376.11 (AF0	4.1
20	436899	AA764852	Hs.291567 Hs.248941		Ts Ts	4.1
30	407624 453361	AW157431 AA035197	Hs.107375	ES	iTs	4.1
	447439	AA313565	Hs.145020	ES	its, Wealdy similar to KIAA1205 protein	4.1
	438372	Al140189	Hs.123191		STS .	4.1 4,1
25	438624	AA889055	Hs.123468 Hs.25017		STs pothetical protein FLJ13158	4.1
35	422493 406872	AW474183 AI760903	ns.23017.	,, at	:wi09h08.x1 NCI_CGAP_CLL1 Homo sapiens	4.1
	425295	AA431366	Hs.37251	E	STs	4.1
	425849	AJ000512	Hs.29632	3 54	erum/glucocorficoid regulated kinase	4.0
40	434206	AW136973	Hs.18047 Hs.99235	9 E	STs, Wealdy similar to S69890 mitogen i gulator of G-protein signaffing 20	4.0
40	420602 400645	AF060877	HS.33230	T	arget Exon	4.0
	456306	AA225313	Hs.22288	18 E	STs, Wealty similar to TRHY_HUMAN TRICH	4.0
	419326	W94915	Hs.42418		STs	4.0 4.0
45	414948		Hs.18215		STs ell division cycle 25A	4.0
45	423198 411537		Hs.1634		b:MR0-BT0551-060300-102-e05 BT0551 Homo	4.0
	421637			m i	tomo saniens clone 23556 mRNA sequence	3.9 3.9
	439231			30 I	tomo sapiens mRNA; cDNA DKFZp434N079 (fr	3.9
50	429433		Hs.2135		ESTs, Weakly similar to KIAA1353 protein Homo sapiens cDNA FLJ10281 fis, clone HE	3.9
30	424188 449932		Hs.2630	24	ESTA	3.9
	43407		Hs.2830	59	Homo sepiens PRO1082 mRNA, complete cds	3.9
	43478	4 AA649051		.07	ESTs MAGG Home	3.9 3.9
55	42514				gb:EST366697 MAGE resequences, MAGC Homo ESTs	3.9
55	42853 44331				ESTS	3.9
	41685				ESTs	3.9
	41168	8 AW95344		***	gb:EST365510 MAGE resequences, MAGB Homo	3.9 3.9
60	44734				ESTs, Highty similar to S02392 alpha-2-m novel C3HC4 type Zinc finger (ring fings	3.8
00	42590 40369		9 Hs.318	304	C4001100*:gi 5852342 gb AAD54015.1 (AF0	3.8
	41588		Hs.134	71	ESTe	3.8
	43264	16 AW7533			gb:RC3-CT0254-031099-012-e05 CT0254 Hamo	3.8 3.8
	4470		7 Hs.157	697	ESTs	3.8
65			5 Hs.468	121	Target Exon hypothetical protein FLJ20086	3.8
	4413: 4166:		Hs.202		ESTs	3.8
	4260				ESTs	3.8
~	4556	46 BE0644			gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.8 3.8
70			Hs.894 7 Hs.344		ets variant gene 1 ESTs	3.8
	4450 4572				ESTs, Wealthy similar to S51797 vasodilat	3.8
	4200				ESTs, Moderately similar to 138022 hypot	3.8
_	4280	60 AA4206	16 Hs.24	9483	ESTs	3.7 3.7
7:	4164	127 BE2440			Rac/Cdc42 guarrine exchange factor (GEF)	3.7 3.7
	4530		415 Hs.20	303	HBV pX associated protein-8 Target Exon	3.7
	4045 447		408 Hs.15	2290	ESTs, Highly similar to JC2463 vasoactiv	3.7
	453	438 AJ4699	35 Hs.22	2792	ESTs	3.7 3.7
8	0 429	643 AA455	889 Hs.16	37279	FYVE-finger-containing RabS effector pro	3.7
		072 A18903 660 M7908		11923	Homo sapiens cDNA: FLJ22785 fis. clone K ESTs	3.7
		660 M7908 188 Al3629		328	solute carrier lamily 7 (cationic amino	3.7

	430744			ESTS	damala internation ambio bigges ?	3.7 3.7
	454392 454457	BE260893 AW753456	Hs.236131	ab-OV	domain-interacting protein kinase 2 2-CT0261-261099-011-d11 CT0261 Homo	3.7
	454457 435095		Hs.4750	hypoth	etical protein OKFZp564K0822	3.7
5	438206	AA780385		ESTS	A LA Di Control de Con	3.7 3.7
	418967	NM_001725	Hs.89535 Hs.180878		icida/permeability-increasing pro otein lipase	3.7
	427809 427722	M26380 AK000123	Hs.180479	hypot	netical protein FLJ20116	3.7
	413986	Z43567	•	gb:HS	C1FC021 normalized infant brain cDN	3.7 3.7
10	438898	AI819863	Hs.106243	ESTS		3.7
	418483	W26076 R20529	Hs.221847 Hs.6806	ESTs ESTs		3.6
	415849 438380	T06430	Hs.6194	chone	troitin suffate proteoglycan BEHAB/b	3.6
	440296	D30829	Hs.180610	splici	ng factor proline/glutamine rich (3.6 3.6
15	438025	AW501360	Hs.258910 Hs.25300	EST	phatidylinositol 4-kinase type II	3.6
	458970 448002	AW246119 Y15227	Hs.20149	detet	ed in lymphocytic leukemia, 1	3.6
	432058	AW665996	Hs.130729	EST	s, Weatty similar to ALU1_HUMAN ALU S	3.6 3.6
~~	409557	BE182896	Hs.211193	EST	o saplens, Similar to nuclear localiz	3.6
20	418049 425331	AA211467 AW962128	Hs.190488	ob:E	ST374201 MAGE resequences, MAGG Horno	3.6
	424051	AL110203	Hs.138411	Horr	o sapiens mRNA; cDNA DKFZp586J1922 (f	3.6
	404185			Targ	et Exon	3.6 3.6
25	427517	AA644142 AW978202	Hs.7107 Hs.289064	E51	s, Weakly similar to ALU7_HUMAN ALU S othetical protein FLJ22251	3.6
25	421094 440388	AI693520	Hs.223000	EST	' \$	3.6
	415934	NM_000928	Hs.992	pho	spholipase A2, group iB (pancreas)	3.6 3.6
	408292	AW178363	Hs.38178	gb:l	RC3-HT0105-010999-002-H06 HT0105 Homo othetical protein FLJ23468	3.6
30	442432 451826	BE093589 AA020741	Hs.171611			3.6
50	427375	AL035460	Hs.177536	me	allocarboxypeptidase CPX-1	3.6 3.6
	419485	AA489023	Hs.99807	ES	Ts, Weakly similar to unnamed protein Ts, Weakly similar to 138022 hypotheti	3.6
	416370 418400	N90470 BE243026	Hs.203697 Hs.301989		A0246 protein	3.6
35	436674	AA725002	Hs.272018	low	molecular mass ubiquinone-binding pr	3.5 3.5
	407013	U35637		gb	Human nebulin mRNA, partial cds ISP00000241415°;Hypothetical 67.7 kDa p	3.5
	403108 422564	Al148006	Hs.222120		its	3.5
	450297	AW901347			pothetical protein FLJ23342	3.5 3.5
40	436338		Hs.11839		STs .	3.5
	447458		Hs.15896	1 E	STs :EST383123 MAGE resequences, MAGK Homo	3.5
	457364 458814		Hs.17086	ı Ě	STs, Weakly similar to Z195_HUMAN ZINC	3.5
	441701		Hs.12749	7 E	STs	3.5 3.5
45	405558		Hs.9071	T:	arget Exon ogesterone membrane binding protein	3.5
	452682 434589			Q.	b:Homo sapiens full length insert cONA	3.5
	44328		Hs.13291	17 È	STs	3.5 3.5
50	40518		Hs.19546		M_016358":Homo sapiens iroquois homeobo Ismin A, alpha (actin-binding protein-	3.5
50	41006- 42523			09 E	STs. Weakly similar to 138022 hypotheti	3.5
	40427			1	arget Exon	3.5 3.5
	42880				STs rypothetical protein FLJ20311	3.5
55	44744 45047			15 I	STs	3.4
,,,	45445			•	ф:QV3-CT0192-211099-008-g02 CT0192 Homo	3.4 3.4
	40037				lomo sapiens ovarian cancer related prot ESTs	3.4
	44094 44961				ESTS	3.4
60	44566		Hs.2823	386	ESTs	3.4 3.4
	4458		Hs.8190 Hs.1697)7 745	ESTs crumbs (Drosophila) homolog 1	3.4
	4375 4429				ESTs	3.4
	4511				FSTs	3.4 3.4
65					gb:RC5-ST0293-140200-014-H05-ST0293-Homo	3.4
	4592 4337		Hs.301 Hs.112		homeodomain-interacting protein kinase 3 ESTs	3.4
	4449				xanthene dehydrogenase	3.4 3.4
	4397	53 BE2622			hypothetical protein from EUROIMAGE 2168	3.4
70					ESTs matrilin 2	3.4
	4477				Target Exon	3.4
	422	18 AK0013		6385	hypothetical protein FLJ10521	3.3 3.3
7:	5 439				gb:zd64c04.r1 Soares_fetal_heart_NbHH19W ESTs, Moderately similar to ZN91_HUMAN Z	3.3
/.	O 416			6313	ESTs	3.3
	432	890 NM_01	4442 Hs.27		siafic acid binding Ig-like lectin 8	3.3 3.3
	412			25E	gb:QV4-NN0038-300300-155-e07 NN0038 Homo S100 calcium-binding protein A4 (calcium	3.3
R		130 AW276 854 AW138			ESTs	3.3
•		048 BE281			ESTs, Moderately similar to A47582 B-cel	3.3 3.3
		632	779		NM_022490:Homo sapiens hypothetical prol gb:MR2-CT0222-011199-007-d06 CT0222 Homo	3.3
	411	565 AW851	1/25		Bring States Att 102-001-000 GLOST HOLD	•.•

				STs erologically defined colon cancer antig	3.3 3.3
	426625 401272	T78300		29000559":gi]12314195jembjCAB99338.1 (A	3.3
_		AB021923 .	Hs.23367 (ST-YD1 protein	3.3
5	401702	********		VM_001171*:Homo sapiens ATP-binding cass	3.3 3.3
		AW816274 AI218517		rypothetical protein FLJ 12973 ESTs	3.3
		AW807321		tb:MR4-ST0062-240300-003-g05 ST0062 Homo	3.3
• •	423784	AK000039	Hs.132826	Homo sepiens cDNA FLJ14913 fis, clone PL	3.3 3.3
10	440688	AW404591	Hs.147440 Hs.12600	ESTs, Wealdy similar to Z192_HUMAN ZINC N-ethylmaleimide-sensitive factor attach	3.3
	410267 455778	AW978005 BE088746	ris. 12000	gb:CM2-BT0693-210300-123-d09 BT0693 Homo	3.3
	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	3.2
1.6	451597	AW295250		ESTS	3.2 3.2
15	451446 421353	A1826288 AW292857	Hs.171637 Hs.255130	hypothetical protein MGC2628 ESTs	3.2
	442710	At015631	Hs.23210	ESTs	3.2
	420560	AW207748	Hs.59115	ESTs	3.2 3.2
20	417404	NM_007350	Hs.82101 Hs.283854	pteckstrin homology-like domain, family at:nz36a03.s1 NCI_CGAP_GCB1 Homo saptens	3.2
20	437834 430694	AA769294 AA810624	Hs.30936	ESTs, Wealdy similar to H2BH_HUMAN HISTO	3.2
	412021	AW885592		gb:RC4-OT0071-090300-011-g11 OT0071 Homo	3.2
	443431	AI056847	Hs.20654	ESTs	3.2 3.2
25	445774 413335	AI254165 AI613318	Hs.339968 Hs.48442	ESTs ESTs	3.2
23	450692	H50603	Hs.94037	hypothetical protein FLJ23053	3.2
	411571	BE049094		ESTs	3.2 3.2
	404592			NM_022739":Homo sapiens E3 ubiquifin lig Target Exon	3.2
30	402747 428500	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	3.2
50	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.2
	445347	AF035318	Hs.12533	Homo sapiens clone 23705 mRNA sequence	3.2 3.2
	458438 442314	AI141520 AI311854	Hs.151464 Hs.129220	ESTs, Weakly similar to ALUC_HUMAN IIII ESTs	3.2
35	435291	BE568452	Hs.344037	protein regulator of cytokinesis 1	3.2
	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	3.2 3.2
	448789	BE539108	Hs.22051	hypothetical protein MGC15548 Target Exon	3.2
	403291 436210	AI825420	Hs.197824	EST8	3.2
40	418079	R40058	Hs.6911	ESTs	3.2
	413951	AW051200	Hs.75640	natriuretic peptide procursor A	3.2 . 3.2
	435828 437722	AA700705 AW292947	Hs.13852 Hs.122872	ESTs ESTs, Wealdy similar to JU0033 hypotheti	3.2
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	3.2
45	405046			C3000978:gij9280045 dbijBAB01579.1 (AB0	3.1 3.1
	444315 453096	R07860 AW294631	Hs.20039 Hs.11325	ESTs ESTs	3.1
	433835	A1806185	113,11020	gb:wf26a10.x1 Soares_NFL_T_GBC_S1 Homo s	3.1
	430608	R45584	Hs.23025	ESTs, Weakly similar to ALUS_HUMAN ALU S	3.1 3.1
50	453324	W26592 R54418	Hs.232089 Hs.183745	ESTs hypothetical protein FLJ13456	3.1
	414884 446862	AV660697	Hs.282700	ESTs	3.1
	427241	AA399988	Hs.112087	Human DNA sequence from clone RP11-530N1	3.1
55	416486	H81336	Hs.37560	ESTs gb:zb87a09.r1 Soares_senescent_fibroblas	3.1 3.1
55	429940 430535	W25215 AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	3.1
	439544	W26354	Hs.28891	hypothetical protein FLJ11360; artemis p	3.1
	437083	AW082597			3.1 3.1
60	435677 458810	AA694142 BE407125	Hs.293726 Hs.231510		3.1
00	443484	AI091458	Hs.134559	ESTs .	3.1
	427581	NM_01478		3 KIAA0129 gene product	3.1 3.1
	444016 423337			gb:xw82h09.r1 Soares_testis_NHT Homo sap 7 axin 2 (conductin, axii)	3.1
65	403288		_ ,,,,,,,,,,	C1001737*:gi[7511201[pir]]T27904 hypothe	3.1
	450125	AA005418		6 ESTs	3.1
	438138		Hs.17750		3.1
	436222 443433		Hs.12281 Hs.30166		3.1
70	443725	AW24568	D Hs.9701	growth arrest and DNA-damage-inducible,	3.1
	43204		7	gb:EST384819 MAGE resequences, MAGL Homo	3.1 3.1
	405760 42378		Hs.13285	Target Exon 11 hypothetical protein FLJ11222	3.1
	41160		1 Hs.1775	O ESTs	3.1
75	41789	3 AA290605			3.1 3.1
	44924 42952				3.1
	42552 45664				3.1
00	41249	0 AW80356	4 Hs.2888	50 Homo sapiens cDNA: FLJ22528 fis, clone H	31 31
80) Hs.2039 Hs.1776		3.1
	43450 45075				3.1
	41529		Hs.1065		3.0
				209	
				207	

	403212			NIM 040505-None aminos internation 2 at	
	422757	AI909935	Hs.65551	NM_019595:Homo sapiens intersectin 2 (IT Homo sapiens, Similar to DNA segment, Ch	3.0 3.0
	427624	AA406245	Hs.24895	EST8	3.0
_	449256	AA059050	Hs.59847	ESTs	3.0
5	411543	AW851248		gb:1L3-CT0220-160200-066-F01 CT0220 Homo	3.0
	409112	BE243971	Hs.50649	quinone oxidoreductase homolog	3.0
	414403	AW969551	Hs.76064	ribosomal protein L27a	3.0
	427418	AA402587	Hs.325520	LAT1-3TM protein	3.0
10	455481	AW948317	14. 4057	gb:RC0-MT0015-280300-021-a09 MT0015 Homo	30
10	444396 407235	T65213 020569	Hs.4257	ESTs	3.0
	431431	AL096711	Hs.169407 Hs.252953	SAC2 (suppressor of actin mutations 2, y	3.0
	451391	AA017410	Hs.40568	Human DNA sequence from clone RP3-403A15 ESTs	3.0 3.0
	430251	AA609246	Hs.181451	ESTs .	3.0
15	420658	AW965215	Hs.130707	ESTs	3.0
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	3.0
	440897	AW104275	Hs.148348	ESTs	3.0
	444509	AW571659	Hs.278081	EST ₈	3.0
20	433062 408523	AK001757 AW833259	Hs.281348	hypothetical protein FU10895	3.0
20	443477	R32325	Hs.314287 Hs.221794	ESTs ESTs	3.0
	423869	BE409301	Hs.134012	C1g-related factor	3.0 3.0
	405488			ENSP00000220888*:ZINC FINGER TRANSCRIPTI	3.0
0.0	414988	C17535		gb:C17535 Human placenta cONA (TFujiwara	3.0
25	440471	AA885146	Hs.307944	ESTA	3.0
	416355	H49875	Hs.268906	ESTs	3.0
	408926	AF217525	Hs.49002	Down syndrome cell adhesion molecule	3.0
	424028 438201	AF055084 AA780243	Hs.153692 Hs.54547	Homo sapiens cDNA FLJ14354 fs, clone Y7 ESTs	2.9
30	413851	AW897510	Hs.137387	ESTs	2.9
	402229	BE262804	113.137307	mitochondrial ribosomal protein S2	2.9 2.9
	444145	BE153823	Hs.282385	ESTs, Weakly similar to 2004399A chromos	2.9
	423770	AW976766	Hs.132776	Homo saplens cDNA FLJ10077 fis, clone HE	2.9
25	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	29
35	414232	W86946	Hs.238246	hypothetical protein FLJ22479	2.9
	400533 440483	41200025	450005	ENSP00000209376":PRED65 protein (Fragmen	2.9
	443502	A1200835 A1074528	Hs.150385 Hs.133949	ESTs ESTs	29
	449667	AB023227	Hs.23860	KIAA1010 protein	2.9
40	446809	AW590171	Hs.101413	ESTs	2.9 2.9
	408788	AL134947	Hs.213956	Homo sapiens BAC clone RP11-10205 from Y	2.9
	413627	BE182082	Hs.246973	ESTs	2.9
	449655	AI021987	Hs.59970	ESTs	2.9
45	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	2.9
43	400090	A1410.400.40		Eas Control	2.9
	454968 423352	AW849046 AA324808	N= 103576	gb:IL3-CT0214-150300-085-H06 CT0214 Homo	2.9
	426197	AA004410	Hs.193576 Hs.100009	ESTs acyt-Coenzyme A oxidase 1, palmitoyt	2.9
	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	2.9 2.9
50	415346	Z43108		gb:HSC13E071 normalized infant brain cDN	2.9
	436726	AA324975	Hs.198689	ESTs, Wealdy similar to T00079 hypotheti	2.9
	442513	AF 150207	Hs.207949	ESTs	2.9
	425012	177666	Hs.92414	Homo sapiens cDNA: FLJ22030 fis, clone H	2.9
55	402322 427235	AI126288	Hs.192232	Target Exon	2.9
-	456412	AW749617	Hs.280776	ESTs tankyrase, TRF1-interacting ankyrin-rela	2.9 2.9
	431196	AW974436	Hs.154929	ESTs	29
	439379	AA835002	Hs.125611	ESTs	2.9
	423757	AL049337	Hs.132571	Homo sapiens mRNA; cDNA DKFZp564P016 (fr	2.9
60	446134	AW161234	Hs.13993	TBP-like 1	2.9
	435645 449385	AI052789 AI650471	Hs.133263	ESTs SOT	2.9
	444161	N52543	Hs.347290 Hs.142940	ESTs	2.9
	406635	U07162	TIS. 14234U	gb:Human clone LNA11 autoantibody to hea	2.9
65	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	2.9 2.9
	458760	AI498831	Hs.111334	ferritin, light potypeptide	2.9
	427245	AA421022	Hs.97739	ESTs	2.9
	400658			ENSP00000237081*:KIAA1217 PROTEIN (FRAGM	29
70	430701	A1760833	Hs.293971	ESTs	2.9
, 0	435294	T84084	Hs.196008		29
	429927 446160	NM_001115 AW392197	Hs.2522 Hs.218003	adenylate cyclase 8 (brain) ESTs	29
	420674	NM_000055	Hs.1327	butyrytcholinesterase	29
	424330	AW073953	Hs.333396	Homo sapiens cDNA FLJ13596 ffs, clone PL	29 29
75	418915	AJ474778	Hs.118977		29
	425922	AL157466	Hs.162751	Homo sapiens mRNA; cDNA DKFZp761E2423 (f	29
	447512	AW958148	Hs.129454	ESTs	29
	449990	AJ279010	Hs.48821	ESTs	2.8
80	423779 427395	AW071837 AW298741	Hs.57971	ESTs Maderatohy similar to 120022 hours	2.8
	416188	BE157260	Hs.97861 Hs.79070	ESTs, Moderately similar to 138022 hypot v-myc avian myelocytomatosis viral oncog	2.8
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orotat	2.8 2.8
	400352	AF068294	Hs.272414		2.8
				The second secon	

	457579	AB030816	Hs.36761 I	IRAS-like suppressor	2.8
			Hs.267150	QAA1409 protein	2.8 2.8
	403903			C5001632*:gi[10645308]gb[AAG21430.1]AC00	2.8
5	444491 455899	AI151091 BE155112	Hs.270714	EST8 gb:PM1-HT0350-151299-003-803 HT0350 Homo	2.8
,	457292	AI921270	Hs.281462	hypothetical protein FLI14251	2.8
	428305	AA446628	Hs.2799	cartilage linking protein 1	2.8 2.8
	435375	AI733610		ESTs	2.8 2.8
10	409078	AW327515 AA922153		ESTs hypothetical protein MGC15729	28
10	436109 444656	AJ277924	Hs.145199	ESTs	2.8
	426384	AJ472078	Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	2.8
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	28 28
1.5	438243	AI581311	No. 400050	ESTs ESTs	2.8
15	434012 402711	AA621425	Hs.186256	Target Exon	2.8
	442955	AI683534	Hs.131583	ESTs	2.8
	418319	AW611703	Hs.190173	ESTs, Wealtly similar to A46010 X-linked	2.8 2.8
20	438934	BE220137	Hs.124323	ESTs	2.8
20	438689	AW129261 AA478847	Hs.181672 Hs.42484	ESTs hypothetical protein FLJ10618	2.8
	420083 400315	U46120	Hs. 193392	Human expressed unknown mRNA	28
	433563	AI732637	Hs.277901	ESTs	2.8
	458093	AJ207788	Hs.343628	sialytransferase 48 (beta-gatactosidase	2.8 2.8
25	409157	AA064631	Hs.207077	gb:z/72c03.s1 Soares_pineal_gland_N3HPG ESTs	2.8
	450597 425300	AI701635 AW601773	Hs.270259	ESTs	2.8
	458817	Z25900	Hs.18724	Homo sapiens mRNA; cONA DKFZp564F093 (fr	2.8
	418312	AW972468	Hs.170307	Ral guanine nucleotide exchange factor R	2.8 2.8
30	430335	D80007	Hs.239499	KIAA0185 protein gb:MR4-ST0118-261099-012-e10 ST0118 Homo	2.8
	454581 419735	AW809189 AW750056	Hs.169577	Homo sapiens cDNA FLJ14743 fis, clone NT	2.8
	436265	AA731331	Hs.190668	ESTs	2.8
	439481	AF086294	Hs.125844	ESTs	2.8 2.8
35	441964	AA972619	Hs.20506	ESTs. Wealdy similar to 138022 hypotheti	2.8
	422648 430503	D86983 AA533574	Hs.118893 Hs.152274	Melanoma associated gene ESTs	28
	403942	AA333574	115.152214	Target Exon	2.8
	420565	AI806770	Hs.30258	ESTs	2.8
40	439069	H63144	Hs.184178		2.8 2.8
	436480	AJ271643	Hs.87459 Hs.29002	putative acid-sensing ion channel KIAA1708 protein	2.8
	408137 451692	AI694131 AL137422	Hs.26849	Homo saplens mRNA; cDNA DKFZp761A1623 (f	2.8
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45	452526	W38537	Hs.280740		2.8 2.8
	414300	AI304870	Hs.188680	ESTs ubiquitin carrier protein E2-C	2.8
	419741 437933	NM_007019 AI276132	Hs.93002 Hs.146155		2.7
	405941	ALTOIDE	15.140100	Target Exon	2,7
50	443210	AI692649	Hs.9451	hypothetical protein MGC13168	2.7 2.7
	450651	W79000	Hs.44545	ESTs, Weakly similar to B34087 hypotheti nucleoponin 88kD	2.7
	426765 418886	AA743503 AA993982	Hs.172100 Hs.130850		2.7
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55	430426	AA478807	Hs.12517		27 27
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	400924 458070		Hs.20940	Target Exon 6 ESTs, Wealthy similar to 138600 zinc fing	2.7
	427299		Hs.21426	3 ESTs, Moderately similar to ALU1_HUMAN A	2.7
60	442621	Al004333	Hs.13055	3 ESTs, Weakly similar to ALUA_HUMAN !!!!	2.7 2.7
	437643			gh:Homo sapiens mRNA full length insert 9 Homo sapiens cONA: FLJ22373 fis, clone H	27
	426925 443397		8 Hs.31568 Hs.29342		2.7
	42997		Hs.23451		2.7
65	438879			9 ESTs	2.7
	42255			gb:EST379359 MAGE resequences, MAGJ Homo	2.7 2.7
	44613		Hs.39749 Hs.2890		2.7
	42911 42861				2.7
70	43994		7 Hs.6788	astrotactin	2.7
. •	43969	9 AF08653	4 Hs.1875	61 ESTs, Moderately similar to ALU1_HUMAN A	2.7 2.7
	43833			68 ESTs	2.7
	45668 41207		3 Hs.1160 Hs.7313		2.7
75	41227			gb:QVO-NN1022-170400-193-c02 NN1022 Homo	27
, ,	43880	1 AA82597	1 Hs.1242	84 ESTs	2.7
	44289	2 AI038379			2.7 2.7
	4329		5 Hs.2790	165 trans-prenyltransferase NM_001334":Homo sapiens cathepsin O (CTS	27
80	40379		Hs.248		2.7
30	4154		Hs.260	274 ESTs	2.7
	4287	15 AW2937	16 Hs.531:	26 ESTs	2.7
	4577	50 AI65147	4 Hs.163	944 ESTs	2.7

	424480	AA341442 1	ts.205299	EST8	2.7
	444822			hypothetical protein FLJ23109	2.7
	432651			ESTS	2.7 2.7
_	439823			ESTS	2.7
5	457021			Homo sapiens cDNA: FLJ21897 fis, clone H	2.7
	440026			ESTs ESTs	2.7
	446960 435046			ESTS, Wealdy similar to ALU1_HUMAN ALU S	2.7
	431999		Hs.272312	Horno sapiens mRNA; cDNA DKFZp434J2235 (I	27
10	458527	AI950256		ESTs	2.7
	445899	AI263738	Hs.145626	ESTs	2.7 2.7
	404254			ENSP0000082468*:DJ45P21.3 (butyrophilin	27
	402344	44000453		Target Exon gb:EST93093 Skin tumor I Homo sapiens cD	27
15	426503 446420	AA380153 AW015693	Hs.135614	ESTs	2.7
13	426914	AA393328	Hs.194303	ESTs	2.7
	407903	AJ287341	Hs.154029	bHLH factor Hes4	2.7
	433009	AA761668		gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens	2.7 2.7
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20	403290	D4007E	Hs.194600	ESTs	2.7
	435143 416569	R12375 H64891	HS.134000	gb:yr68h03.r1 Soares fetal liver spleen	2.7
	428690	AI948490	Hs.98765	ESTs	2.7
	425128	BE561929	Hs.154718	tumor protein 052-like 2	2.7
25	443361	AF792628	Hs.133273	ESTs	2.7 2.7
	404053			Target Exon	26
	435113	AA665469	Hs.117135	ESTs CX000838:gij10092633[ref[NP_055314.1] pu	2.6
	405717 413098	BE065279		gb:RC1-BT0314-030500-016-b09 BT0314 Homo	2.6
30	444884	AI201094	Hs.148540	ESTs	2.6
50	419015	179262	Hs.14463	ESTs	2.6
	423234	AA323534	Hs.296162	AD037 protein	2.6 2.6
	406871	AA993857	Hs.180842	ribosomal protein L13	2.6
26	428670	AA431682	Hs.134832		26
35	408371 413929	AF161545 BE501689	Hs.44439 Hs.75617	hypothetical protein collagen, type IV, alpha 2	2.6
	408369	R38438	Hs.182575		2.6
	419817	AA743434	Hs.193778	ESTs	2.6
	415788	AW628686	Hs.78851	KIAA0217 protein	2.6 2.6
40	427388	BE379610	Hs.177592	ribosomal protein, large, P1	2.6
	451018	AW965599	Hs.247324	mitochondrial ribosomal protein S14 Target Exon	2.6
	405863 454037	AW998716		gb:PM4-BN0067-250300-002-f11 BN0067 Homo	2.6
	430147	R60704	Hs.234434		2.6
45	425480	AB023198	Hs.158135		2.6
	407182		Hs.230157		2.6 2.6
	439538		Hs.56407		2.8
	449249		Hs.193115 Hs.138343		2.6
50	429569 402936		113.1300	ENSP00000217246": DJ803K15.1 (novel prote	2.6
50	420670			ESTs	26
	455409			gb:PM2-DT0023-050400-003-h03 DT0023 Hamo	2.6 2.6
	413151		Hs.14197		26
55	422484		Hs.12315	NM_007325":Homo sepiens glutamate recept	2.6
23	400780 429258			gb:zx10e09.r1 Soares_total_fetus_Nb2HF8_	2.6
	44897			ob:UI-H-BI1-acw-a-06-0-UI.s1 NCI_CGAP_Su	2.6
	40261			C1003844*:gif6912550jref[NP_036483.1] ol	2.6 2.6
	41709	9 BE537357	Hs.30699	hypothetical protein MGC5457	26
60	42839			gb:zw50e02:r1 Soares_total_fetus_Nb2HF8_ 55 ESTs	2.6
	44916 41258		Hs.26416 Hs.74089		2.6
	44363		Hs.1342		2.6
	40298			Target Exon	2.6 2.6
65	43325		Hs.2073		2.6
	42891				2.6
	41855				2.6
	44521 40442		1 13,1102	C8000067*:gij10432400jembjCAC10290.1j (A	2.6
70	4359		Hs.1141		2.6
	4359		3 Hs.1197		2.6
	4392		0 Hs.1304	117 ESTs, Wealthy similar to 2195_HUMAN ZINC	2.6 2.6
	4195			gb:zd50c01.s1 Soares_fetal_heart_NbHH19W	2.6
75	4368				2.6
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	4437	70 AW81593	24	gb:MR3-ST0218-191199-012-a10 ST0218 Homo	2.0
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	447587	AW292139	Hs.115789	ESTs	2.6
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5	426411	AK000708	Hs.169764	hypothetical protein FLJ20701	2.6
,	432668 436682	AA558601 AI590055	Hs.43296 Hs.124110	ESTs ESTs	2.6 2.6
	426894	AJ204209	Hs.143911	ESTs	2.6
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10	457554	AA570111	Hs.155873	ESTs. Wealty similar to ALUE_HUMAN IIII	2.8
10	438166 443021	N30158 AA368546	Hs.122645 Hs.8904	ESTs Ig superfamily protein	2.6 2.6
	427005	AA394228	Hs.97494	ESTs	26
	437085	AA743935	Hs.202329	ESTs .	2.6
15	408603	R25283	Hs.326416	Homo saplens mRNA; cDNA DKFZp564H1916 (f	2.6
13	431019 437287	NM_005249 AA748180	Hs.2714 Hs.159346	forkhead box G1B hypothetical protein FLJ21369	2.5
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20	447930	R44574	Hs.107510	ESTs	2.5
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40	453362	H14988	Hs.107375	ESTs	2.5
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	432036	AF224266	Hs.272373		2.5 2.5
	422752	BE247253	Hs.21263	suppressor of potassium transport defect	2.5
55	413786	AW613780	Hs.13500	ESTs	2.5
	439706 451533	AW872527 NM_004657	Hs.59761 Hs.26530	ESTs, Weskly similar to DAP1_HUMAN DEATH	2.5
	414959	D59968	Hs.45184	serum deprivation response (phosphatidyl Homo sapiens cDNA FLJ12284 fis, clone MA	2.5 2.5
	449919	AI674685	Hs.200141		2.5
60	458891	A1659166	Hs.207144		2.5
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                          1364506_1
                          1381547_1
            455899
                          168294_1
176820_1
                                           ALD40357 AAB83621 AA203230
AI820973 AI734077 AI820984 AA225796 AA225060 AA225101
            456232
             456304
10
                                            AW971037 AA508019 AA492345
            457364
             TABLE 12C:
            Pkey:
Ref:
                                    Unique Eos probeset identifier number
                                    compared sources. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." reters to the publication entitled "The DNA sequence of human chromosome 27" Dunham, et al. (1939) Nature 402-489-495. Indicates DNA strand from which exons were predicted.
15
             Strand:
                                    indicates nucleotide positions of predicted exons.
             Nt_position:
                                                            Nt_position
123881-124090
                                             Strand
20
             400492
400533
                           9213749
6981826
                                            Minus
                                                             277132-277595
                                             Minus
              400645
                           8117693
                                             Minus
                                                             58471.58716
                                             Minus
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                           8131663
8569925
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72840-72924,74761-74849
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                                                             98374-98509
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              401272
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              401454
                                             Minus
                                                             114659-114832
68182-68325
                            1871197
                                             Minus
 30
                                                              15739-15951,16165-16779
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                            9965022
                                              Minus
                            2935596
              402274
                                              Phis
                                                              5604-6527
                            7630359
                                              Minus
                                                             75078-75203
76812-79040
              402322
              402344
                            8099258
                                              Mirnes
                                                              37870-37923,39664-39717,71711-71764
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                            7705171
                                              Plus
 35
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                                              Minus
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114306-115418
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                                                              7105-7357
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Minus
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7230870
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                                                               143467-143634
                             8084957
7708855
                                               Minus
                                                               87826-87947,89835-90002
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                                                                135775-136000
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9367203
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                                                                 138651,139153
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                               9857511
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                                                                 39067-39225
                                                Minus
                 404592
                               9943965
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Minus
                                                                45096-45229
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                 404632
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                 405046
                               7596829
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                 405238
405239
                               7249119
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43310-43462
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9588573
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                  405760
                               6056938
                                                 Minus
                                                                 37424-38045
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                               7657810
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                                                 Plus
                  405863
                  405941
                               6758796
9256242
                                                 Plus
                                                                 2798-3444
20805-20960
                  406395
                                                 Mirus
                                                                  68314-68523.68853-68950
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                                                                  91439-91579
                                 9864741
                  406481
     80
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TABLE 134: 964 GENES UP-REGULATED IN LOWER GRADE GUOSLASTOMA COMPARED TO NORMAL ADULT TISSUES Table 13A fists about 678 genes up-regulated in lower grade glioblastoma (LGG) compared to normal normal adult tissues. These were selected from 59680 probesets on the Affyrmetriu/Eos Hu03 GeneChip array such that the ratio of "average" LGG to "average" normal tissues was greater than or equal to 3.0. The "average" LGG tevet was set to the 85°

PCT/US02/29560 WO 03/025138

percentile amongst various LGG tumors. The "average" normal tissue level was set to the 85° percentile amongst various non-matignant eduit tissues. In order to remove genespecific background levets of non-specific hybridization, the 10° percentile value emongst the various non-matignant tissues was subtracted from both the numerator and the
denominator before the ratio was evaluated.

Unique Ecs probeset Identifier number
ExAcon: Exemplar Accession number, Genbank accession number
UniquelD: Unique mumber
Unique Title: Unique gene title
Rt: Ratio of LOWER GRADE GLIOBLASTOMA to NORMAL ADULT TISSUES

5

	Ki.				
10	Pkey	ExAcon	UnigenelD (Unigene Tide	R1 67.6
. •		AI880044	He 176977 1	protein kinase C binding protein 2	58.2
	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	53.8
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 29kD	50.6
16	431917	D16181	Hs.2868	peripheral myelin protein 2 peripheral myelin protein 2	48.3
15	428321	AJ599994	Hs.2868 Hs.169309	myelin-associated oligodendrocyte basic	44.3
	426325 435147	O28114 AL133731	Hs.4774	Homo sapiens mRNA; cDNA DXFZp761C1712 (I	44.2
	456759	BE259150	Hs.127792	delta (Orosophila)-like 3	43.8
	415817	U88967	Hs.78867	nmiein tymsine phosphatase, receptor-1	40.8 40.1
20	429007	D80642		gb:HUM092E09B Human fetal brain (TFujiwa	38.8
20	417183	R52089	Hs_172717	ESTs	35.8
	430838	N46664	Hs.169395	hypothetical protein FLJ12015	34.9
	413472	BE242870	Hs.75379	soute carrier family 1 (glial high affi	34.4
0.5	425088	AA663372	Hs.169395 Hs.198612	hypothetical protein FLJ 12015 G protein-coupled receptor 51	34.2
25	429276	AF056085 Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	33.9
	424140 450133	AW969769	Hs.105201	ESTe	33.8
	423849	AL157425	Hs.133315	Homo saplens mRNA; cDNA DKFZp761J1324 (f	32.8
	413333	M74028	Hs.75297	fibroblest growth factor 1 (acidic)	32.8 31.3
30	449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	30.3
•	402604			Target Exon	28.8
	412733	AA984472	Hs.74554	KIAA0080 protein catenin (cadherin-associated protein), d	28.2
	416829	AB013805	Hs.80220	ESTs	27.9
26	439239	AI031540	Hs.235331 Hs.47860	neurotrophic tyrosine kinase, receptor,	27.1
35	444378	R41339 F05538	Hs.4273	ESTs	· 26.2
	439415 425048	H05468	Hs.164502	ESTs	25.5
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	25.3 24.0
	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	23.5
40	425799	T08133	Hs.182906	Homo sapiens mRNA for KIAA1872 protein.	23.5
	447359	NM_012093	Hs.18268	adenylata kinase 5	23.2
	425842	AI587490	Hs.159623		23.2
	423853	AB011537 AI362949	Hs.133466 Hs.75169	ESTs	22.9
45	435708 437268	A1362949 A1754847	Hs.227571		21.6
47	409395	U48745	Hs.336678	dystrobrevin, alpha	21.1
	441285	NM_002374		microtubule-associated protein 2	20.4 20.0
	422656	AI870435	Hs.1569	LIM homeobox protein 2	19.7
	425523	AB007948	Hs.158244	KIAA0479 protein	19.5
50	437204	AL110216	Hs.22826	ESTs, Weathy similar to 155214 salivary	19.4
	416370	N90470	Hs.203697		19.3
	441497		Hs.23172 Hs.32964	SRY (sex determining region Y)-box 11	19.1
	453392 408604		Hs.21925		18.9
55	413597			3 ESTs	18.8
"	422980		Hs.76722	CCAATenhancer binding protein (C/EBP).	18.8 18.6
	428392		Hs.2265	secretory granute, neuroendocrine protes	18.2
	429466		Hs.12827		18.2
	448302		Hs.18290		17.4
60	439199		Hs.26299		17.4
	448743 41833				17.3
	44451				17.2
	44478				17.1
65	44700		8 Hs.1575	39 ESTs	16.8 16.5
	42598				16.1
	44867				15.8
	45237		Hs.2284		15.7
70	42412		Hs.2907		15.6
70			Hs.1509 4 Hs.1330	C ESTE Weekly similar to 2004399A CITOMOS	15.4
	42479 42620		Hs.168	350 Homo sapiens mRNA; CDNA DXF2p000A1U40 (I	15.2
	4466		15.100	Homo sapiens mRNA for KIAA1763 protein.	15.2
	4536		6 Hs.340	74 dipepiidylpeptidase VI	14.9 14.7
7:	5 4290		Hs.194	765 H.sapiens GENX-5624 mRNA, 3 UTR	14.6
	4414	40 AJ80798		95 ESTs	14.6
	4299	27 NM_001	115 Hs.252	2 adenylate cyclase 8 (brain)	14.4
	4158			6 ESTs	14.2
0	4181				14.0
8		277 X77748	Hs.378		14.0
	4096		90 Hs.77		13.9
	441; 415				13.7
	713			216	

	424945 426344	AI221919 H41821	Hs.322469	hypothetical protein FLJ10582	13.6
	446372	AB020644	Hs.14945	transcriptional activator of the c-los p long fatty acyl-CoA synthetase 2 gene	13.4 13.3
A 1	429946	R49390	Hs.254129	KIAA1678	13.3
5	444119	R41231	Hs.184261	ESTs, Weakly similar to T26686 hypotheti	13.3
	438380	T06430	Hs.6194	chandraitin sulfate proteoglycan BEHAB/o	13.2
	415910 412266	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	13.2
	436878	N59006 BE465204	Hs.26133 Hs.47448	ESTs ESTs	13.2 13.1
10	428536	Al143139	Hs.2288	visinin-fike 1	13.1
	425649	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	13.1
	428982	NM_005097	Hs.194704	leucine-rich, glioma inactivated 1	13.0
	437948 444124	AA772920 R43097	Hs.303527	ESTs	13.0
15	428342	AI739168	Hs.6818	ESTs Homo sapiens cDNA FLJ13458 fis, clone PL	12.9 12.7
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	12.7
	412959	D87458	Hs.75090	KIAA0282 protein	12.6
	419863	AW952691	Hs.93485	Homo sapiens mRNA; cDNA DKFZp761D191 (fr	12.6
20	431467 431019	N71831 NM_005249	Hs.256398 Hs.2714	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	12.6
20	420547	AF155140	Hs.98738	forkhead box G18 gonadotropin-regulated testicular RNA he	12.4 12.4
	430091	AB032958	·Hs.233023	KIAA1132 protein	12.4
	448595	AB014544	Hs.21572	KIAA0644 gene product	12.2
25	447342	Al199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	12.2
23	409049 421264	AI423132 AL039123	Hs.146343 Hs.103042	ESTs microtubule-associated protein 18	12.0 11.9
	451952	AL120173	Hs.301663	ESTs	11.9
	411305	BE241596	Hs.69547	myelin basic protein	11.8
20	433551	AI985544	Hs.12450	protocadherin 9	11.6
30	431988 415170	AC002302 R44386	Hs.77202	protein kinase C, beta 1	11.6
	408562	AI436323	Hs.164578 Hs.31141	ESTs Horno saplens mRNA for KIAA1568 protein,	11.5 11.4
	435501	AW051819	Hs.129908	KIAA0591 protein	11.4
25	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	11.1
35	423419	R55336	Hs.23539	ESTs	11.1
	424432 433896	AB037821 AW294729	Hs.146858 Hs.274461	protocadherin 10 ESTs	10.9
	415293	R49462	Hs.106541	ESTS	· 10.9 10.9
40	447101	N72185	Hs.44189	ESTs	10.9
40	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	10.9
	438054 433597	AA776626 AA708205	Hs.169309 Hs.100343	ESTS ESTS	10.8
	421659	NM_014459	Hs.106511	protocadherin 17	10.7 10.6
	445102	AW204610	Hs.22270	ESTs	10.6
45	425154	NM_001851	Hs.154850	collagen, type IX, sipha 1	10.6
	451625	R56793	Hs.106576	alanine-glyoxylate aminotransferase 2-li	10.6
	435191 450154	R15912 R15891	Hs.4817 Hs.281587	Homo sapiens clone 24461 mRNA sequence Human (clone CTG-A4) mRNA sequence	10.6
	407886	AW969688	Hs.100826	ESTs	10.5 10.4
50	420345	AW295230	Hs.25231	ESTs	10.4
	428728	NM_016625	Hs.191381	hypothetical protein	10.3
	424997 440184	AL138167 AB002297	Hs.96920 Hs.7022	ESTs	10.3
	419078	M93119	Hs.89584	dedicator of cyto-kinesis 3 insufinoma-associated 1	10.2 10.2
55	445495	BE622641	Hs.38489	ESTs, Wealdy similar to (38022 hypotheti	10.1
	416857	AA188775	Hs.292453	ESTs	10.0
	445041 419271	T64183 N34901	Hs.282982 Hs.238532	solute carrier ESTs	10.0
	446711	AF 169692	Hs.12450	protocadherin 9	9.8 9.8
60	426847	S78723	Hs.298623	5-hydroxytryptamine (sérotonin) receptor	9.7
	427304	AA761526	Hs.163853	ESTs	9.7
	418097 449300	R45137 AI656959	Hs.21868 Hs.346514	ESTs ESTs	9.7
	419985	H66373	Hs.5856	ESTs, Highly similar to bA393J16.3 [H.sa	9.7 9.7
65	443785	AW449952	Hs.190125	basic-helix-loop-helix-PAS protein	9.5
	415486	H12214	Hs.13284	ESTs, Wealdy similar to 2109260A B cell	9.5
	453220 438209	AB033089 AL120659	Hs.32452 Hs.6111	Homo saplens mRNA for KIAA1263 protein,	9.5
	424028	AF055084	Hs.153692	aryl-hydrocarbon receptor nuclear transl Homo sapiens cDNA FLJ14354 fis, clone Y7	9.4 9.4
70	419683	AA248897	Hs.48784	ESTs	9.4
	414175	AJ308876	Hs.103849		9.2
	400292	AA250737	Hs.72472	BMP-R1B	9.2
_	408947 454048	AL080093 H05626	Hs.49117 Hs.6921	Homo sapiens mRNA; cDNA DKFZp564N1662 (f ESTs	9.2 9.2
75	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	9.2 9.1
	441016	AW138653	Hs.25845	ESTs	9.0
	425187	AW014486	Hs.22509	ESTs	9.0
	445568 453941	H00918 U39817	Hs.36820	KIAA1796 protein Bloom syndrome	8.9
80	422411	AW749443	Hs.22511	ESTs	8.9 8.8
	447350	Al375572	Hs.172634	ESTs	8.8
	424481	R19453	Hs.1787	proteofipid protein 1 (Pelizaeus-Merzbac	8.7
	448902	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp76111912 (f	8.7

	448986	H42169	No 242240	h	
	423135	N67655	Hs.347310 Hs.26411	hypothetical protein FLJ14627 ESTs	8.6
	418030	BE207573	Hs.83321	neuromedin B	8.5
_	448769	N66037	Hs.38173	ESTs	8.4 8.4
5	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	8.3
	400293	N51002	Hs.306480	Homo sapiens mRNA; cDNA DKFZp761E2112 (f	8.3
	415279	F04237	Hs.1447	glial fibrillary acidic protein	8.2
	451516 419629	AI800515 AB020695	Hs.12024	ESTs	8.2
10	437034	AA742643	Hs.91662	KIAA0888 protein	8.2
	456965	AW131888	Hs.172792	gb:ny91c01.s1 NCI_CGAP_GCB1 Homo sapiens ESTs, Wealdy similar to hypothetical pro	8.2
	417417	F05745	Hs.89512	ATPase, Ca transporting, plasma membrane	8.1 8.1
	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	8.1
16	422864	AA318323	Hs.12827	gb:EST20390 Retina II Homo seplens cONA	8.1
15	452526	W38537	Hs.280740	hypothetical protein MGC3040	8.0
	435793	AB037734	Hs.4993	KIAA1313 protein	7.9
	415669 407168	NM_005025 R45175	Hs.78589 Hs.117183	serine (or cysteine) proteinase inhibito	7.9
	447414	D82343	Hs.74376	ESTs neuroblastoma (nerve tissue) protein	7.9
20	442710	AI015631	Hs.23210	ESTs	7.8
	416836	D54745	Hs.80247	cholecystokinin	7.8 7.8
	419721	NM_001650	Hs.288650	aquaporin 4	7.7
	438080	AA777381	Hs.291530	ESTs. Weakly similar to ALUC_HUMAN !!!!	7.7
25	436109 428845	AA922153	Hs.132760	hypothetical protein MGC15729	7.7
23	448321	AL157579 NM_005883	Hs.153610 Hs.20912	KIAA0751 gene product	7.7
	410305	AF030409	Hs.62185	adenomatous polyposis coli like	7.7
	443392	AI055821	Hs.293420	solute carrier family 9 (sodium/hydrogen ESTs	7.6
	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	7.6 7.5
30	418738	AW388633	Hs.6682	solute carrier family 7, (cationic arnino	7.5
	423361	AW170055	Hs.47628	ESTs	7.5
	447198	D61523	Hs.283435	ESTs	7.5
	448555 458332	A1536697 A1000341	Hs.159863	ESTs	7.5
35	407034	U84540	Hs.220491	ESTs	7.4
	425354	U62027	Hs.155935	gb:Human dystrobrevin isoform DTN-3 (DTN complement component 3a receptor 1	7.4
	426814	AF036943	Hs.172619	myelin transcription factor 1-like	7.4 7.4
	448507	AL133109	Hs.21333	Homo sapiens mRNA; cDNA DKFZp566N1047 (f	7.4
40	439845	AL355743	Hs.56663	Homo sapiens EST from clone 41214, full	7.4
40	449078	AK001256	Hs.22975	KIAA1576 protein	7.3
	410102 425741	AW248508 AF052152	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	7.2
	440210	AW674562	Hs.159412 Hs.125296	Homo sapians clone 24628 mRNA sequence ESTs	7.2
	415651	AJ207162	Hs.3815	stathmin-like-protein RB3	7.2
45	428409	AW117207	Hs.98523	ESTs	7.2 7.1
	413409	AI638418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	7.1
	443992	AW022228	Hs.322922	ESTs	7.1
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	7.1
50	427540 439979	R12014 AW500291	Hs.20976 Hs.6823	ESTs	7.0
-	424893	AW295112	Hs.153648	hypothetical protein FLJ10430 Homo septens cDNA FLJ13303 fis, clone OV	7.0
	452355	N54926	Hs.29202	G protein-coupled receptor 34	7.0
	414596	AF002020	Hs.76918	Niemann-Pick disease, type C1	7.0 7.0
55	440152	AB002376	Hs.7006	KIAA0378 protein	7.0
55	454293	H49739	Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	7.0
	425782 416805	U86468 F13271	Hs.159525	cell growth regulatory with EF-hand doma	7.0
	419991	AJ000098	Hs.79981 Hs.94210	Human clone 23560 mRNA sequence	7.0
	424343	AW956360	Hs.4748	eyes absent (Drosophila) homolog 1 adenylate cyclase activating polypeptide	7.0
60	408369	R38438	Hs.182575	solute carrier family 15 (H777) transport	6.9 6.9
	449605	AW138581	Hs.198416	ESTs	6.9
	444396	T65213	Hs.4257	ESTs	6.9
	444165 414245	AL137443 BE148072	Hs.10441	hypothetical protein FLJ11236	6.9
65	412155	R38167	Hs.75850 Hs.12449	WAS protein family, member 1	6.9
•-	424524	AB032947	Hs.151301	Homo sapiens transmembrane protein HTMP1 Ca2+dependent activator protein for secr	6.9
	448681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	6.9
	411379	AJ816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	6.9 6.9
70	446782	AI653048	Hs.144006	ESTs	6.8
70	426919	AL041228	11- 400444	ELAV (embryonic lethal, abnormal vision,	6.8
	423346 436643	AJ267677 AA757626	Hs.127416 Hs.10941	synaptojanin 1	6.8
	414922	D00723	Hs.77631	ESTs, Wealdy similar to IPP1_HUMAN PROTE glycine cleavage system protein H (amino	6.8
7.	410037	AB020725	Hs.58009	grycine ceavage system protein in (amino KIAA0918 protein	6.8
75	442613	A1004002	Hs.130522	Kv channel-interacting protein 1	6.8 6.8
	413589	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	6.8
	422175	N79885	Hs.6382	ESTs. Highly similar to T00391 hypotheti	6.8
	421141	AW117261	Hs.125914	EST8	6.7
80	452786 441916	R61362 AA993571	Hs.106642 Hs.129075	ESTs, Weakly similar to T09052 hypotheti	6.7
	448533	AL119710	Hs.21365	ESTs nucleosome assembly protein 1-tike 3	6.7
	428037	N47474	Hs.89230	potassium Intermediate/small conductance	6.7 6.7
	423343	AA324643	Hs.246106	ESTs	6.7 6.7

	456723	Z43902	Hs.4748 :	adenytate cyclase activating polypeptide	6.7
	414214			tycocrotein MSA	6.7
	434811	AW971205	Hs.114280	ESTs	6.7
_	424922	BE386547		hypothetical protein MGC10825	6.7 6.6
5	449328			ESTS	6.6
	431553 420156	X78075 AW449258		cartitage linking protein 1 ESTs	6.6
	431117	AF003522		detia (Urosophila)-like 1	6.6
	422960	AW890487		cadherin 13, H-cadherin (heart)	6.6 8.5
10	429239	AA448419		ESTs ESTs	6.5
	453924 433929	R49295 Al375499	Hs.27379	ESTS	6.5
	426529	AF090100	Hs.170241	Homo sapiens clone IMAGE 23915	6.5
	414683	S78295	Hs.76888	hypothetical protein MGC12702	6.4
15	409746	NM_004794	Hs.56294	RAB33A, member RAS oncogene family	6.4 6.4
	419169 453590	AW851980 AF150278	Hs.262346 Hs.33578	ESTs, Wealdy similar to S72482 hypotheti KIAA0820 protein	6.4
	422263	AA307639	Hs.129908	KIAAD591 protein	6.4
	421688	AK000307	Hs.106825	hypothetical protein FLJ20300	6.4
20	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	6.3 6.3
	425588	F07396 AI267589	Hs.46627 Hs.302689	ESTs hypothetical protein	6.3
	410366 419498	AL036591	Hs.20887	hypothetical protein FLJ10392	6.3
	446997	AA383439	Hs.16758	Spir-1 protein	6.3
25	427958	AA418000	Hs.98280	potassium intermediate/smail conductance	6.3 6.3
	445908	R13580 S72043	Hs.13436 Hs.73133	Homo sapiens clone 24425 mRNA sequence metallothionein 3 (growth inhibitory fac	6.3
	412068 452834	AI638627	Hs.105685	KIAA1688 protein	6.3
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	6.3
30	418512	AW498974		diacytglycerol kinase, zeta (104kD)	6.2 6.2
	410099	AA081630	N= 246107	KIAA0036 gene product Homo sepiens mRNA; cDNA DKFZp434E082 (fr	6.2
	452744 427897	AI267652 NM_017413	Hs.246107 Hs.303084	apelin; peptide tigand for APJ receptor	6.2
	416427	BE244050	Hs.79307	Rac/Cdc42 guaraine exchange factor (GEF)	6.2
35	439274	AFD85092	Hs.48372	ESTs	6.2
	431552	AI815863	Hs.259873	exonal transport of synaptic vesicles	6.2 6.2
	439607 408950	BE540565 AA707814	Hs.159460 Hs.14945	ESTs long fatty acyl-CoA synthetase 2 gene	6.2
	412709	AL022327	Hs.74518	KIAA0027 protein	6.2
40	435624	AF218942	Hs.24889	formin 2	6.1
	425977	R15138	Hs.165570	Homo sapiens clone 25052 mRNA sequence	6.1 6.1
	420077 457005	AW512260 AJ007421	Hs.87767 Hs.172597	ESTs sal (Drosophila)-like 3	6,1
	440471	AA886146	Hs.307944	ESTS	6.1
45	423770	AW976766	Hs.132776	Homo sapiens cDNA FLJ10077 fis, clone HE	6.1
	438624	AA889055	Hs.123468	ESTs	6.1 6.1
	452752 438208	AW044058 AL041224	Hs.33578 Hs.65379	KIAA0820 protein ESTs	6.1
	416072	AL110370	Hs.79000	growth associated protein 43	6.1
50	407808	AA663559	Hs.279789	histone deacetylase 3	6.1
	433701	AW445023	Hs.15155	ESTs	6.1 6.1
	419704 429250	AA429104 H56585	Hs.45057 Hs.198308	ESTs tryptophan rich basic protein	6.1
	433244		Hs.271285		6.0
55	422544		Hs.118140	KIAA0716 gene product	6.0
	420133		Hs.155543		6.0 6.0
	440491 422728		Hs.130558 Hs.103262		6.0
	415257		Hs.27513	ESTs	5.9
60	417160	N76497	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	5.9
	430188		Hs.23479		5.9 5.9
	437372 430471				5.9
	433523		113.27132	ESTs	5.9
65	408926	AF217525		Down syndrome cell adhesion molecule	5.9
	427317				5.9 5.9
	426140 409892			8 Homo sapiens clone 25119 mRNA sequence gb:EST368183 MAGE resequences, MAGD Homo	5.8
	459516		Hs.24685		5.8
70	44291		Hs.11307	ESTs, Weakly similar to T19326 hypotheti	5.8
	41473	7 Al160386	Hs.12508	7 ESTs	5.8
	42433		Hs.10161	5 ESTs NM_002706*;Homo saplens protein phosphat	5.8 5.8
	40314 42011		,	gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	5.8
75	45081			6 ESTs	5.8
	40214	5		Target Exon	5.8
	43479				5.8 5.8
	42242			73 hypothetical protein FLJ22672 5 KIAAD455 gene product	5.8 5.8
80	44574 42060				5.8
	45140	7 AA13137	6 Hs.3438	09 fibroblest growth factor 128	5.7
	44110	2 AA97390		intermediate filament protein syncotiin	5.7 5.7
	42456	30 AA15872	7 Hs.1505	55 protein predicted by clone 23733	3.7

	420207	AW182459	Hs.125759 (STs, Weakly similar to LEUS_HUMAN LEUKE	5.7
	430287 405238		1	larget Exon	5.7 5.7
	432890			uaic acid binding Ig-like lectin 8 hypothetical protein DKFZp547J036	5.7 5.7
5	4.0.00	R39127 Q87470		NAA0280 protein	5.7
3	413492 427624	AA406245		ESTs	5.7
	418079	R40058 '		ESTs	5.6 5.6
	424458	M29273	Hs.1780 Hs.20887	myelin associated glycoprotein hypothetical protein FLJ10392	5.6
10	448299	AA497044 A1685086	Hs.26339	ESTs, Wealdy similar to S21348 probable	5.6
10	429698 430228	AW950939	Hs.6382	ESTs, Highly similar to T00391 hypotheti	5.6
	445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	5.6 5.6
	436887	AW953157	Hs.193235	hypothelical protein DKFZp547D155	5.6
15	452898 435638	AA814497 AB011540	Hs.78792 Hs.4930	ESTs low density Epoprotein receptor-related	5.6
13	436035	AA703679	Hs.106999	ESTs. Weekly similar to SYT5_HUMAN SYNAP	5.5
	412190	R16180	Hs.274461	EST8	5.5 5.5
	459278	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fts, clone H regulator of G-protein signalling 7	5.5
20	416490 423449	AF090116 Al497900	Hs.79348 Hs.33067	ESTs	5.5
20	440856	AI703103	Hs.271360	hypothetical protein MGC16275	5.5
	432154	AI701523	Hs.112577	ESTs DOE 10/5C1	5.4 5.4
	423476	AL035633	45-105701	Human DNA sequence from clone RP5-1046G1 Homo saplens mRNA full length insert cDN	5.4
25	428588 447773	F12101 AJ423930	Hs.185701 Hs.36790	ESTs, Wealthy similar to putative p150 [H	5.4
23	436936	AL134451	Hs.197478	ESTs	5.4
	427250	R35941	Hs.25418	ESTS	5.4 5.4
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fs, clone HE protein tyrosine phosphatase, receptor t	5.4
30	452856 428795	AF034799 R45503	Hs.30881 Hs.97469	ESTs, Highly similar to A39769 N-acetyl	5.4
20	407385	AA610150	Hs.272072	ESTs. Weakly similar to 138022 hypotheti	5.4
	405348			C7001664:gi 12698061 dhi BAB21849.1 (AB	5.4 5.3
	438330	AW450572	Hs.257316	gb:E6T93093 Skin tumor I Homo sapiens cD	5.3
35	426503 44B14B	AA380153 NM_016578	Hs.20509	HBV pX associated protein-8	5.3
55	410386	W26187	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	5.3 5.3
	445225	AI216555	Hs.202398	ESTs	5.3
	428784	Y12851	Hs.193470 Hs.187621		5.3
40	418759 402605	AA227879	115.107021	Target Exon	5.3
40	412046	Y07847	Hs.73088	RAS-related on chromsome 22	5.3 5.2
	423869	BE409301	Hs.134012		5.2
	430130	AL137311 AW294631	Hs.234074 Hs.11325	ESTs	5.2
45	453096 450475				5.2
73	429139		Hs.66087	EST8	5.2 5.2
	451783		Hs.21086		5.2
	436568 424330		Hs.91564 Hs.33339		5.2
50	408453		Hs.45127		5.2
50	447499			4 protocadherin beta 15	5.2 5.2
	402855		11- 000 47	NM_001839*:Homo sapiens calponin 3, acid	5.2
	420805 426457		Hs.99947 Hs.16996		5.2
55	41735		Hs.82002	endothelin receptor type B	5.1
	429469	3 M64590	Hs.27	glycine dehydrogenase (decarboxylating;	5.1 5.1
	45063		Hs.27717	74 ESTs ESTs	5.1
	41281 40037		32	Homo sepiens ovarian cancer related prot	5.1
60	44186		47 Hs.8004	huntingtin-associated protein interactin	5.1 5.1
	44283				5.1
	42270				5,1
	41155 41904		Hs.8956		5.0
65	43097			10 FSTs	5.0 5.0
	45132			diacytglycerol kinase, zeta (104kD)	5.0
	42357				5.0
	4299° 45278				5.0
70	4531		16 Hs.3179	11 acytohosphatase 2, muscle type	5.0 5.0
	4280		Hs.219	907 ESTs, Moderately similar to Transforming	5.0 5.0
	4301			gb:PM3-BN0176-100400-001-g04 BN0176 Homo 187 Homo sapiens cDNA FLJ14337 fis, clone PL	5.0
	4499 4391			7 synaptogydn 3	5.0
7:	4262			047 chondroitin sulfate proteoglycan 3 (neur	5.0 6.0
	4517	52 AB0329	97 Hs.269		5.0 4.9
	4205				4.9
	4273 4281				4.9
8	0 4451		346 Hs.198	689 ESTs	4.9
	4100	359 R38624		313 ESTs	4.9 4.9
	427				4.9
	448	340 KI32V3	m3.214	113 SQUIR CAIRS ISSUIT 12, DOCUMENT	

	453554	44334647	No anger		
	457561	AA331517 H98216	Hs. 286055	chimerin (chimaerin) 2	4.9
	409100 437117	AL049256	Hs.42245 Hs.122593	ESTs, Moderately similar to 138022 hypot ESTs	4.9
	415101	R45531	Hs. 144534	ESTs	4.9
5	438458	AW975186		gb:EST387294 MAGE resequences, MAGN Homo	4.9 4.9
_	442026	AJ243749	Hs.6074	brain-specific angiogenesis inhibitor 3	4.9
	438283	AI458931	Hs.37282	ESTs	4.9
	449714	AB033015	Hs.23941	KIAA1189 protein	4.9
10	420871	AA702972	Hs.65300	ESTs .	4.9
10	425256	BE297611	Hs.155392	collapsin response mediator protein 1	4.9
	424001	W67883	Hs.137476	paternally expressed 10	4.9
	419103 446727	240229 AB011095	Hs.96423	hypothetical protein FLJ23033	4.B
	408670	AF160967	Hs.16032 Hs.46784	KIAA0523 protein	4.8
15	428189	AA424030	Hs.46627	potassium large conductance calcium-acti ESTs	4.8
	420092	AA814043	Hs.88045	ESTS	4.B 4.B
	410631	AA086469	Hs.47171	ESTs	4.8
	449277	AA001064	Hs.43670	ESTs	4.8
00	436282	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.8
20	414706	AW340125	Hs.76989	KIAA0097 gene product	4.8
	438703	AI803373	Hs.31599	ESTs	4.8
	439340	AB032436	Hs.6535	brain-specific Na-dependent inorganic ph	4.8
	445890	AF055019	Hs.21906	Homo sapiens cione 24670 mRNA sequence	4.7
25	438734 408177	AI937612 AI241733	Hs.273758 Hs.43871	hypothetical protein FLJ23112 ESTs	4.7
	445740	178281	Hs. 13226	Homo sapiens clone 25181 mRNA sequence	4.7
	459527	AW977558	Hs.291735	ESTs, Wealthy similar to 178885 serine/th	4.7 4.7
	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	4.7
20	409172	Z99399	Hs.122593	ESTS	4.7
30	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	4.7
	421637	AF035290	Hs.106300	Homo sapiens clone 23556 mRNA sequence	4.7
	448044	A1458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	4.7
	459311	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	4.7
35	447891 426968	R41754 U07618	Hs.6496 Hs.173034	ESTs	4.7
55	404819	00/0/0	rts.173034	amphiphysin (Stiff-Mann syndrome with br NM_002688*:Homo sapiens peanut (Drosophi	4.7
	409125	R17268	Hs.343567	axonal transport of synaptic vesicles	4.7 4.7
	437762	T78028	Hs.154679	synaptologmin I	4.7
40	441668	AI611973	Hs.136313	ESTs	4.7
40	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	4.6
	429269	AA449013	Hs.99203	ESTs	4.6
	433009	AA761668		gb:nz24c08.s1 NCI_CGAP_GC81 Homo sapiens	4.6
	416586	D44643	Hs.14144	secreted modular calcium-binding protein	4.5
45	427701 426925	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	4.6
43	410264	NM_001196 AK001853	Hs.315689 Hs.61508	Homo sapiens cDNA: FLJ22373 fis, clone H	4.6
	437698	R61837	Hs.7990	Homo sapiens cDNA FLJ10991 fls, clone PL ESTs, Moderately similar to I84505 calci	4.6
	445813	Z42023	Hs.106576	alanine-glyoxylate aminotransferase 2-li	4.6 4.6
	424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	4.6
50	448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4,6
	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	4.6
	424282	R75421	Hs.135694	ESTs	4.6
	429401	AW296102	Hs.99272	ESTs, Wealthy similar to S32567 A4 protei	4.6
55	426413 407896	AA377823 D76435	Un 41164	gb:EST90805 Synovial sarcoma Homo sapien	4.5
55	413248	T64858	Hs.41154 Hs.21433	Zic family member 1 (odd-paired Drosophi hypothetical protein DKFZpS47J036	4.5
	443731	AI083928	Hs.145418	ESTs	4.5
	449539	W80363	Hs.58446	ESTs	4.5 4.5
	420362	U79734	Hs.97206	huntingtin interacting protein 1	4.5
60	443301	AI733614	Hs.220587	ESTs, Moderately similar to ALU5_HUMAN A	4.5
	423178	AI033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	4.5
	437933	AI276132	Hs.146155	ESTs	4.5
	446544 411642	AI631932 NM_014932	Hs.7047	ESTs, Weakly similar to Unknown [H.sapie	4.5
65	428282	N34905	Hs.71132 Hs.44653	neuroligin 1	4.5
0.5	411498	NM_014210	Hs.70499	Homo sapiens cDNA: FLJ22669 fis, clone H ecotropic viral integration site 2A	4.5
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	4.5 4.5
	436637	AJ783529	Hs.26766	EST8	4.5
	438456	AA913381	Hs.20594	ESTs	4.5
70	400533			ENSP00000209376":PRED65 protein (Fragmen	4.4
	413951	AW051200	Hs.75640	natriuratic peptide precursor A	4.4
	417632	R20855	Hs.5422	glycoprotein M6B	4.4
	425138	H08849	Hs.167464	glutamate receptor, lonotropic, N-methyl	4.4
75	457211 413812	AW972565	Hs.32399	ESTs. Wealdy similar to S51797 vasoditat	4.4
	448451	AW188687 AW015994	Hs.44748 Hs.345433	ESTs gb:UI-H-BIOp-abh-g-09-0-UI.s1 NCI_CGAP_S	4.4
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	4.4
	458760	Al498631	Hs.111334	ferritin, light polypeptide	4.4 4.4
90	405819			NM_002578:Homo sapiens p21 (CDKN1A)-acti	4.4
80	447877	AI435184	Hs.164252	ESTs .	4.4
	431342	AW971018	Hs.21659	ESTs	4.4
	408577	H50572	Hs.19515	ESTs, Highly similar to NRG3_HUMAN PRO-N	4.4
	445729	H21066	Hs.13223	Homo sapiens mRNA full length insert cON	4.4

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	422253	W81526	Hs.118329	ESTs, Moderately similar to GAD_HUMAN GA	4.4
	419088	A1538323	Hs.52620	integrin, beta 8	4.4
	428305	AA446628	Hs.2799	cartilage linking protein 1	4.4
_	410768	AF038185	Hs.66187	Homo sapiens clone 23700 mRNA sequence	4.4
5	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	4.4
	451621 424240	AI879148 AB023185	Hs.26770 Hs.143535	fatty acid binding protein 7, brain	4.4 4.3
	433932	AW954599	Hs.169330	calcium/calmodulin-dependent protein kin neuronal protein	4.3
	439935	S75105	Hs.8358	gfutamate receptor, ionotropic, kainate	4.3
10	436039	AW023323	Hs.121070	ESTs	4.3
	416220	N49776	Hs.170994	hypothetical protein MGC10946	4.3
	409953	AA332277 AW967956	Hs.57691 Hs.123648	cacherin 18, type 2	4.3 4.3
	456497 420352	8E258835	FIS. 123040	ESTs, Wealty similar to AF108460 1 ubinu gb:601117374F1 NIH_MGC_16 Homo sapiens c	4.3
15	454032	W31790	Hs.194293	ESTs, Wealty similar to I54374 gene NF2	4.3
	421790	AW896201	Hs.22654	sodium channel, voltage-gated, type I, a	4.3
	444218	AF070641	Hs.10684	Homo sapiens clone 24421 mRNA sequence	4.3
	436391	AJ227892	Hs.146274	ESTs	4.3
20	452106 422465	A1141031 AF073710	Hs.21342 Hs.117149	ESTs regulator of G-protein signaling 9	4.3 4.3
	439285	AL133916		hypothetical protein FLJ20093	4.3
	404541			NM_030795:Homo sapiens stathmin-like 4 (4.3
	424572	M19650		2,3-cyclic nucleotide 3 phosphodieste	4.3
25	449048	Z45051	Hs.22920	similar to \$68401 (cattle) glucose induc	4.3
23	409182 444600	AA064970 R41398	Hs.122593 Hs.6996	ESTs ESTs	4.3 4.3
	408838	AI669535	Hs.40369	ESTs	4.3
	410592	R94088	Hs.43569	ESTs	4.3
20	440168	AA868507	Hs.126141	ESTs	4.2
30	445078	AI869975	Hs.4775	Junctophilin 3	4.2
	428870 411666	AA431682 AF106564	Hs.134832 Hs.71346	ESTs neurofilament 3 (150kD medium)	4.2 4.2
	412505	AA974491	Hs.21734	ESTs	4.2
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	4.2
35	441707	R42637	Hs.21963	hypothetical protein DKFZp761B0514	4.2
	449433	AI672096	Hs.9012	ESTs. Weakly similar to \$26650 DNA-bindi	4.2
	441523 448243	AW514263 AW369771	Hs.301771 Hs.52620	ESTs, Wealthy similar to ALUF_HUMAN !!!! integrin, beta 8	4.2 4.2
	429149	AW193360	Hs.197962	ESTs, Weakly similar to I38022 hypotheti	4.2
40	430676	AF084866		gb:Homo sapiens envelope protein RIC-3 (4.2
	404584			Target Exon	4.2
	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.2
	451254 428585	AI571016 AB007863	Hs.172967 Hs.185140	ESTS KIAAAAA	4.2 4.2
45	439231	AW581935	Hs.141480	KIAAD403 protein Homo sapiens mRNA; cDNA DKFZp434N079 (fr	4.2
	425287	R88249	Hs.155524	peanut (Drosophila)-like 2	4.2
	425790	AW136286	Hs.288446	ESTs	4.2
	450407	NM_000810	Hs.24969	gamma-aminobutyric acid (GABA) A recepto	4.2
50	425241 445292	AA324624 AV653264	Hs.155247 Hs.13982	aldotase C, fructose-bisphosphate Homo sapiens cDNA FUJ14666 fis, clone NT	4.2 4.1
30	400777	AVOODZON	ris. 1330Z	NM_007325*:Homo sapiens glutamate recept	4.1
	422170	AI791949	Hs.112432	anti-Mullerian hormone	4.1
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	4.1
55	425402	AI215881	Hs.24970	ESTs, Wealdy similar to B34323 GTP-bindi	4.1
22	438461 421268	AW075485 Al126821	Hs.286049 Hs.30514	phosphoserina aminotransferase ESTs	4.1
•	416439	AA180363	Hs.118769		4.1 4.1
	419687	AJ638859	Hs.227699		4.1
60	435040	A1932350	Hs.152825		4.1
60	439774	AL360257	Hs.213493		4.1
	458435 410320	AM18718 AA084071	Hs.144121 Hs.93816	ESTs, Weakly similar to T46916 hypotheti Homo sepiens mRNA; cDNA DKFZp547N093 (fr	4.1 4.1
	436899	AA764852	Hs.291567		4,1
	454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	4.1
65	453118	AW195849	Hs.252757		4,1
	428771	AB028992	Hs.193143		4.1
	444185 422374	AW298350 AW732869	Hs.66020 Hs.1519	ESTs protein kinase, cAMP-dependent, regulato	4.1 4.1
	430147	R60704	Hs.234434		4.1
70	456060	C14904	Hs.45184	Homo sapiens cDNA FLJ12284 fis, clone MA	4.1
	433819	AW511097	Hs.112765	ESTs	4,1
	415827	H17462	Hs.23079	ESTs	4,1
	437397 441390	AA349847 AI692560	Hs.4221 Hs.131175	hypothetical protein DKFZp761H039 i ESTs	4.1
75	440483	AI200836	Hs.150386		4.1 4.0
. •	435294	T84084	Hs.196008		4.0
	447397	BE247676	Hs.18442	E-1 enzyme	4.0
	425390	AI092634	Hs.156114		4.0
80	432022 420602	AL162042 AF060877	Hs.272348 Hs.99236		4.0 4.0
-	408081	AW451597		regulator of G-protein signalling 20 ESTs	4.0
	453313	BE005771	Hs.15374	hypothetical protein FLJ22490	4.0
	436511	AA721252	Hs.29150		4.0

	448944	AB014605	Hs.22599	strophin-1 interacting protein 1; activi	4.0
	419412	AW181058	Hs.90297	synuclein, beta	4.0
	409091 453438	AW970386 AI469935	Hs.269423 Hs.22792	ESTs ESTs	4.0 4.0
5	450582	AJ339732	113.22.732	G-rich RNA sequence binding factor 1	4.0
	440553	AA889416	Hs.344043	Homo sapiens cDNA FLJ14459 fis, clone HE	4.0
	437449 445888	AL390153	Hs.208339 Hs.13415	Homo sapiens mRNA; cDNA DKFZp762G113 (fr	4.0
	439450	AF070564 R51613	Hs. 125304	Homo sapiens clone 24571 mRNA sequence ESTs	4.0 4.0
10	453792	AL134539	Hs.254129	KIAA1678	4.0
	459080	AW192083	Hs.290855	ESTs	4.0
	438810 446233	AW897846 AI282028	Hs.6421 Hs.25205	hypothetical protein DKFZp761N09121 ESTs	4.0
	412754	AW160375	Hs.74565	amyloid beta (A4) precursor-like protein	4.0 4.0
15	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	4.0
	434859	BE255080	Hs.299315	collapsin response mediator protein-5; C	4.0
	423279 416340	AW959861 N31772	Hs.290943 Hs.79226	ESTs fasciculation and elongation protein zet	4.0
	410126	BE169274	113.7 3220	KIAA0036 gene product	3.9 3.9
20	431173	AW971198	Hs.294068	ESTs	3.9
	446936	H10207	Hs.47314	ESTs	3.9
	424899 419038	AL119387 AW134924	Hs.119062 Hs.190325	ESTs ESTs	3.9 3.9
	450530	NM_006668	Hs.25121	cytochrome P450, subfamily 46 (cholester	3.9
25	438142	T90309	Hs.269651	ESTS	3.9
	412659	AW753865	Hs.74376	offactomedin related ER localized protei	3.9
	412788 410909	AA120960 AW898161	Hs.198416 Hs.53112	ESTs ESTs, Moderately similar to ALU8_HUMAN A	3.9 3.9
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	3.9
30	432809	AA565509	Hs.131703	ESTs	3.9
	424186	AI536021	Hs.288706	Homo sapiens cDNA FLJ10281 fis, clone HE	3.9
	425480 449932	AB023198 Al675444	Hs.158135 Hs.263024	KIAA0981 protein ESTs	3.9 3.9
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.9
35	450590	AJ701507	Hs.273740	ESTs	3.9
	419586	AI088485	Hs.144759	ESTs, Weakly similar to 138022 hypotheti	3.9
	414040 436480	N58513 AJ271643	Hs.32171 Hs.87469	ESTs putative acid-sensing ion channel	3.9 3.9
	443210	AI692649	Hs.9451	hypothetical protein MGC13168	3.9
40	448448	NM_014954	Hs.21239	KIAA0985 protein	3.9
	447067 413199	R42098	Hs.21964 Hs.75236	ESTS	3.9
	429421	M62843 AL031658	ns./3230	ELAV (embryonic lethat, abnormat vision, Human DNA sequence from clone RP1-310O13	3.9 3.9
	415796	R87548	Hs.78854	ATPase, Na? transporting, beta 2 polypep	3.8
45	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	3.8
	418771 417565	AA807881 AJ203405	Hs.25329	ESTs	3.8
	412420	AL035668	Hs.47831 Hs.73853	ESTs bone morphogenetic protein 2	3.8 3.8
	450202	AW969756	Hs.34145	ESTs, Wealdy similar to 849847 GTP-bindi	3.8
50	435312	AJ243396	Hs.4865	voltage-gated sodium channel beta-3 subu	3.8
	435832 435854	AA425688 AJ278120	Hs.41641 Hs.4996	Bruno (Orosophila) -like 4, RNA binding	3.8
	459079	AI821122	115.4350	pulative ankyrin-repeat containing prote gb:ns91g10.y5 NCI_CGAP_Pr3 Homo sapiens	3.8 3.8
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	3.8
\$ 5	421977	W94197	Hs.110165		3.8
	437756 403696	AA767537	Hs.197096	ESTs C4001100*:gij5852342 gb AAD54015.1 (AF0	3.8 3.8
	453033	AA325869	Hs.31463	KIAA0281 gene product	3.8
60	441732	AW298818	Hs.127341	ESTs	3.8
60	415884 432646	H22966 AW753310	Hs.13471	ESTs ab: PC3 CT0354 031099 013 -05 CT0364 Users	3.8
	451059	AW297465	Hs.267150	gb:RC3-CT0254-031099-012-c05 CT0254 Homo KIAA1409 protein	3.8 3.8
	447057	AJ423407	Hs.157697		3.8
65	418915	Al474778	Hs.118977		3.8
05	441111 447818	A1806867 W79940	Hs.126594 Hs.21906	ESTs Homo sapiens clone 24670 mRNA sequence	3.8
	457183	H91882	Hs.118569		3.8 3.8
	418358	L02840	Hs.B4244	potassium voltage-gated channel, Shab-re	3.8
70	410711	AB002316	Hs.65746	KIAA0318 protein	3.8
70	428878 438944	AA435884 AA302517	Hs.48926 Hs.92732	ESTs KIAA1444 protein	3.8
	420898	AB002379	Hs.100113		3.8 3.8
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	3.8
75	427209	H06509	Hs.92423	KIAA1566 protein	3.7
13	445319 428841	AF052108 AI418430	Hs.12513 Hs.104935	Homo sapiens clone 23687 mRNA sequence ESTs	3.7 3.7
	414821	M63835	Hs.77424	Fc tragment of IgG, high affinity ta, re	3.7
	443310	BE552018	Hs.133152	! ESTs	3.7
80	407728	AW071502	Hs.175931		3.7
30	429643 444127	AA455889 N63620	Hs.167279 Hs.13281	FYVE-finger-containing Rab5 effector pro ESTs	3.7 3.7
	425652	AB021742	Hs.322431	neurogenic differentiation 2	3.7
	458072		Hs.271923		3.7

	450550	A CTOOOD		505	
	459660 432188	M79082	N= 2020	ESTs	3.7
	437627	A1362952	Hs.2928	solute carrier family 7 (cationic amino	3.7
	408508	AW469925 AI806109	Hs.257837	ESTs	3.7
5	448999	AF179274	Hs.135736	KIAA1580 protein	3.7
	410623	AW958932	Hs.22791 Hs.293833	transmembrane protein with EGF-like and	3.7
	430744	AA485229	Hs.105649	ESTs .	3.7
	454392	BE260893	Hs.236131		3.7
	453739	AL120266	115.230131	homeodomain-interacting protein kinase 2 ESTs	3.7
10	407198	H91679		gbryv04a07.s1 Soares fetal liver splaen	3.7
	405239	UB9281		oxidative 3 alpha hydroxysteroid dehydro	3.7
	433615	AA732982	Hs.269607	ESTs. Weakly similar to ALU1_HUMAN ALU S	3.7
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.7
	451027	AW519204	Hs.40808	ESTs	3.7 3.7
15	415131	D61119		gb:HUM158C118 Clontech human fetal brain	3.7
	443454	AI057494	Hs.133421	ESTs	3.7
	423779	AW071837	Hs.57971	ESTs	3.7
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	3.7
20	435910	AI084152	Hs.21782	ESTs. Wealty similar to ALU7_HUMAN ALU S	3.6
20	447028	AI973128	Hs.167257	brain link protein-1	3.6
	452997	N64777	Hs.44656	ESTs	3.6
	408601	U47928	Hs.86122	protein A	3.6
	407332	AI801565	Hs.200113	Homo sapiens cDNA FLJ11379 fis, clone HE	3.6
25	455646	BE064420	41- 0404	gb:RC4-BT0311-241199-012-008 BT0311 Homo	3.6
23	433657 421679	AI244368	Hs.8124	PH domain containing protein in retina 1	3.6
	448985	AI475110	Hs.203933	ESTS	3.6
	414709	AA324885 AA704703	Hs.22777	carbonic anhydrase XI	3.6
	411775	H08342	Hs.77031	Sp2 transcription factor	3.6
30	439099	AB037800	Hs.6462	gb:yt87b09.r1 Soares Infant brain 1NIB H protein kinase C and casein kinase subst	3.6
	436315	BE390513	Hs.27935	hypothetical protein MGC4837	3.6
	423611	AB011163	Hs.129908	KIAA0591 protein	3.6
	453169	AB037815	Hs.32156	KIAA1394 protein	3.6 3.6
	436954	AA740151	Hs.130425	ESTs	3.6
35	439249	AF086060	Hs.170053	G-protein coupled receptor 88	3.6
	432058	AW665996	Hs.130729	ESTs. Wealty similar to ALU1_HUMAN ALU S	3.6
	419390	A1701162	Hs.90207	hypothetical protein MGC11138	3.6
	428483	AI908539	Hs.184592	KIAA0344 gene product	3.6
40	409557	BE182896	Hs.211193	ESTs	3.6
40	418049	AA211467	Hs.190488	Homo sapiens, Similar to nuclear localiz	3.6
	443774	AL117428	Hs.9740	DKFZP434A236 protein	3.6
	425331	AW962128		gb:EST374201 MAGE resequences, MAGG Homo	. 3.6
	445105	AF238869	Hs.283955	Homo sapiens clone GLSH-2 similar to gli	3.6
45	424051 446420	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.6
73	428138	AW015693 AA773842	Hs.135614 Hs.293799	ESTS	3.6
	404185	AA113042	H2.233/33	EST8	3.6
	427517	AA644142	Hs.7107	Target Exon	3.6
	443150	AI034467	Hs.34650	ESTs, Wealdy similar to ALU7_HUMAN ALU S ESTs	3.6
50	408065	AW954272		gb:EST366342 MAGE resequences, MAGC Horno	3.6 3.6
	435092	AL137310	Hs.4749	Homo sapiens mRNA; cDNA DKFZp761E13121 (3.6
	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	3.6
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	3.6
EE	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	3.6
55	412350	A1659306	Hs.73826	protein tyrosine phosphatase, non-recept	3.6
	439753	BE262233	Hs.7423	hypothetical protein from EUROIMAGE 2168	3.6
	451734	NM_006176	Hs.26944	neurogranin (protein kinase C substrate,	3.6
	437056	Al147061		gb:ok33a11.s1 Soares_NSF_F8_9W_OT_PA_P_S	3.6
60	438328 451489	AJ492261 NM 005503	Hs.32450	ESTs	3.6
	423541	AL137256	Hs.26468 Hs.130489	artyloid beta (A4) precursor protein-bind	3.6
	434784	AA649051	Hs.164007	ATPase, aminophospholipid transporter-li ESTs	3.6
	441834	AL138034	Hs.7979	KJAA0736 gene product	3.5
	421183	AL135740	Hs.102447	TSC-22-fike	3.5
65	452108	AW135982	Hs.203013	hypothetical protein FLJ12748	3.5 3.5
	425870	R13406	Hs.56782	ESTs	3.5
	425115	R44664	Hs.123956	ESTs	3.5
	444471	AB020684	Hs.11217	KIAA0877 protein	3.5
70	419929	U90268	Hs.93810	cerebral cavernous malformations 1	3.5
70	407792	AI077715	Hs.39384	putative secreted figand homologous to f	3.5
	422564	AI148006	Hs.222120	ESTs	3.5
	433323	AA805132	Hs.159142	ESTs	3.5
	435743	T66861	Hs.12962	ESTs	3.5
75	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.5
, ,	403341 443761	A1825742	LL 24540-	Target Exon	3.5
	458743	AI525743 R53169	Hs.345187	EST8	3.5
	447925	AW292271	Hs.80712 Hs.250718	KIAA0202 protein	3.5
	445424	AB028945	Hs.12698	ESTs cortactin SH3 domain-binding protein	3.5
80	416874	H98752	Hs.42568	ESTs	3.5
	430456	AA314998	Hs.241503	hypothetical protein	3.5 3.5
	419647	AA348947	Hs.91816	hypothetical protein	3.5 3.5
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	3.5

	*****	05044500			
	444458 451066	BE041526	Hs.31746 Hs.206132	hypothetical protein OKFZp547F072	3.5
	425234	AI758660 AW152225	Hs.165909	ESTs	3.5
	420071	AB028985	Hs.94806	ESTs, Wealth similar to I38022 hypotheti ATP-binding cassette, sub-family A (ABC)	3.5
5	432625	AJ243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.5 3.5
-	442118	AA976718	Hs.202242	ESTS	3.5
	421685	AB011156	Hs.106794	KIAA0584 protein	3.5
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	3.5
10	444326	Al939357	Hs.270710	ESTs	3.5
10	443361	AI792628	Hs. 133273	ESTs	3.5
	427627 434542	R87582	Hs.179915	guarine nucleotide binding protein (G pr	3.4
	419235	AA769310 AW470411	Hs.61260 Hs.288433	hypothetical protein FLJ13164 neurotrimin	3.4
	440700	AW952281	Hs.296184	guanine nucleotide binding protein (G pr	3.4
15	417084	H08370	Hs.33067	ESTs	3.4 3.4
	432925	AA878324		ESTs	3.4
	439920	H05430	Hs.288433	neurotrimin	3.4
	453710	AL119135	Hs.236131	homeodomain-Interacting protein kinase 2	3.4
20	412783	BE276738	Hs.74578	DEAD/H (Asp-Gtu-Ala-Asp/His) box polypep	3.4
20	435977	AL138079	Hs.5012	brain-specific membrane-anchored protein	3.4
•	431725 449611	X65724	Hs.2839	Norrie disease (pseudoglioma)	3,4
	448543	AJ970394 AW897741	Hs.197075 Hs.21380	ESTs	3.4
	430968	AW972830	10.21300	Homo sepiens mRNA; cDNA DKFZp586P1124 (1 gb:EST384925 MAGE resequences, MAGL Homo	3.4
25	413530	AA130158	Hs.19977	ESTs, Moderately similar to ALUS_HUMAN A	3.4
	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRN	3.4 3.4
	445666	R59960	Hs.282386	ESTs	3.4
	412820	BE001238		gb:CM3-BN0075-240200-101-d11 BN0075 Homo	3.4
20	458912	AI911066		ESTs	3.4
30	452449	AW068658	Hs.20943	ESTs	3.4
	437085 419852	AA74393S AW503756	Hs.202329	ESTs	3.4
	448750	U95020	Hs.286184 Hs.21903	hypothetical protein dJ551D2.5	3,4
	435741	AJ240668	Hs.113099	calcium channel, voltage-dependent, beta ESTs	3.4
35	445828	F05802	Hs.81907	ESTs	3.4 3.4
	419347	C15944	Hs.90005	superiorcervical ganglia, neural specifi	3.4
	431733	AW298410	Hs.21475	ESTs	3.4
	415949	H10562	Hs.21691	ESTs	3.4
40	400205			NM_006265°:Homo sapiens RAD21 (S. pombe)	3.4
40	437528	N59646	Hs.169745	crumbs (Drosophila) homolog 1	3.4
	442593 442927	R39804 AI024347	Hs.31961	ESTs	3.4
	429528	AI985303	Hs.131519	EST6	3.4
	450756	AI733488	Hs.99361 Hs.144052	ESTs ESTs	3.4
45	437387	AI198874	Hs.28847	AD026 protein	3.4
	430347	NM_002039	Hs.239706	GRB2-associated binding protein 1	3.4
	404283			ENSP00000244751*:Copine-like protein KIA	3.4 3.4
	433229	AB040925	Hs.91625	KIAA1492 protein	3.4
60	440274	R24595	Hs.7122	scrapie responsive protein 1	3.4
50	435114	AA778232	Hs.19515	ESTs, Highly similar to NRG3_HUMAN PRO-N	3.4
	439690	AA843868	Hs.190567	ESTs	3.4
	450784 417868	AW246803 AI078534	Hs.47289	ESTs	3.3
	439793	AA018825	Hs.122592 Hs.7934	ESTs	3.3
55	456209	W60633	Hs.297792	Kruppel-like factor 4 (gut) ESTs	3.3
	421458	NM_003654	Hs.104576	carbohydrate (keratan suffate Gal-6) sul	3.3 3.3
	438201	AA780243	Hs.54647	ESTs	3.3
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	3.3
60	425897	AA935315	Hs.48965	Homo sapiens cDNA: FLJ21693 ffs, clone C	3.3
60	423169	8E047009	Hs.21837	ESTs, Wealdy similar to KIAA0927 protein	3.3
	415539 450337	AI733881 AI693256	Hs.72472	8MP-R1B	3.3
	408447	AK002089	Hs.202427 Hs.45080	ESTS	3.3
	423420	AI571364	Hs.128382	Homo sepiens cDNA FLJ11227 fis, clone PL Homo sepiens mRNA; cDNA DKFZp76111224 (f	3.3
65	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.3
	440435	AL042201	Hs.21273	transcription factor NYD-sp10	3.3 3.3
	453785	AI368236	Hs.283732	ESTs. Moderately similar to ALU1_HUMAN A	3.3
	448048	BE281291	Hs.170408	ESTs. Moderately similar to A47582 B-cel	3.3
70	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.3
, 0	404632	ALARE 4790		NM_022490:Homo sapiens hypothetical prot	3.3
	411565 416845	AW851728 H95279	Hs.293788	gb:MR2-CT0222-011199-007-d06 CT0222 Homo	3.3
	436267	AW450938	Hs.180115	gb:yu20h02.s1 Soares fetal liver spieen ESTs	3.3
	426625	178300	Hs.300842	Serologically defined colon cancer antig	3.3
75	401272			C9000559":gij12314195jembjCA899338.1j (A	3.3 3.3
	435071	D60683	Hs.35495	ESTs	3.3 3.3
	433128	AB021923	Hs.23367	EST-YD1 protein	3.3
	426920	AA393351	Hs.132121	ESTs	3.3
80	423668	Y10148	Hs.131138	neurotensin receptor 2	3.3
55	435056 445534	AW023337	Hs.5422	glycoprotein M6B	3.3
	425010	AL038823 T16837	Hs.12840 Hs.4241	Homo sapiens germline mRNA sequence	3.3
	445260	AI218133	Hs.147617	ESTs ESTs	3.3
				COTO	3.3
				225	

	421094	AW978202	Hs.289064	hypothetical protein FLJ22251	3.3
	450358	AB010098	Hs.24907	coronin, actin-binding protein, 2B	3.3
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	3.3
5	432488	AA551010	Hs.216640	ESTs	3.3
,	443672 412719	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	3.3
	420050	AW016610 AL118615	Hs.816 Hs.94653	ESTs	3.3
	410082	AA081594	Hs.158311	neurochondrin	3.3
	408554	AA836381	Hs.315111	Musashi (Drusophila) homolog 1 nuclear receptor co-repressor/HDAC3 comp	3.3
10	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	3.3 3.2
••	434574	AI424458	Hs.33470	ESTs	3.2
	432715	AA247152	Hs.200483	ESTs, Wealty similar to KIAA1074 protein	3.2
	426757	AW205640	Hs.158206	ESTs	3.2
	428187	AA770021	Hs.16332	ESTs	3.2
15	451597	AW295250	Hs.207536	ESTs .	3.2
	400362	AF068294	Hs.272414	Homo sapiens HDCMB45P mRNA, partial cds	3.2
	417675	A1808607	Hs.3781	similar to murine leucine-rich repeat pr	3.2
	429550	AW293055	Hs.119357	ESTs	3.2
20	404120			C5000537":gij3298595 gb AAC41376.1 (AF0	3.2
20	417123	BE326521	Hs.159450	ESTs	3.2
	450313	A1038989	Hs.332633	Bardet-Biedl syndrome 2	3.2
	425999	AW513051	Hs.332981	ESTs, Wealdy similar to 138022 hypotheti	3.2
	430526 452619	AF181862 AW298597	Hs.242407 Hs.61884	G protein-coupled receptor, family C, gr	3.2
25	415558	AA885143	Hs.125719	Homo sapiens, clone IMAGE:4298026, mRNA, ESTs	3.2
~	451996	AW514021	Hs.245510	ESTs	3.2
	420560	AW207748	Hs.59115	ESTs	3.2 3.2
	432328	A1572739	Hs.195471	6-phosphofructo-2-kinese/fructose-2,6-bi	3.2
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	3.2
30	414300	AJ304870	Hs.188680	ESTs	3.2
	437834	AA769294	Hs.283854	gbmz36g03.s1 NCI_CGAP_GC81 Homo saplens	3.2
	430694	AA810624	Hs.30936	ESTs, Weakly similar to H2BH_HUMAN HISTO	3.2
	447714	AW296313	Hs.255537	ESTs	3.2
3.5	412021	AW885592		gb:RC4-OT0071-090300-011-g11 OT0071 Homo	3.2
35	443431	AI056847	Hs.20654	ESTs	3.2
	445774	AJ254165	Hs.339968	ESTs .	3.2
	431327	AW972220	Hs.105426	ESTs	3.2
	413335	AI613318	Hs.48442	ESTs	3.2
40	430809 445858	AI791150 AL133811	Hs.262009	ESTs, Moderately similar to (38022 hypot	3.2
40	450692	H50603	Hs.94037	solute carrier family 1 (gilal high affi	3.2
	439039	AI656707	Hs.48713	hypothetical protein FLI23053 ESTs	3.2
	401720	74000101	113.40713	NM_014587":Homo sapiens SRY (sex determi	3.2
	453740	AL120295	Hs.311809	ESTs, Moderately similar to PC4259 femi	3.2 3.2
45	451032	W03692	Hs.323079	Homo sapiens mRNA; cDNA DXFZp564P116 (fr	3.2
	413834	BE296896	Hs.224179	ESTs. Weakly similar to I38022 hypotheti	3.2
	438138	R98299	Hs.177502	ESTs	3.2
	436338	W92147	Hz.118394	ESTs	3.2
FΛ	417169	R13550	Hs.246773	ESTs	3.2
50	424066	Z99348	Hs.112461	ESTs, Weakly similar to I38022 hypotheti	3.2
	435767	H73505	Hs.117874	ESTs	3.2
	415314	N88802	Hs.5422	glycoprotein M68	3.2
	448475 414699	BE613134 Al815523	Hs.247474	hypothetical protein FLJ21032	3.2
55	438549	BE386801	Hs.76930 Hs.21858	synuclein, atpha (non A4 component of am trinucleotide repeat containing 3	3.2
	453896	AW293483	Hs.255205	KIAA1853 protein	3.2 3.2
	419539	AF070590	Hs.90869	Homo sapiens clones 24522 and 24623 mRNA	3.1
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	3.1
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	3.1
60	429046	X57438	Hs.194772	oligodendrocyte myelin głycoprotein	3.1
	421896	N62293	Hs.45107	ESTs	3.1
	413995	BE048148	Hs.75671	syntaxin 1A (brain)	3.1
	414734	AA151712	Hs.82572	ESTs	3.1
65	446147	AL133064	Hs.14051	Homo sepiens mRNA; cDNA DKFZp434A2417 (f	3.1
03	427712	AJ368024	Hs.283696	ESTs	3.1
	406481 453204	R10799	Lin 101000	Target Exon	3.1
	422890	Z43784	Hs.191990	ESTs	3.1
	422991	H10940	Hs.48965	ankyrtin 3, node of Ranvier (ankyrtin G) Homo sapiens cDNA: FLJ21693 fis, clone C	3.1
70	421030	AW161357	. 40.503	microtubula-associated protein tau	3.1 3.1
-	423603	AB007880	Hs.129883	Homo sapiens KIAA0420 mRNA, complete cds	3.1
	413985	AI018666	Hs.75667	synaptophysin	3.1
	431721	A8032996	Hs.268044	KIAA1170 protein	3.1
75	434164	AW207019	Hs.148135	serine/threonine kinase 33	3.1
75	429876	AB028977	Hs.225974	KIAA1054 protein	3.1
	423175	W27595	Hs.347310		3.1
	412799	AI267606		gb:aq91h03.x1 Stanley Frontal SB pool 1	3.1
	459318	NM_000038		gli:Homo sapiens adenomatosis polyposis c	3.1
80	453324	W26592	Hs.232089	ESTs	3.1
Ų.	424009 436222	F11690 Al208737	U- 122012	gb:HSC300041 normalized infant brain cDN	3.1
	414884	R54418	Hs.122810 Hs.183745	Homo sepiens cDNA FLJ11489 fis, clone HE	3.1
	446862	AV660697	Hs.282700	hypothetical protein FLJ13456 ESTs	3.1
					3.1
				007	

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	402041	AA399988	No. 4 4 2000		
	427241 455388	AW936234	Hs.112087	Human DNA sequence from clone RP11-530N1 gb:QV0-DT0020-090200-106-g05 DT0020 Homo	11
	415838	R44336	Hs.7093	ESTs	3.1 3.1
_	451692	AL137422	Hs.26849	Homo saplens mRNA; cDNA DKFZp751A1623 (f	3.1
5	445294	Z45978		Human clone 23826 mRNA sequence	3.1
	434460	AA478485	Hs.3852	KIAA036B protein	31
	449919	AJ674685	Hs.200141	ESTs	3.1
	440688	AW404591	Hs.147440	ESTs, Wealthy similar to Z192_HUMAN ZINC	3.1
10	416801	X98834	Hs.79971	sal (Orosophila)-like 2	3.1
10	428060 423597	AA420616	Hs.249483	ESTs	3.1
	452454	AL043117 AW820480	Hs.129872	sperm associated artigen 9	3.1
	445337	NM_013280	Hs.12523	gb:CV2-ST0298-140200-042-f10 ST0298 Homo fibronectin leucine rich transmembrane p	3.1
	413974	BE208636	Hs.27788	ESTs	3.1 3.1
15	422772	AL119585	Hs.120228	KIAA0749 protein	31
	423872	AB020316	Hs.134015	uronyl 2-sulfotrensferese	3.1
	435375	AJ733610	Hs.187832	ESTs	3.1
	450661	AW952160	Hs.83849	ESTs	3.1
20	428547	AA830050	Hs.124344	EST8	3.1
20	400658	41500004	11- 440 105	ENSP00000237081":KIAA1217 PROTEIN (FRAGM	3.0
	443845 446619	AI590084 AU076643	Hs.148485 Hs.313	ESTs, Weakly similar to A47161 Mac-2-bin	3.0
	433980	AA137152	Hs.286049	secreted phosphoprotein 1 (osteopontin, phosphoserine aminotransferase	3.0
	437738	AA766914	Hs.203475	ESTS, Weakly similar to ALU1_HUMAN ALU S	3.0 3.0
25	444772	AW450800	Hs.176859	ESTs	3.0
	453825	AL157475	Hs.35453	Homo sapiens mRNA; cDNA DKFZp761G151 (fr	3.0
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	3.0
	408449	NM_004408	Hs.166161	dynamin 1	3.0
30	432821	BE170702	Hs.279005	solute carrier family 21 (organic anion	3.0
20	453657	W23237	Hs.296162	AD037 protein	3.0
	407235 428862	D20569 NM_000348	Hs.169407 Hs.2316	SAC2 (suppressor of actin mutations 2, y	3.0
	424726	AK001007	Hs.138760	SRY (sex determining region Y)-box 9 (ca Homo sapiens cDNA FLJ 10145 fis, clone HE	3.0
	454253	AV660717	Hs.47144	DKFZP586N0819 protein	3.0 3.0
35	450650	T65617	Hs.101257	hypothetical protein MGC3295	3.0
	418211	BE244746	Hs.247474	hypothetical protein FLJ21032	3.0
	440461	R52728	Hs.7193	KIAA1183 protein	. 3.0
	452850	H23230	Hs.22481	ESTs, Moderately similar to A46010 X-lin	3.0
40	431431	AL096711	Hs.252953	Human DNA sequence from clone RP3-403A15	3.0
4 0	447881 454042	BE620886	Hs.75354	GCN1 (general control of amino-acid synt	3.0
	429168	H22570 AA984682	Hs.146589	hypothetical protein FLJ20093	3.0
	451391	AA017410	Hs.40568	ESTs, Weakly similar to JC5238 galactosy ESTs	3.0
	446377	AW014022	Hs.170953	ESTs	3.0 3.0
45	430251	AA609246	Hs.181451	ESTs	3.0
	420658	AW985215	Hs.130707	ESTs	3.0
	454119	BE549773	Hs.40510	uncoupling protein 4	3.0
	451018	AW965599	Hs.247324	mitochondrial ribosomal protein S14	10
50	435321	R16814	Hs.112062	ESTs	3.0
30	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.0
	423858 431242	AL137326 AA987742	Hs.133483 Hs.347534	Horno sapiens mRNA; cDNA DKFZp434B0650 (f KIAA1201 protein	3.0
	403022	70101142	113.347334	C21000178*:gij7341207 gb AAF61215.1 AF22	3.0 3.0
	445899	AI263736	Hs.145626	ESTs	3.0
55	440261	M81888	Hs.7117	glutamate receptor, ionotropic, AMPA 1	3.0
	446809	AW590171	Hs.101413		3.0
	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	3.0
	418951	F07809	Hs.89506	paired box gene 6 (aniridia, keratitis)	3.0
60	448499 432229	BE613280	Hs.77550	hypothetical protein MGC1780	3.0
00	443726	AW290976 AI083825	Hs.143587 Hs.148382	ESTs ESTs	3.0
		70000023	115.140002	6018	3.0
	TABLE 13	18 :			
	Pkey:		ue Eas probe	set identifier number	
65	CAT num		duster numl		
	Accession	ı: Geni	bank accessio	n numbers	
	•				
	Pkey	CAT Number			
70	408065 410099	103646_1 117647_1		AI003154 AA059300 AA046911 T08671 A1374364 D03074 AMPERICA A A3C4503 A A5C4	407 444 408 408 408 408 408 408 408 408 408
, 0	410033	11/04/_1	T07775 AA	1000/1 A11/4234 D838/4 AW333843 AA3645Q3 AA693 484640 W60000 D63686 T33844 D6333043 AM004368	467 AW993370 BE327037 AA167714 N79906 AW901977 AW901980 W52882
			RIBARNAA	404349 WOWSO LGZOOS 123611 BE32/043 AWSU1/08 RE467738 AMOS636 AIRB7863 AIRB7663 AA436640 AIR	BE551237 AA917004 AA716027 AI439658 AA283724 AI805992 AI457096
			AA211402	AI204899 AI366472 AW827081 AA788593 T32736 AI76	57419 Al418634 T31586 AA436630 AA706191 Al041169 Al422304 T03534
	410126	117761_1	BE169274	AW893230 AA210998 H24222 AA081774 BE000935 BE	DORSA AARRA
75	411585	1249756_1	AW851728	AW851607 AW851621 AW851702 AW851647 AW8517	77 AWR51658 AWR51617 AWR51628
	411775	125757_1	H08342 R5	2430 Z42067 AA095285	
	412021	1272156_1		AW885594 AW885579 AW885651	
	412799	132817_1	AI267606	A121045 AA126521	
80	412811	132943_1	P30007 A	V30//JU RAJOZU14 K13591 AA1212U1 D60420 BE2632 .e.13483 AWA16463 WA6363 D446A7 A13449AA	53 BE047852 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148 AA598689
	412820	1330039_1	REDOTOSE PEROTOSE	813482 AWU16452 HU6383 H41807 AI364268 AA62052 BE001177 BE001180 BE001234	8 AIZ41940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734
	415131	1523680_1		11508 D81734	

	418512	176394_1	AW498974 T09332 R58460 AA350990 T33786 T30936 AA350905 T08592 T09274 AA224297 D54678 T08951 R15346 AW953188 AA350074 AW890649
	420111	190755_1	AA255652 AA280911 AW987920 AA262684
_	420352	192979_1	BE258835 AW968316 AA259918 AW843305 R14744 AI580388 BE071923 R36280
5	421030	19864_1	AW161357 AI879062 AI928938 AW161097 AW161167 BE314465 AA351715 F07096 AA179034 F08510 F00653 AI936671 AA476718 AW772464
			AI807703 R44253 AA976667 AI985186 AI650254 H38942 R84829 AA018724 AA001000 MR5934 AA019126 MR5609 AA017000 AA220366 AA020666
			D51397 AA213981 BE548002 AID56359 AA001560 AW952113 AA317769 AIB57477 AIB57475 AW249771 AW162661 H38943 AA018628 RB5885
			A)584613 A)934765 A)796172 AW157488 A)929191 R85523 D51221 D53851 H85610 A)749674 F21582 AA323145 AA019127 AA687444 T06745 A)699293 H29532 AA214029 AA223656 NM_016834 X14474 R19697 H09695 R17455 R13812 R19056 A)681231 A)590200 R37671 AA681828
10			A990023 AF935669 AW005821 AA324581 H17335 R37659 R42802 R46242 R60936 R59731 H28993 AA479907 R44570 AIRORGO AA308994
			AA507078 R41274 AJ365507 T16348 AJ560453 F03259 F04722 T16312 AAD16081 AW073061 RE314R24 W2R930 R4409R R51045
	422890	222707_1	443/84 R13382 AW5/2911 AA449369 H17037 R19603 AI532565 AW004030 RF502530 725032 AAR05324 AA449241 AI551825 AI2CAR63 AW100040
			AA948Z67 AI953735 AI263703 AA319159 AW964436 AI903440 AW594171 AI857447 AW204071 AW956110 C15616 D81142 H17038 AW162343 T87230 AI366013 H10064 AI190479 AI093318 AI867923 BE219303 BE048820 AI198397 AA654667 Z39851 F02655 Z28734 F04161 T16575 F10145
15			A318815 R40898
	423476	22861_1	AL035633 F11794 F11783 H18042 T66089 H29379 R19493 AW134660 Al299437 AL133995 AA057405 N78357 AA917450 A1002692 T09262 T65008
	424000	201122 4	H29290 AI200874 AA894415 AI732887 AI791768 AI733447 AA988785 N62128 T09261 AW956938
	424009 424572	234177_1 24097_1	F11690 AW966370 AA333586 030830
20	424072	24037_1	M19650 R18810 R18721 AW896146 AW889520 AA192362 AA176814 F12085 BE255264 BE251393 T65248 AA380585 AA380465 BE408684 AA459037 AW498869 AA776107 BE274289 D45269 M61958 AA378818 AW663180 AW672958 H08611 M78164 BE393721 AA348660 R36303
			AW498662 AA019090 AA001087 AA054302 AA019775 AA018808 AA019132 AI858240 R73218 H30477 H17776 AA666570 RE276750 AL1106E7
			AA375861 AA352427 AW581695 AI141188 N63474 AA654162 H17659 AL120696 T28867 AW498868 AL355918 AA902349 AA569099 AI088233
,			A042604 AA555133 A183811 AI608822 A1275941 AW316805 AA349486 A1355233 R85117 AW613626 R49234 AA458846 N20669 H18693 AA977567
25			T15423 AW002084 AIB24721 N36242 AI417281 AI018212 AA912337 F09722 AA749449 AW879172 AA885477 AA916639 AIB72560 F00482 H45184 AI217251 AA775807 BE390071 AA303517 AA001050 BE515169 N44066 AL133684 AI807085 AA808009 AA915914 F00007 AA019749 AL121560
			AW675544 AW090233 AW072071 AB10932 A089733 AW026222 AA770155 Al089647 A085733 AW516061 AL037636 AL037635 Al863947 H50420
			R11203 AAU19133 N94772 N71842 N29047 AA778138 AA554338 AA179865 N59453 T65212 AA054270 AW806630 AA513375 D13148 AA349487
	424945	245223_1	AU077160 BE255571 BE276795 BE250823 AL 120301 BE311390 BE252483 Al231010 210567 A. 148790 AU6767 AU6
- 30	724343	243223_1	Al221919 Z19967 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 Al341345 AW298800 AA724961 AA931158 AI741227 Al806660 Al982626 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 Al492961 Al361526 F04002 AA452141 T23551 Al472555
			Al193667 Al341984 N92658 T32870 R52664 N50428 AW089291 Al934175 Al423737 D60665
	425331	250199_1	AW962128 AA355353 AA427363
	426413 426503	266650_1 268283_1	AA377823 AW954494 AI022688 AA380153 AA380233 AW963529
35	426919	273507_1	AL041228 D82004 D61361 Al203314 Al990307 AW900295 Al018308 AW087473 AW183530 AA393346 H50055 AA935601
	428342	290035_2	AI/39168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377778 AW293682 AI928140 AA721439 AID92404
	429007	298301_1	AI085630 AA731340 D80842 AA443145 AL119015 AW904500
	429421	30431_1	AL031658 AI693758 AL040619 AW977914 AAB11957 AI352198 AW104364 AA648367 AA897604 AW341668 AI201392 AL040620
40	430183	31412_2	BE010038 AA676833 Al311783 T86895 W68032 BE064393 BE064394 BE157228 BE183282 Al936370 AA652514 T67280 AA039000
	430676	32168_1	AF084866 AF084870 AF084864 AF084867 AF084869 AF084865 AF084868 AW818206 AW812038 BE144813 BE144812 AW812041 AW812040
	430968	326269_1	AW812067 BE061583 BE061604 T05808 A1352469 AA580921 BE141783 BE141782 BE061601 AW814393 AW885029 AW972830 AA527647 AA489820 AA570362
4.5	432646	351909_1	AW753310 AW974000 AA557840 AA558570 AW751539
45	432925	356372_1	AA878324 AI863159 AI619686 AA570406 AID14377
	433009 433523	357371_1 368873_1	AA761668 AA573621 R92814 R09670 H29882 AW665533 AW149901 AI572917 AA598500 AI686465 AI336390 AW864390 AW864320
	437034	431713_1	AA742643 AA808575 AW976669
50	437056	432262_1	A1147061 AA743380 AA765223 AW976398 A1803927
30	438458 439285	457837_1 47065_1	AW975186 AA807807 D2548 A 11373016 A70413 ACRESON ATCC 21 AMPERODO A A 2010 AMPERODO A 100 AMPER
	100200	_	AL 133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AJ346341 AJ867454 N54784 AJ655270 AJ421279 AW014882 AA775552 N62351 N59253 AA626243 AJ341407 BE175639 AA456968 AJ358918 AA457077
	441102	509604_1	AA973905 AI299888 AA917019 H63235 T90771
55	445294	6352_1	245978 U79248 T77277 R24952 AA361008 AW953678 T10376 AW860579 AW860657 AW364889 AW860635 AW860658 AW905164 W21226
			AA448954 W69484 AA993098 AA287413 AA449682 AI961815 W57612 AW271363 R45215 AW136256 AI865103 W69577 AI961826 AA747542 AA173748 AI961816 F07706 R39461 F04829 F05938 AA172385
	445858	6525_1	AL133811 M78538 T07792 AW895859 AW895859 AL119422 T79876 R19494 AF131756 H18570 T0R285 F11532 742038 AW081084 AA683301
			MOZUTZ AL 119616 ZZ1141 AA663820 Z19748 H18462 AL 120152 R43841 R37594 AA775980 F09194 A1207884 Z39142 F01555 AA020727 AL 120362
60	446692	689623_1	AW952737 T04912 Z44514 AJ352097 AJ803984 AW235923 AW196558 AJ954637 AJ336983
	447197	711623_1	R36075 Al366546 R36167
	448044	747196_1	A458692 H24240 R14537 R18426 AW867082
	450582 451320	83933_1 86576_1	A339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA855829 AW935878 AW14872 A16310827 116324 A274106 AT101 A160 A1740 A760 A760 A760 A760 A760 A760 A760 A76
65			AW118072 Al631982 T15734 AA224195 Al701458 W20198 F26326 AA890570 N90552 AW071907 Al671352 Al375892 T03517 R88265 Al124088 AA224388 Al084316 Al354886 T33652 Al140719 Al720211 T03490 Al372637 T15415 AW205836 AA630384 T03515 T33230 AA017131 AA443303
			133623 A/222556 T33511 T33785 A/419606 D55612
	452454 453739	918306_1 979419_1	AW820480 AW820288 Ai902522
	454042	99636_3	AL120266 AW269469 AW890114 H22570 AW292267 AW137298 AW874199 AI206120 H45263 AA788851 R49056 AW241428 AI921013 AW129293 AI684910 BE466753 AA340613
70			AWU25969 AI2U2561 AI243913 AW771106 F04969 AI654847 AI494436 AW771447 AW103715 N64350 AA347011 AI491597 AA770107 AA041105
			AU30894 AU421078 AU18523 AA707199 AA410309 AU366468 AW020049 AU880103 AL119553 R42410 R55722 T66767 R43035 H17396 H45331
	454171	1049240_	F01659 Z38381 AA708586 A1081305 R53955 AA041432 W27787
	455388	1287904	
75	455646	1348557_	BE064420 BE084435 BE084429 BE064414 BE064400 BE064517
	458912 459079	823104_1	AI911066 AI933734 AI680888 AJ003599
	433013	888710_1	AJ821122 AJ821866
90	TABLE 1		
80	Pkey: Ref:	ŭ	nique number corresponding to an Eos probese!
	rvel.	S)	equence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA equence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
	Strand:	lr.	dicates DNA strand from which exons were predicted.

	Nt_position	n: Indica	ites nucleotide	positions of predicted exons.	
	Pkey	Ref	Strand	MI maritim	
	400533	6981826	Minus	Nt_position 277132-277595	
5	400658	8118459	Minus	73525-73644	
	400777	8131663	Plus	70745-71121	
	401272	9797373	Minus	98374-98509	
	401720	6468551	Ptus	7783-8468	
10	402145	8018280	Ptus	113086-114800	
10	402604 402605	9909420 9909420	Phus	20393-20767	
	402855	9662953	Minus Minus	47680-47973	
	403022	3132351	Plus	59763-59909 92097-92864	
	403142	9444521	Plus	89286-90131	
15	403341	8569175	Plus	30699-30910	
	403696	3135242	Minus	143467-143634	
	404120	7342152	Plus	135775-136000	
	404185	4572584	Minus	129171-129327	
20	404283	2276311	Minus	99460-99564	
20	404541 404584	8318559	Plus	103456-103664	
	404632	9857511 9796668	Plus Plus	138651-139153	
	404819	4678240	Plus	45096-45229	70 47007 47000 47500 40054 40057 40440
	405238	7249119	Minus	16223-16319,16427-16513,16736-16859,16941-17075,171: 51728-51838	(0-1/20/,1/389-1/529,18261-1835/,18443-18578
25	405239	7249119	Plus	144345-144464,144690-144836,151750-151883,152407-15	2484
	405348	2914717	Minus	43310-43462	
	405819	4007557	Plus	2830-2967	
	406481	9864741	Minus	91439-91579	
30					
50	TARLE 14	A- AROUT 111	CENES NO	SECULATED IN CUIDOLACTORA COMPADED TO MODILIA	
	Table 14A	lists about 1111	Denes inven	REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL	CENTRAL NERVOUS SYSTEM stem (CNS). These were selected from 59680 probesets on the Affyrnetric/Eos
	Hu03 Gen	eChio array suc	h that the ratio	of "sversoe" dishipsions to "sversoe" CNS fireves was ever	stern (CNS). These were selected from 59680 probesets on the Affyrnetrix/Eoster than or equal to 2.5. The "average" glioblastoma level was set to the 85*
	percentile	amongst various	brain tumors.	The "average" normal CNS tissue level was set to the 850 a	ercentile amongst various CNS tissues, In order to remove gene-specific
35	oackgroun	IO IBAGIZ OI UOU-I	specific hybridia	zation, the 10th percentile value amonost various non-mationa	nt tissues was subtracted from both the numerator and the denominator before
	RIG 1910 M	ras evaluated.			THE STATE OF THE PARTY OF THE PROPERTY OF THE STATE OF TH
	Pkey:			et identifier number	
	ExAcon:	Exen	nplar Accession	number, Genbank accession number	
40	UnigenetC Unigene T		ene number ene gene title		•
10	R1:		of GLIOBLAS	TOMA IN CHE	
	••••	. 4000	0.00000	TOWN ID CAS	
	Pkey	ExAcon	UnigenetD	Unigene Title	· R1
4.5	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Dani	32.8
45	423961	D13666	Hs.138348	periostin (OSF-2os)	28.0
	433001	AF217513	Hs 279905	done HQ0310 PR00310p1	25.3
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	04.2
			11- 4-5000		24.3
	424800	AL035588	Hs.153203	MyoD family inhibitor	22.6
50	424800 417308	AL035588 H60720	Hs.81892	KIAA0101 gene product	22.6 22.2
50	424800 417308 449539	AL035588 H60720 W80363	Hs.81892 Hs.58446	KIAA0101 gene product ESTs	22.6 22.2 20.7
50	424800 417308	AL035588 H60720	Hs.81892 Hs.58446 Hs.32964	KiAA0101 gene product ESTs SRY (sax determining region Y)-box 11	22.6 22.2 20.7 18.7
50	424800 417308 449539 453392	AL035588 H60720 W80363 U23752	Hs.81892 Hs.58446 Hs.32964 Hs.77432	KiAA0101 gene product ESTs SRY (sex determining region Y)-box 11 epidermal growth factor receptor (avian	22.6 22.2 20.7 18.7 18.6
	424800 417308 449539 453392 414825 444190 412420	AL035588 H60720 W80363 U23752 X06370	Hs.81892 Hs.58446 Hs.32964	KIAA0101 gene product ESTs SRY (sax determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2	22.6 22.2 20.7 18.7 18.6 17.2
50 55	424800 417308 449539 453392 414825 444190 412420 417130	AL035588 H60720 W80363 U23752 X06370 AI878918 AL035668 AW276858	Hs.81892 Hs.58446 Hs.32964 Hs.77432 Hs.10526 Hs.73853 Hs.81256	KiAA0101 gene product ESTs SRY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenelic protein 2	22.6 22.2 20.7 18.7 18.6 17.2 16.7
	424800 417308 449539 453392 414825 444190 412420 417130 414217	AL035588 H60720 W80363 U23752 X06370 AI878918 AL035668 AW276858 AI309298	Hs.81892 Hs.58446 Hs.32964 Hs.77432 Hs.10526 Hs.73853 Hs.81256 Hs.279898	KİAA0101 gene product ESTs SRY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenelic protein 2 5100 calcium-binding protein A4 (calcium Homo sapiens cDNA: FLJZ3165 fis, clone L	22.6 22.2 20.7 18.7 18.6 17.2
	424800 417308 449539 453392 414825 444190 412420 417130 414217 431941	AL035588 H60720 W80363 U23752 X06370 AI878918 AL035668 AW276858 AI309298 AK000106	Hs.81892 Hs.58446 Hs.32964 Hs.77432 Hs.10526 Hs.73853 Hs.81256 Hs.279898 Hs.272227	KiAA0101 gene product ESTs SRY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenetic protein 2 5100 catclum-binding protein A4 (catcium Homo sapiens cDNA: FLJ23165 fs., clone L Homo sapiens cDNA FLJ2099 fs., clone CO	22.6 22.2 20.7 18.7 18.6 17.2 16.7
	424800 417308 449539 453392 414825 444190 412420 417130 414217 431941 425397	AL035588 H60720 W80363 U23752 X06370 AI878918 AL035668 AW276858 AI309298 AK000105 J04088	Hs.81892 Hs.58446 Hs.32964 Hs.77432 Hs.10526 Hs.73853 Hs.81256 Hs.279898 Hs.272227 Hs.156346	KiAA0101 gene product ESTs SRY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenetic protein 2 S100 catclum-binding protein A4 (catclum Homo sapiens cDNA: FLJ23165 fs, clone L Homo sapiens cDNA FLJ20099 fs, clone CO topoisomerase (DNA) II alpha (170x0)	22.6 22.2 20.7 18.7 18.6 17.2 16.7 16.7 14.3 14.3
55	424800 417308 449539 453392 414825 444190 412420 417130 414217 431941 425397 446584	AL035588 H60720 W80363 U23752 X06370 AI878918 AL035669 AW276858 AI309298 AIK000105 J04088 U53445	Hs.81892 Hs.58448 Hs.32964 Hs.77432 Hs.10526 Hs.73853 Hs.81256 Hs.279289 Hs.272227 Hs.156346 Hs.15432	KiAA0101 gene product ESTs SRY (sex detarmining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenelic protein 2 5100 calcium-binding protein A4 (calcium Homo sapiens cDNA: FLJ23165 fis, clone L Homo sapiens cDNA FLJ20099 fis, clone CO topoisomerase (DNA) II alpha (170kD) downregulated in ovarian cancer 1	22.6 22.2 20.7 18.7 18.6 17.2 16.7 14.3 14.3 14.1
	424800 417308 449539 453392 414825 444190 412420 417130 414217 431941 425397 446584 422672	AL035588 H60720 W80363 U23752 X06370 AI878918 AL035668 AW276858 AI309298 AK000105 J04088	Hs.81892 Hs.58446 Hs.32964 Hs.77432 Hs.10526 Hs.73853 Hs.81256 Hs.279898 Hs.272227 Hs.156346	KiAA0101 gene product ESTs ESTs (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenetic protein 2 5100 catclum-binding protein A4 (catcium Homo sapiens cDNA: FLJ23155 fs., clone L Homo sapiens cDNA FLJ20099 fs., clone CO topoisomerase (DNA) II alpha (170kD) downregulated in ovarian cancer 1 collagen, type IV, alpha 1	22.6 22.2 20.7 18.7 18.6 17.2 16.7 14.3 14.3 14.1 13.9
55	424800 417308 44939 453392 414825 444190 412420 417130 414217 431941 425397 445884 422672 402604	AL035588 H60720 W80363 U23752 X06370 AI878918 AL033568 AW276858 AI309286 AK000106 J04088 U53445 X12784	Hs.81892 Hs.58446 Hs.32964 Hs.77432 Hs.10526 Hs.73853 Hs.81256 Hs.279898 Hs.272227 Hs.156346 Hs.15432 Hs.119129	KiAA0101 gene product ESTs SRY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenetic protein 2 S100 catchum-binding protein A4 (catchum Homo sapiens cDNA: FLJ23165 fs, clone L Homo sapiens cDNA: FLJ23165 fs, clone CO topoisomerase (DNA) II alpha (170kD) downregulated in ovarian cancer 1 collagen, type IV, alpha 1 Target Exon	22.6 22.2 20.7 18.7 18.6 17.2 16.7 16.7 14.3 14.3 14.1 13.9
55	424800 417308 449539 453392 414825 444190 412420 417130 414217 431941 425397 446584 422672	AL035588 H60720 W80363 U23752 X06370 Al876918 AL035668 AW276858 AX000106 J04088 U53445 X12784 AA420687	Hs.81892 Hs.58446 Hs.77432 Hs.10526 Hs.77432 Hs.10526 Hs.278898 Hs.272227 Hs.156346 Hs.15432 Hs.119129	KiAA0101 gene product ESTs ESTs (sex determining region Y)-box 11 epidermal growth factor receptor (evian cysteine and glycine-rich protein 2 bone morphogenetic protein 2 5100 calctum-binding protein A4 (calcium Homo aspiens CDNA-FLJ23165 fis., done L Homo sapiens CDNA-FLJ2099 fis., clone CO topoisomerase (DNA) II alpha (170kD) downregulated in ovarian cancer 1 collagen, type IV, alpha 1 Target Exon Homo sapiens CDNA-FLJ14259 fis., clone PL	22.6 22.2 20.7 18.7 18.6 17.2 16.7 14.3 14.3 14.1 13.9 13.6 13.6
55 60	424800 417308 449392 453392 414825 444190 412420 417130 414217 431941 425397 448584 422672 402604 424835	AL035588 H60720 W80363 U23752 X06370 AI878918 AL033568 AW276858 AI309286 AK000106 J04088 U53445 X12784	Hs.81892 Hs.58446 Hs.32964 Hs.77432 Hs.10526 Hs.73853 Hs.81256 Hs.279898 Hs.272227 Hs.156346 Hs.15432 Hs.119129	KiAA0101 gene product ESTs SRY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenetic protein 2 S100 catclum-binding protein A4 (catcium Homo sapiens cDNA: FLJ23165 fs., clone L Homo sapiens cDNA: FLJ23165 fs., clone CO lopoisomerase (DNA) II alpha (170k.D) downregulated in ovarian cancer 1 collagen, type IV, alpha 1 Target Exon Homo sapiens cDNA FLJ14259 fs., clone PL matrix metalfoproteinase 7 (matifysin,	22.6 22.2 20.7 18.7 18.6 17.2 16.7 14.3 14.3 14.1 13.9 13.6 13.6
55	424800 417308 449539 453392 414825 444120 417130 414217 431941 425397 445584 422672 402604 424635 428330 434078 434078	AL035588 H60720 W80363 U23752 X06370 Al876918 AL035668 AW276858 AX000106 J04088 U53445 X12784 AA420687 L22524 AW880709 AU077228	Hs.81892 Hs.58446 Hs.32964 Hs.77432 Hs.10526 Hs.73853 Hs.81256 Hs.273227 Hs.156346 Hs.119129 Hs.115432 Hs.119129	KiAA0101 gene product ESTs SRY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenetic protein 2 S100 catchum-binding protein A4 (catchum Homo sapiens cDNA: FLJ23165 fs, clone C Homo sapiens cDNA: FLJ23165 fs, clone CO topoisomerase (DNA) II alpha (170kD) downregulated in ovarian cancer 1 collagen, type IV, alpha 1 Target Exon Homo sapiens cDNA FLJ14259 fs, clone PL matrix metafloproteinase 7 (matritysin, chromosome 8 open reading frame 4	22.6 22.2 20.7 18.7 18.6 17.2 16.7 14.3 14.3 14.1 13.9 13.6 13.6 13.0 12.9 12.5
55 60	424800 417308 449539 453392 414825 444190 412420 417130 414217 413941 42539 448589 42604 42604 42603 42603 434078 414761 442432	AL035588 H60720 W80363 U23752 X06370 Al876918 AL035668 AW276858 AI309288 AK000105 J04088 U53445 X12784 AA420687 L22524 AW880709 AL077228 BE093389	Hs.81892 Hs.58448 Hs.77432 Hs.10526 Hs.73853 Hs.81256 Hs.279898 Hs.272227 Hs.156346 Hs.15432 Hs.119129 Hs.11945 Hs.2256 Hs.283683	KiAA0101 gene product ESTs SRY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenetic protein 2 S100 catclum-binding protein A4 (catcium Homo sapiens cDNA: FLJ23165 fs., clone L Homo sapiens cDNA: FLJ23165 fs., clone CO lopoisomerase (DNA) II alpha (170k.D) downregulated in ovarian cancer 1 collagen, type IV, alpha 1 Target Exon Homo sapiens cDNA FLJ14259 fs., clone PL matrix metalfoproteinase 7 (matifysin,	22.6 22.2 20.7 18.7 18.6 17.2 16.7 14.3 14.3 14.1 13.9 13.6 13.6 13.0 12.9 12.5
55 60	424800 417308 449539 453392 414829 414190 412420 417130 414217 431941 425397 448584 426072 402604 424635 428330 434078 414761 442435 434078 43	AL035588 H60720 W80363 U23752 X06370 AU878918 AL03568 AW276858 AI309288 AK000105 J04088 U53445 X12784 AA420687 L2252 AW880709 AU077228 BE093589 BE259150	Hs.81892 Hs.58446 Hs.77432 Hs.10526 Hs.10526 Hs.173853 Hs.81256 Hs.279898 Hs.272227 Hs.156346 Hs.15432 Hs.119129 Hs.119455 Hs.283683 Hs.77256 Hs.283683 Hs.77256 Hs.38178 Hs.127792	kiAA0101 gene product ESTs SRY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenetic protein 2 S100 catchum-binding protein A4 (catchum Homo sapiens cDNA: FLJ23165 fis, clone C Homo sapiens cDNA: FLJ23165 fis, clone CO topoisomerase (DNA) III alpha (170kD) downregulated in ovarian cancer 1 collagen, type IV, alpha 1 Target Exon Homo sapiens cDNA FLJ14259 fis, clone PL matrix metafloproteinase 7 (matrilysin, chromosome 8 open reading frame 4 enhancer of zestic (Drosophila) homolog 2 hypothetical protein FLJ23468 deta (Drosophila) libe 3	22.6 22.2 20.7 18.7 18.6 17.2 16.7 14.3 14.3 14.1 13.9 13.6 13.6 13.0 12.9 12.5
55 60	424800 417308 449539 453392 414825 444190 412420 41713 416217 431941 425394 42672 402603 424035 42633 42633 42432 42432 42432 42672 42432 42432 42672 42432 42432 42673	AL035588 H60720 W80363 U23752 X06370 Al876918 AL035668 AW276858 AX000106 J04088 U53445 X12784 AA420687 L22524 AW880709 AU077228 BE033589 BE259150 AW4504420	Hs. 81892 Hs. 58446 Hs. 77432 Hs. 10526 Hs. 10526 Hs. 173853 Hs. 81256 Hs. 272227 Hs. 156346 Hs. 15432 Hs. 119129 Hs. 115455 Hs. 2256 Hs. 283683 Hs. 127792 Hs. 127792 Hs. 127785 Hs. 127793	kiAAJ101 gene product ESTs SRY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenelic protein 2 5100 calcium-binding protein A4 (calcium Homo sapiens cDNA FLJ20165 fs., clone L Homo sapiens cDNA FLJ20165 fs., clone CO topoisomerase (DNA) II alpha (170kD) downregulated in ovarian cancer 1 collagen, type IV, zipha 1 Target Exon Homo sapiens cDNA FLJ14259 fs., clone PL matrix metafloproteinase 7 (matrilysin, chromosome 8 open reading frame 4 enhancer of zeste (Drosophila) homolog 2 hypothetical protein FLJ23468 delta (Drosophila)-like 3 ESTs	22.6 22.2 20.7 18.7 18.6 17.2 16.7 14.3 14.3 14.1 13.9 13.6 13.6 13.0 12.9 12.5 12.4
556065	424800 417309 453392 453392 414825 444190 412420 417130 414217 431941 42583 442672 402604 424635 42635 42635 434078 414761 442432 456759 409638 441269	AL035588 H60720 W80363 U23752 X06370 Al876918 AL035668 AW276858 AI309298 AK000106 J04088 U53445 X12784 AA420687 L22524 AW880709 AU077228 BE093589 BE259150 AW450420 AW015206	Hs.81892 Hs.58446 Hs.72964 Hs.77432 Hs.10526 Hs.73853 Hs.81256 Hs.279898 Hs.272227 Hs.156346 Hs.15432 Hs.119129 Hs.119129 Hs.119129 Hs.12256 Hs.283683 Hs.77256 Hs.38178 Hs.127792 Hs.1127792 Hs.11335 Hs.178784	kiAA0101 gene product ESTs ESTs SRY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenetic protein 2 S100 calcium-binding protein A4 (calcium Homo sapiens cDNA FLJ23165 fs, clone L Homo sapiens cDNA FLJ20099 fs, clone CO lopoisomerase (DNA) II alpha (170kD) downregulated in ovarian cancer 1 collagen, type IV, alpha 1 Target Exon Homo sapiens cDNA FLJ14259 fs, clone PL matrix metafloproteinase 7 (matritysin, chromosome 8 open reading frame 4 enhancer of zeste (Drosophila) homolog 2 hypothetical protein FLJ23468 detta (Drosophila)-like 3 ESTs ESTs	22.6 22.2 20.7 18.7 18.6 17.2 16.7 14.3 14.3 14.1 13.9 13.6 13.6 13.6 13.2 12.9 12.5 12.4 12.2 12.1 11.5 10.5
55 60	424800 417308 449539 453392 414429 414190 412420 417130 414217 431941 425397 446584 422672 402604 424635 426072 402604 424635 42672 40603 414761 442434 442675 4426	AL035588 H60720 W80363 U23752 X06370 AU878918 AL03568 AW276858 AI309280 AK000106 J04088 U53445 X12784 AA420687 L22524 AW880709 AU077228 BE093589 BE259150 AW450420 AW505076	Hs.81892 Hs.58446 Hs.77432 Hs.10526 Hs.10526 Hs.279898 Hs.272227 Hs.156346 Hs.15432 Hs.119129 Hs.11945 Hs.283683 Hs.77256 Hs.283683 Hs.77256 Hs.283683 Hs.77256 Hs.283683 Hs.77256 Hs.283683 Hs.77256 Hs.1844 Hs.301855	kiAA0101 gene product ESTs SRY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenetic protein 2 S100 calcium-binding protein A4 (calcium Homo sapiens cDNA: FLJ23165 fis, clone C Iopoisomerase (DNA) II alpha (170kD) downregulated in ovarian cancer 1 collagen, type IV, alpha 1 Target Exon Homo sapiens cDNA FLJ14259 fis, clone PL matrix metafloproteinase 7 (matrilysin, chromosome 8 open reading frame 4 enhancer of zestic (Drosophila) homolog 2 hypothetical protein FLJ23468 deta (Drosophila)-like 3 ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	22.6 22.2 20.7 18.7 18.6 17.2 16.7 14.3 14.3 14.1 13.9 13.6 13.0 12.9 12.5 12.4 12.2 12.1 11.5 10.5
556065	424800 417308 449539 453392 444829 444190 412420 41713 431941 425394 42672 402603 424035 42403 42403 42403 42403 42403 42403 42403 42403 42403 42403	AL035588 H60720 W80363 U23752 X06370 Al876918 AL035668 AW276858 AX000106 J04088 U53445 X12784 AA420687 L22524 AW880709 AU077228 BE093589 BE259150 AW450420 AW15206 AW505076 AF027208	Hs. 81892 Hs. 58446 Hs. 77432 Hs. 10526 Hs. 10526 Hs. 173853 Hs. 81256 Hs. 279227 Hs. 156346 Hs. 15432 Hs. 119129 Hs. 115455 Hs. 2256 Hs. 283683 Hs. 127792 Hs. 127792 Hs. 178784 Hs. 178784 Hs. 178784 Hs. 178784 Hs. 301855	kiAA0101 gene product ESTs ESTs SRY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenetic protein 2 5100 calcium-binding protein A4 (calcium Homo sapiens cDNA-FLJ20165 fis, clone CO topoisomerase (DNA) II alpha (170kD) downregulated in ovarian cencer 1 collagen, type IV, alpha 1 Target Exon Homo sapiens cDNA FLJ14259 fis, clone PL matrix metafloproteinase 7 (matritysin, chromosome 8 open reading frame 4 enhancer of zeste (Drosophila)-homolog 2 hypothetical protein FLJ23468 detta (Drosophila)-like 3 ESTs ESTs DiSeorge syndrome critical region gene 8 prominin (mouse)-like 1	22.6 22.2 20.7 18.7 18.6 17.2 16.7 14.3 14.3 14.3 14.1 13.9 13.6 13.6 13.0 12.9 12.5 12.4 12.2 12.1 11.5 10.5 10.5
556065	424800 417303 449539 453392 414825 444190 412420 4171307 414217 431941 425397 446584 422672 402604 424635 428330 434078 414761 442432 456759 409659 441269 435020 422163 441269 4	AL035588 H60720 W80363 U23752 X06370 Al876918 AL035668 AW276858 AI309299 AK000106 J04088 U53445 X12784 AA420687 L22524 AW880709 AL0777228 BE093589 BE259150 AW450420 AW015206 AW505076 AF0272708 AI203334	Hs.81892 Hs.58446 Hs.72964 Hs.77432 Hs.10526 Hs.73853 Hs.81256 Hs.279898 Hs.272227 Hs.156346 Hs.15432 Hs.119129 Hs.119129 Hs.115455 Hs.2256 Hs.283683 Hs.77256 Hs.38178 Hs.127792 Hs.117378 Hs.117378 Hs.117378 Hs.117378 Hs.11736 Hs.11736 Hs.11736 Hs.11736 Hs.11736 Hs.11736 Hs.11736 Hs.11736 Hs.11736 Hs.11736 Hs.11736	kiAA0101 gene product ESTs STY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenetic protein 2 S100 calcium-binding protein A4 (calcium Homo sapiens cDNA FLJ23165 fs, clone L Homo sapiens cDNA FLJ23165 fs, clone CO lopoisomerase (DNA) II alpha (170k.D) downregulated in ovarian cancer 1 collagen, type IV, alpha 1 Target Exon Homo sapiens cDNA FLJ14259 fs, clone PL matrix metafloproteinase 7 (matritysin, chromosome 8 open reading frame 4 enhancer of zeste (Drosophila)-line a enhancer of zeste (Drosophila)-line 3 ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	22.6 22.2 20.7 18.7 18.6 17.2 16.7 14.3 14.3 14.3 14.1 13.9 13.6 13.6 13.0 12.9 12.5 12.4 12.2 12.1 11.5 10.5 10.5
55606570	424800 417308 449539 453392 444829 444190 412420 41713 431941 425394 42672 402603 424035 42403 42403 42403 42403 42403 42403 42403 42403 42403 42403	AL035588 H60720 W80363 U23752 X06370 Al876918 AL035668 AW276858 AX000106 J04088 U53445 X12784 AA420687 L22524 AW880709 AU077228 BE093589 BE259150 AW450420 AW15206 AW505076 AF027208	Hs.81892 Hs.58446 Hs.77432 Hs.10526 Hs.10526 Hs.173853 Hs.81256 Hs.279898 Hs.272227 Hs.156346 Hs.15432 Hs.119129 Hs.115455 Hs.22366 Hs.283683 Hs.77256 Hs.283683 Hs.77256 Hs.21335 Hs.17792 Hs.21335 Hs.178784	kiAA0101 gene product ESTs SRY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenetic protein 2 S100 calcium-binding protein A4 (calcium Homo sapiens cDNA: FLJ23165 fis, clone L Homo sapiens cDNA FLJ2395 fis, clone CO lopoisomerase (DNA) II alpha (170kD) downregulated in ovarian cancer 1 collagen, type IV, alpha 1 Target Exon Homo sapiens cDNA FLJ14259 fis, clone PL matrix metalloproteinase 7 (matrilysin, chromosome 8 open reading frame 4 enhancer of zestic (Drosophila) homolog 2 hypothetical protein FLJ23468 deta (Drosophila)-like 3 ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	22.6 22.2 20.7 18.7 18.6 17.2 16.7 14.3 14.3 14.1 13.9 13.6 13.0 12.9 12.5 12.4 12.2 12.1 11.5 10.5 10.5 10.1 9.9
556065	424800 417308 449539 453392 414429 414190 412420 417130 414217 431941 425397 448584 422672 402604 424835 424835 424835 424835 424835 424835 424835 43498 414761 442423 44559 43592 4	AL035588 H60720 W80363 U23752 X06370 Al876918 AL035668 AW276858 AI309289 AK000106 J04088 U53445 X12784 AA420687 L22524 AW880709 AU077228 BE093589 BE259150 AW450420 AW	Hs.81892 Hs.58446 Hs.77432 Hs.10526 Hs.77353 Hs.81256 Hs.279898 Hs.272227 Hs.156346 Hs.15432 Hs.119129 Hs.119129 Hs.119129 Hs.127592 Hs.23683 Hs.77256 Hs.38178 Hs.127792 Hs.117378 Hs.1173784 Hs.117369 Hs.117369 Hs.117369 Hs.117369 Hs.117369 Hs.117369 Hs.117369 Hs.117369 Hs.117369 Hs.117369 Hs.117369	kiAA0101 gene product ESTs ESTs SRY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich grotein 2 5100 catchum-binding protein A4 (catchum Homo sapiens cDNA: FLJ23155 fis., clone tC Homo sapiens cDNA: FLJ23155 fis., clone tC Homo sapiens cDNA FLJ2099 fis., clone tC Homo sapiens cDNA FLJ20099 fis., clone tC Homo sapiens cDNA FLJ20099 fis., clone tC Homo sapiens cDNA FLJ2019 fis., clone tC Homo sapiens cDNA FLJ14259 fis., clone tC Homo sapiens cDNA FLJ14259 fis., clone PL matrix metalloproteinase 7 (matritysin, chromosome 8 open reading frame 4 enhancer of zeste (Drosophila)-fixe 3 ESTs ESTs DiGeorge syndrome critical region gene 8 prominin (mouse)-fixe 1 ESTs hypothetical protein FLJ20647 caspass 6, apoptosis-related cysteine pr	22.6 22.2 20.7 18.7 18.6 17.2 16.7 14.3 14.3 14.3 14.1 13.9 13.6 13.0 12.9 12.5 12.4 12.2 12.1 11.5 10.5 10.5 10.1 9.9 9.4
55606570	424800 417308 449539 453392 414823 444190 412420 417130 414217 431941 425397 448584 422672 402604 424835 42835 424308 434078 434078 441269 435072 435	AL035588 H60720 W80363 U23752 X06370 Al876918 AL035668 AW276858 AX000106 J04088 U53445 X12784 AA420687 L22524 AW880709 AU077228 BE093589 BE259150 AW450420 AW15206 AW505076 AF027208 AI203334 AA204586 U20536	Hs. 81892 Hs. 58446 Hs. 77432 Hs. 10526 Hs. 10526 Hs. 173853 Hs. 81256 Hs. 277227 Hs. 156346 Hs. 15432 Hs. 119129 Hs. 115455 Hs. 2256 Hs. 283683 Hs. 127792 Hs. 178784 Hs. 17878	kiAA0101 gene product ESTs STY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenetic protein 2 S100 catclum-binding protein A4 (catcium Homo sapiens cDNA: FLJ23165 fs., clone L Homo sapiens cDNA: FLJ23165 fs., clone CO lopoisomerase (DNA) II alpha (170k.D) downregulated in ovarian cancer 1 collagen, type IV, alpha 1 Target Exon Homo sapiens cDNA FLJ14259 fs., clone PL matrix metalloproteinase 7 (matritysin, chromosome 8 open reading frame 4 enhancer of zeste (Drosophila)-homolog 2 hypothetical protein FLJ23468 detta (Drosophila)-lüke 3 ESTs ESTs DiGeorge syndrome critical region gene 8 prominin (mouse)-läke 1 ESTs hypothetical protein FLJ20647 caspase 6, apoptosis-related cysteine pr Homo sapiens mRNA; cDNA DKF2p686C1019 (f	22.6 22.2 20.7 18.7 18.6 17.2 16.7 14.3 14.3 14.3 14.1 13.9 13.6 13.6 13.0 12.9 12.5 12.4 12.2 12.1 11.5 10.5 10.5 10.1 10.1 9.9 9.4
55606570	424800 417308 449539 453392 414829 444190 412420 41713 431941 425394 42672 402603 424035 424035 424035 424035 424035 424035 424035 424035 424035 424035 424035 424035 424035 424035 434030 434078 43503 43503 434078 43503	AL035588 H60720 W80363 U23752 X06370 Al876918 AL035668 AW276858 AX000106 J04088 U53445 X12784 AA420687 L22524 AW880709 AL077228 BE093589 BE259150 AW450420 AW15206 AW505076 AF027208 AI203334 AA204586 U20536 T75202 BE501689 AW014486	Hs.81892 Hs.58446 Hs.77432 Hs.10526 Hs.173853 Hs.81256 Hs.272227 Hs.156346 Hs.15432 Hs.119129 Hs.115455 Hs.283683 Hs.283683 Hs.283683 Hs.283683 Hs.127792 Hs.112799 Hs.112350 Hs.112360 Hs.123144 Hs.234149 Hs.234149 Hs.234149 Hs.234149 Hs.235147 Hs.125147 Hs.25509	kiAA0101 gene product ESTs ESTs SRY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich grotein 2 5100 catchum-binding protein A4 (catchum Homo sapiens cDNA: FLJ23155 fis., clone tC Homo sapiens cDNA: FLJ23155 fis., clone tC Homo sapiens cDNA FLJ2099 fis., clone tC Homo sapiens cDNA FLJ20099 fis., clone tC Homo sapiens cDNA FLJ20099 fis., clone tC Homo sapiens cDNA FLJ2019 fis., clone tC Homo sapiens cDNA FLJ14259 fis., clone tC Homo sapiens cDNA FLJ14259 fis., clone PL matrix metalloproteinase 7 (matritysin, chromosome 8 open reading frame 4 enhancer of zeste (Drosophila)-fixe 3 ESTs ESTs DiGeorge syndrome critical region gene 8 prominin (mouse)-fixe 1 ESTs hypothetical protein FLJ20647 caspass 6, apoptosis-related cysteine pr	22.6 22.2 20.7 18.7 18.6 17.2 16.7 14.3 14.3 14.3 14.1 13.9 13.6 13.0 12.9 12.5 12.4 12.2 12.1 11.5 10.5 10.5 10.1 9.9 9.4
55606570	424800 417308 449539 453392 414829 414190 412420 417130 414217 431941 425397 448584 422672 402604 424635 428307 434761 43	AL035588 H60720 W80363 U23752 X06370 AU876918 AL035668 AW276858 AI309298 AK000105 J04088 U53445 X12784 AA420687 L22524 AW880709 AU077228 BE093589 BE259150 AW450420 AW5502076 AF027208 AV505076 AF027208	Hs.81892 Hs.58446 Hs.77432 Hs.10526 Hs.77353 Hs.81256 Hs.279898 Hs.272227 Hs.156346 Hs.15432 Hs.119129 Hs.119129 Hs.115455 Hs.2256 Hs.283683 Hs.77256 Hs.38178 Hs.127792 Hs.1735 Hs.17796 Hs.301855 Hs.17378 Hs.301855 Hs.1736628 Hs.234149 Hs.33280 Hs.75617 Hs.75617 Hs.25599 Hs.25599	kiAA0101 gene product ESTs STY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenetic protein 2 S100 catcium-binding protein A4 (catcium Homo sapiens cDNA FLJ23165 fs., clone C lopoisomerase (DNA) II alpha (170k.D) downregulated in ovarian cancer 1 collagen, lype IV, alpha 1 Target Exon Homo sapiens cDNA FLJ14259 fs., clone PL matrix metafloproteinase 7 (matritysin, chromosome 8 open reading frame 4 enhancer of zeste (Drosophila)-homolog 2 hypothetical protein FLJ23468 detta (Drosophila)-lüke 3 ESTs ESTs DiGeorge syndrome critical region gene 8 prominin (mouse)-läke 1 ESTs hypothetical protein FLJ20647 caspasa 6, apoptosis-related cysteine pr Homo sapiens mRNA; cDNA DXFZp586C1019 (f collagen, type IV, alpha 2 ESTs ESTs ESTs ESTs	22.6 22.2 20.7 18.7 18.6 17.2 16.7 14.3 14.3 14.3 14.1 13.9 13.6 13.6 13.0 12.9 12.5 12.4 12.2 12.1 11.5 10.5 10.5 10.1 10.1 9.9 9.4
5560657075	424800 417308 449539 453392 414825 444190 412420 417130 414217 431941 425397 448584 422672 402604 424835 42839 434078 4414761 442439 445759 409638 441269 435020 422163 44963 44963 44963 44978 44978 44978 44978 44978 44978 44978 44978 44978 44978 44978 44978	AL035588 H60720 W80363 U23752 X06370 Al876918 AL035668 AW276858 Al309288 AK000105 J04888 AK000105 J04888 BE259150 AW450420 AW80779 AL077228 BE093589 BE259150 AW450420 AW50420	Hs. 81892 Hs. 58446 Hs. 77432 Hs. 10526 Hs. 10526 Hs. 173853 Hs. 81256 Hs. 279227 Hs. 155346 Hs. 155346 Hs. 119129 Hs. 115455 Hs. 2256 Hs. 283683 Hs. 127792 Hs. 1178784 Hs. 1178784 Hs. 106628 Hs. 160628 Hs. 160628 Hs. 160628 Hs. 12314 Hs. 75617 Hs. 22509 Hs. 23960 Hs. 23960 Hs. 23960	kiAA0101 gene product ESTs SRY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenelic protein 2 5100 calcium-binding protein A4 (calcium Homo sapiens cDNA FLJ20165 fis., done L Homo sapiens cDNA FLJ20165 fis., done CO topoisomerase (DNA) II alpha (170kD) downregulated in ovarian cancer 1 collagen, type IV, alpha 1 Target Exon Homo sapiens cDNA FLJ14259 fis., clone PL matrix metafloproteinase 7 (matrifysin, chromosome 8 open reading frame 4 enhancer of zeste (Drosophilla) homolog 2 hypothetical protein FLJ23468 detta (Drosophilla)-like 3 ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	22.6 22.2 20.7 18.7 18.6 17.2 16.7 14.3 14.3 14.3 14.1 13.9 13.6 13.0 12.9 12.5 12.4 12.2 12.1 11.5 10.5 10.5 10.1 10.1 9.9 9.4 9.2 9.1
55606570	424800 417308 449539 453392 414825 444190 412420 417130 416217 431941 42535 42635 42635 42635 42635 42433 434078 434078 435078 44963 435078 44969 435025 44969 4351263 44969 4351263 44969 4351263 44969 4351263 44969 44961 4	AL035588 H60720 W80363 U23752 X06370 Al878918 AL035668 AW276858 AX000106 J04088 U53445 X12784 AA420687 L22524 AW880709 AL077228 BE093589 BE259150 AW450420 AW15206 AW505076 AF027208 AI203334 AA204586 U20536 T75202 BE501689 AW1014486 BE250074 AI970394 AI970394	Hs.81892 Hs.58446 Hs.77432 Hs.10526 Hs.77432 Hs.10526 Hs.279898 Hs.272227 Hs.156346 Hs.179129 Hs.115432 Hs.119129 Hs.115455 Hs.283683 Hs.283683 Hs.127792 Hs.127792 Hs.127998 Hs.127999 Hs.23900 Hs.12314 Hs.75617 Hs.22509 Hs.23950 Hs.197075 Hs.22509	kiAA0101 gene product ESTs SRY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenetic protein 2 S100 catclum-binding protein A4 (catcium Homo sapiens cDNA: FLJ23185 fs., clone t. Homo sapiens cDNA FLJ2099 fs., clone CO lopoisomerase (DNA) II alpha (170kD) downregulated in ovarian cencer 1 collagen, type IV, alpha 1 Target Exon Homo sapiens cDNA FLJ14259 fs., clone PL matrix metalloproteinase 7 (matritysin, chromosome 8 open reading frame 4 enhancer of zeste (Drosophila)-tilke 3 ESTs ESTs DiGeorge syndrome critical region gene 8 prominin (mouse)-tilke 1 ESTs hypothetical protein FLJ20647 caspase 6, apoptosis-related cysteine pr Homo sapiens mRNA: cDNA DKFZp586C1019 (I collagen, type IV, alpha 2 ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	22.6 22.2 20.7 18.7 18.6 17.2 16.7 14.3 14.3 14.3 14.3 14.1 13.9 13.6 13.0 12.9 12.5 12.4 12.2 12.1 11.5 10.5 10.5 10.1 10.1 9.9 9.4 9.2 9.1 9.1 8.9
5560657075	424800 417308 449539 453392 414829 414190 412420 417130 414217 431941 425397 425397 425397 42635 428307 424635 42407 424635 42407 424635 43407 4	AL035588 H60720 W80363 U23752 X06370 AU876918 AL035668 AW276858 AI309298 AK000105 J04088 U53445 X12784 AA420687 L22524 AW880709 AU077228 BE093589 BE259150 AW450420 AW015206 AW505076 AF027208 AV505076 AF027208 AV505076 AF027208 AV505076 AF027208 AV505076 AF027208 AV505076 AF027208 AV505076 AF03334 AA204686 U20536 T75202 BE501689 AW014485 BE280074 AIS70394 H55709 AA468183	Hs.81892 Hs.58446 Hs.77432 Hs.10526 Hs.77353 Hs.81256 Hs.279898 Hs.272227 Hs.156346 Hs.15432 Hs.19129 Hs.115455 Hs.2256 Hs.283683 Hs.77256 Hs.38178 Hs.127792 Hs.11335 Hs.17796 Hs.301855 Hs.1735 Hs.17378 Hs.127792 Hs.234149 Hs.301855 Hs.1234149 Hs.36628 Hs.75617 Hs.22509 Hs.197075 Hs.22509 Hs.197075 Hs.22509 Hs.197075 Hs.22509 Hs.197075 Hs.22509 Hs.197075 Hs.22509 Hs.197075	kiAA0101 gene product ESTs STY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenetic protein 2 S100 catcium-binding protein A4 (catcium Homo sapiens cDNA: FLJ23165 fs., clone L Homo sapiens cDNA: FLJ20099 fs., clone CO lopoisomerase (DNA) II alpha (170k.D) downregulated in ovarian cancer 1 collagen, type IV, alpha 1 Target Exon Homo sapiens cDNA FLJ14259 fs., clone PL matrix metafloproteinase 7 (matritysin, chromosome 8 open reading frame 4 enhancer of zeste (Drosophila)-homolog 2 hypothetical protein FLJ23468 detta (Drosophila)-lüke 3 ESTs ESTs DiGeorge syndrome critical region gene 8 prominin (mouse)-läke 1 ESTs hypothetical protein FLJ20647 caspasa 6, apoptosis-related cysteine pr Homo sapiens mRNA: cDNA DXFZp586C1019 (f collagen, type IV, alpha 2 ESTs ESTs ESTs ESTs ESTs ESTs ESTs Lexical Region (chodinergic Homo sapiens cDNA: FLJ23241 fs, clone C	22.6 22.2 20.7 18.7 18.6 17.2 16.7 14.3 14.3 14.1 13.9 13.6 13.6 13.6 13.0 12.9 12.5 12.4 12.2 12.1 11.5 10.5 10.5 10.1 10.1 9.9 9.4 9.2 9.1 8.9 8.9
5560657075	424800 417308 449539 453392 4444950 412420 417420 4174217 431941 425397 446584 4225397 442635 4243078 434078 414761 442432 456759 45675	AL035588 H60720 W80363 U23752 X06370 Al878918 AL035668 AW276858 AX000106 J04088 U53445 X12784 AA420687 L22524 AW880709 AL077228 BE093589 BE259150 AW450420 AW15206 AW505076 AF027208 AI203334 AA204586 U20536 T75202 BE501689 AW1014486 BE250074 AI970394 AI970394	Hs.81892 Hs.58446 Hs.77432 Hs.10526 Hs.77432 Hs.10526 Hs.279898 Hs.272227 Hs.156346 Hs.179129 Hs.115432 Hs.119129 Hs.115455 Hs.283683 Hs.283683 Hs.127792 Hs.127792 Hs.127998 Hs.127999 Hs.23900 Hs.12314 Hs.75617 Hs.22509 Hs.23950 Hs.197075 Hs.22509	kiAA0101 gene product ESTs STY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenelic protein 2 5100 calcium-binding protein A4 (calcium Homo sapiens cDNA FLJ20165 fs., clone C Homo sapiens cDNA FLJ20165 fs., clone CO topoisomerase (DNA) II alpha (170kD) downregulated in ovarian cancer 1 collagen, type IV, alpha 1 Target Exon Homo sapiens cDNA FLJ14259 fs., clone PL matrix metafloproteinase 7 (matrilysin, chromosome 8 open reading frame 4 enhancer of zeste (Drosophila) homolog 2 hypothetical protein FLJ23468 delta (Drosophila)-like 3 ESTs ESTs ESTs DiGeorge syndrome critical region gene 8 prominin (mouse)-like 1 ESTs Lest Stappens of the stappens of the special protein FLJ20647 caspase 6, apoptosis-related cysteine pr Homo sapiens mRNA; cDNA DXFZp586C1019 (f collagen, type IV, alpha 2 ESTs Lest Stappens of the stappens of the special protein FLJ20241 fs, clone C ESTs Leukemia inhibitory factor (cholinergic Homo sapiens cDNA: FLJ23241 fs, clone C ESTs	22.6 22.2 20.7 18.7 18.5 17.2 16.7 14.3 14.3 14.1 13.9 13.6 13.6 13.6 13.6 13.0 12.9 12.5 12.4 12.2 12.1 11.5 10.5 10.1 9.9 9.4 9.2 9.1 9.1 8.9 8.9 8.9 8.9
5560657075	424800 417308 449539 453392 414829 414190 412420 417130 414217 431941 425397 425397 425397 42635 428307 424635 42407 424635 42407 424635 43407 4	AL035588 H60720 W80363 U23752 X06370 AU876918 AL035668 AW276858 AI309298 AK000105 J04088 U53445 X12784 AA420687 L22524 AW880709 AU077228 BE093589 BE259150 AW450420 AW015206 AW505076 AF027208 AV505076 AF027208 AV505076 AF027208 AV505076 AF027208 AV505076 AF027208 AV505076 AF027208 AV505076 AF03334 AA204686 U20536 T75202 BE501689 AW014485 BE280074 AIS70394 H55709 AA468183	Hs.81892 Hs.58446 Hs.77432 Hs.10526 Hs.77353 Hs.81256 Hs.279898 Hs.272227 Hs.156346 Hs.15432 Hs.19129 Hs.115455 Hs.2256 Hs.283683 Hs.77256 Hs.38178 Hs.127792 Hs.11335 Hs.17796 Hs.301855 Hs.1735 Hs.17378 Hs.127792 Hs.234149 Hs.301855 Hs.1234149 Hs.36628 Hs.75617 Hs.22509 Hs.197075 Hs.22509 Hs.197075 Hs.22509 Hs.197075 Hs.22509 Hs.197075 Hs.22509 Hs.197075 Hs.22509 Hs.197075	kiAA0101 gene product ESTs STY (sex determining region Y)-box 11 epidermal growth factor receptor (avian cysteine and glycine-rich protein 2 bone morphogenetic protein 2 S100 catcium-binding protein A4 (catcium Homo sapiens cDNA: FLJ23165 fs., clone L Homo sapiens cDNA: FLJ20099 fs., clone CO lopoisomerase (DNA) II alpha (170k.D) downregulated in ovarian cancer 1 collagen, type IV, alpha 1 Target Exon Homo sapiens cDNA FLJ14259 fs., clone PL matrix metafloproteinase 7 (matritysin, chromosome 8 open reading frame 4 enhancer of zeste (Drosophila)-homolog 2 hypothetical protein FLJ23468 detta (Drosophila)-lüke 3 ESTs ESTs DiGeorge syndrome critical region gene 8 prominin (mouse)-läke 1 ESTs hypothetical protein FLJ20647 caspasa 6, apoptosis-related cysteine pr Homo sapiens mRNA: cDNA DXFZp586C1019 (f collagen, type IV, alpha 2 ESTs ESTs ESTs ESTs ESTs ESTs ESTs Lexical Region (chodinergic Homo sapiens cDNA: FLJ23241 fs, clone C	22.6 22.2 20.7 18.7 18.6 17.2 16.7 14.3 14.3 14.1 13.9 13.6 13.6 13.6 13.0 12.9 12.5 12.4 12.2 12.1 11.5 10.5 10.5 10.1 10.1 9.9 9.4 9.2 9.1 8.9 8.9

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	447747	A14000C0	W- 10300		
	447342 410102	A1199268 AW248508	Hs.19322 Hs.279727	Homo sapiens, Similar to RIKEN CONA 2010	8.6
	420602	AF060877	Hs.99236	ESTs; homologue of PEM-3 (Ciona savignyi regulator of G-protein signalling 20	8.5 8.4
_	417426	NM_002291	Hs.82124	laminin, beta 1	8.4
5	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	8.3
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	8.1
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	8.1
	414622	AI752666	Hs.76669	nicotinamide N-methyltransferase	8.1
10	430691	C14187	Hs.103538	ESTs	8.0
10	447726 417043	AL137638 NM_004369	Hs.19368	matriin 2	8.0
	447004	AW296968	Hs.80988 Hs.157539	coffagen, type VI, alpha 3 ESTs	7.9
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	7.9
	426075	AW513691	Hs.270149	ESTs. Wealdy similar to 2109260A B cell	7.8 7.8
15	419938	AU078772	Hs.1279	complement component 1, r subcomponent	7.7
	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	7.7
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	7.5
	435291	BE568452	Hs.344037	protein regulator of cytokinesis 1	7.5
20	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	7.5
20	406972 442802	M32053 AL133035	LL 0720	gb:Human H19 RNA gene, complete cds.	7.4
	427581	NM_014788	Hs.8728 Hs.179703	hypothetical protein DKFZp434G171	7.4
	409142	AL136877	Hs.50758	KIAA0129 gene product SMC4 (structural maintenance of chromoso	7.3 7.3
	409902	AI337658	Hs.156351	ESTs	7.3
25	418113	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	7.2
	449961	AW265634	Hs.133100	ESTA	7.2
	418203	X54942	Hs.83758	CDC28 protein kinase 2	7.2
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	7.2
30	428728 429183	NM_016825 AB014604	Hs.191381 Hs.197955	hypothetical protein	7.1
50	439451	AF086270	Hs.278554	KIAA0704 protein	7.1
	422106	D84239	Hs.111732	heterochromalin-like protein 1 Fc tragment of IgG binding protein	7.1 7.0
	406850	A1624300	Hs.172928	collagen, type I, alpha 1	7.0
25	453941	U39817	Hs.36820	Bloom syndrome	6.9
35	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	6.9
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	6.8
	411078	AJ222020	Hs.182364	CocoaCrisp	6.7
	427019 448769	AA001732	Hs.173233	hypothetical protein FLJ10970	6.7
40	418400	N66037 BE243026	Hs.38173 Hs.301989	ESTs KIAA0246 protein	6.7
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	6.6
	440210	AW674562	Hs.125296	ESTs	6.6 6.6
	437036	AI571514	Hs.133022	ESTs	6.6
45	411968	AJ207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	6.6
45	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	6.6
	449300	AI656959	Hs.346514	ESTs	6.5
	440052	AI633744	Hs.195648	ESTs, Wealty similar to 138022 hypotheti	6.5
	412326 434808	R07566 AF155108	Hs.73817 Hs.256150	small inducible cytoldine A3 (homotogous	6.5
50	452461	N78223	Hs.108106	Homo sapiens, Similar to RIKEN cDNA 2810 transcription factor	6.5
	408243	Y00787	Hs.624	interleukin 8	6.5 6.5
	424954	NM_000546	Hs.1848	tumor protein p53 (Li-Fraumeni syndrome)	6.4
	450375	AA009647		a disintegrin and metalloproteinase doma	6.4
55	406478			Target Exon	6.4
23	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	6.4
	439710 458814	AF086543 AI498957	LL 1700C1	gb:Homo sapiens full length insert cDNA	6.4
	410276	AI554545	Hs.170861 Hs.68301	ESTs, Wealdy similar to Z195_HUMAN ZINC analopoletin-2	6.4
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	6.4 6.3
60	427871	AW992405	Hs.59622	Homo sapiens, done IMAGE:3507281, mRNA,	6.3
	436895	AF037335	Hs.5338	carbonic anhydrase XII	6.3
	447458	AI741082	Hs.158961	ESTs	6.3
	447439	AA31356\$	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	6.3
65	413719 449969	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	6.3
05	440704	AW295142 M69241	Hs.180187 Hs.162	Homo sapieris cONA FLJ14337 fis, clone PL	6.2
	400419	AF084545	115.102	Insulin-like growth factor binding prote Target	6.2
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabidnes	6.2 6.2
70	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	6.2
70	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.2
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	6.1
	430630	AW269920	Hs.2621	cystatin A (stefin A)	6.0
	410064 432281	X53416	Hs.195464	filamin A, alpha (actin-binding protein-	6.0
75	432261	AK001239 BE182082	Hs.274263	hypothetical protein FLJ10377	6.0
. •	413063	AL035737	Hs.246973 Hs.75184	ESTs chilinase 3-like 1 (cartilage glycoprote	6.0
	421899	AJ011895	Hs.109281	Nef-associated factor 1	5.9 5.9
	407182	AA312551	Hs.230157	ESTs	5.9 5.9
00	410286	AI739159	Hs.61898	OKFZP586N2124 protein	5.9
80	409829	M33552	Hs.56729	lymphocyte-specific protein 1	5.9
	446657	Al335191	Hs.260702	ESTs, Weakly similar to 2109260A B cell	5.8
	418097 428450	R45137 NM_014791	Hs.21868 Hs.184339	ESTs	5.8
	720730	014131	15.104339	KIAA0175 gene product	5.8

			11 00000		
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	5.7
	421988	AW450481	Hs.161333	ESTs	5.7
	422283	AW411307	Hs.114311	COC45 (cell division cycle 45, S.cerevis	5.7
5	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (5.7
)	434846	AW295389	Hs.119768	ESTs	5.7
	412567	A)750979	Hs.74034	Homo sapiens clone 24651 mRNA sequence	5.7
	452372	AI885742	Hs.228474	ESTs	5.6
	443247	BE614387	Hs.333893	c-Myc target JPO1	5.6
10	423198	M81933	Hs.1634	cell division cycle 25A	5.6
10	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	5.6
	437034	AA742643		gb:ny91c01.s1 NCI_CGAP_GCB1 Homo sapiens	5.6
	429447	AW812452	Hs.83286	ESTs, Weakly similar to \$14747 sphingomy	5.6
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	5.6
1.5	437695	AA769202	Hs.192142	ESTs	5.6
15	426935	NM_000088	Hs.172928	collagen, type I, aspha 1	5.6
	453361	AA035197	Hs.107375	ESTs	5.5
	418293	AI224483	Hs. 16063	hypothetical protein FLJ21877	5.5
	405348			C7001664:gi]12698061 dbj BAB21849.1 (AB	5.5
20	458079	AJ796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.4
20	452799	A1948829	Hs.213786	ESTs	5.4
	448935	AL078596	Hs.22591	nuclear receptor subfamily 2, group E, m	5.4
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	5.4
	442547	AA306997	Hs.217484	ESTs, Wealdy similar to ALU1_HUMAN ALU S	5.4
25	424009	F11690		gb:HSC30D041 normalized infant brain cDN	5.4
25	440332	AI218517	Hs.188051	ESTs	5.4
	422094	AF129535	Hs.272027	F-box only protein 5	5.4
	443884	N20617	Hs.194397	leptin receptor	5.4
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	5.4
20	432731	R31178	Hs.287820	fibronectin 1	5.4
30	426108	AA622037	Hs.166468	programmed cell death 5	5.3
	407624	AW157431	Hs.248941	ESTs	5.3
•	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	5.3
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platel	5.3
25	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	5.2
35	414774	X02419	Hs.77274	plasminogen activator, urokinase	5.2
	413786	AW613780	Hs.13500	ESTs	5.2
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	5.2
	428037	N47474	Hs.89230	potassium intermediate/small conductance	5.2
40	420311	AW445044	Hs.38207	Human DNA sequence from clone RP4-530115	5.1
40	416737	AF154335	Hs.79691	LIM domain protein	5.1
	445837	AI261700	Hs.145544	ESTs	5.1
	425882	U83115	Hs.161002	absent in melanoma 1	5.1
	415682	AI347128	Hs. 191870	ESTs	5.1
45	414053	BE391635	Hs.75725	transgelin 2	5.1
47	453884	AA355925	Hs.36232	KIAA0186 gene product	5.1
	431512	BE270734	Hs.2795	lactate dehydrogenase A	5.1
	432593	AW301003	Hs.51483	ESTs, Wealthy similar to hypothetical pro	5.0
	433323	AA805132	Hs.159142	ESTs	5.0
50	443744	A\$084326	Hs.271548	ESTs, Weakly similar to 178885 serine/th	5.0
50	410434	AF051152	Hs.63668	tofl-like receptor 2	5.0
	420018	U56387	Hs.94376	proprotein convertase subtilisin/kexin t	5.0
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	4.9
	446131 412777	NM_000929	Hs.290	phospholipase A2, group V	4.9
55	449246	AJ335773 AW411209	Hs.270123	ESTs	4.9
55	433244	AB040943	Hs.23363	hypothetical protein FLJ10983	4.9
	407235	D20569	Hs.271285	KIAA1510 protein	4.9
	445118	AJ208762	Hs.169407 Hs.345572	SAC2 (suppressor of actin mutations 2, y ESTs	4.9
	417404	NM_007350	Hs.82101		4.9
60	420092	AA814043	Hs.88045	pleckstrin homology-like domain, family ESTs	4.9
•	412811	H06382	110.00043	ESTS	4,9
	436607	AW661783	Hs.211061	ESTS ESTS	4.9
	438456	AA913381	Hs.20594	ESTs	4.9
	443883	AA114212	Hs.9930		4.9
65	431553	X78075	Hs.2799	serine (or cysteine) proteinase inhibito	4.9
	439999	AA115811	Hs.6838	cartilage linking protein 1 ras homolog gene family, member E	4.9
	411252	AB018549	Hs.69328	MD-2 protein	4.9
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	4.9
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	4.8
70	403349	NM_001406		ephrin-83	4.8
. •	402274	.400.400			4.8
	426044	AA502490	Hs.170290	C19000498*:gij4567179;gbtAAD23607.1(AC00 ESTs	4.8
	423600	AI633559	Hs.310359	ESTS	4.8
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	4.8
75	431117	AF003522	Hs.250500		4.8
	418054	NM_002318		delta (Drosophila)-like 1 hysyl oxidase-like 2	4.8
	441703	AW390054	Hs.192843		4.7
	439627	8E621702	Hs.29076	hypothetical protein FLJ21841	4.7
	445900	AF070526	Hs.125038		4.7
80	435937	AA830893	Hs.119769	ESTs Cone 24787 mk/kA sequence	4.7
	403961	,,,,,,,,,,,,,,		Target Exon	4.7
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	4.7
	408523	AW833259	Hs.314287	ESTs	4.6
					4.6

	403481			T	
	423529	T87318	Hs.120411	Target Exon ESTs	4.6
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	4.6 4.6
•	453362	H14988	Hs. 107375	ESTs	4.6
5	407013 423757	U35637	14- 120024	gb:Human nebulin mRNA, partial cds	4.6
	432363	AL049337 AA534489	Hs.132571	Homo sapiens mRNA; cDNA DKFZp564P016 (fr gb:n/76g11.s1 NCI_CGAP_Co3 Homo sapiens	4.6
	408380	AF123050	Hs.44532	diabiguitin	4.6 4.6
10	429149	AW193360	Hs.197962	ESTs, Wealthy similar to (38022 hypotheti	4.6
10	422170	AI791949	Hs.112432	anti-Mutlerian hormone	4.6
	405558 410295	AA741357	Hs.5174	Target Exon nidogen (enactin)	4.6
	450166	AA429504	110.0117	ESTs	4.6 4.6
16	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	4.5
15	420075	AF142482	Hs.203846	TEA domain family member 3	4.5
	422158 457465	L10343 AW301344	Hs.112341 Hs.122908	protease inhibitor 3, skin-derived (SKAL	4.5
	436827	H72187	Hs.5322	ONA reptication factor guanine nucleotide binding protein (G pr	4.5 4.5
20	452620	AA436504	Hs.119286	ESTs	4.5
20	424381	AA285249	Hs.146329	protein kinase Chk2	4.5
	444656 450639	A1277924 A1703186	Hs.145199 Hs.277174	ESTs SET-	4.5
	424247	X14008	Hs.234734	ESTs hysozyme (renal amyloidosis)	4.5
0.5	423178	AJ033140	Hs.124983	Homo sepiens mRNA; cDNA DKFZp564C142 (tr	4.5 4.5
25	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.5
	447444 401454	AK000318	Hs. 18616	hypothetical protein FLJ20311	4.4
	420560	AW207748	Hs.59115	NM_014226":Homo sapiens renal turnor enti ESTs	4.4
	409205	AI952884	Hs.14832	ESTs, Moderately similar to unnamed prot	4.4 4.4
30	451129	BE072881		gb:RC2-BT0548-200300-012-e09 BT0548 Homo	4.4
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	4.4
	447752 429083	M73700 Y09397	Hs.105938	lactotranslerrin	4.4
	418283	S79895	Hs.227817 Hs.83942	BCL2-related protein A1 cathepsin K (pycnodysostosis)	4.4
35	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	4.3 4.3
	416379	N38857	Hs.203933	ESTs	4.3
	452994	AW962597	Hs.31305	KIAA1547 protein	4.3
	437834 441035	AA769294 A1694309	Hs.283854	gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens	4.3
40	425292	NM_005824	Hs.126458 Hs.155545	ESTs 37 kDa leucine-rich repeat (LRR) protein	4.3
	418030	BE207573	Hs.83321	neuromedin B	4.3 4.3
	450811	A1739486	Hs.245497	ESTs	4.3
	438458	AW975186		gb:EST387294 MAGE resequences, MAGN Homo	4.3
45	442201 429732	AW516704 U20158	Hs.208726 Hs.2488	ESTs	4.3
	435677	AA694142	Hs.293726	lymphocyte cytosolic protein 2 (SH2 doma ESTs, Wealdy similar to TSGA RAT TESTIS	4.3 4.3
	442832	AW206560	Hs.253569	ESTs	4.3
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	4.2
50	421027 414300	AA761198 AJ304870	Hs.55254	ESTs	4.2
30	452874	AK001061	Hs.188680 Hs.30925	ESTs hypothetical protein FLJ10199	4.2
	444161	N52543	Hs.142940	ESTs	4.2 4.2
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	4.2
55	418483 443318	W26076 AI051603	Hs.221847	ESTs	4.2
22	415079	R43179	Hs.133141 Hs.22895	ESTs hypothetical protein FLJ23548	4.2
	416871	H98716	10322030	gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	4.2 4.2
	423678	AW963357	Hs.7847	ESTs	4.2
60	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	4.2
90	438875 428600	AA827640 AW853261	Hs.189059 Hs.242413	ESTS	4.2
	430968	AW972830	115.242413	hypothetical protein DKFZp434K1421 gb:EST384925 MAGE resequences, MAGL Homo	4.2 4.2
	406872	AI760903		gb:wi09h08.x1 NCI_CGAP_CLL1 Homo sapiens	4.2
65	403790			NM_001334":Homo sapiens cathepsin O (CTS	4.1
05	409112 435703	BE243971 AW830133	Hs.50649	quinone axidoreductase homolog	4.1
	432625	AJ243596	Hs.83313 Hs.94830	GK003 protein ESTs, Moderately similar to T03094 A-kin	4.1
	404407			Target Exon	4.1 4.1
70	412568	A1878826	Hs.74034	caveolin 1, caveolae protein, 22kD	4.1
70	422087	X58968	Hs.111301	matrix metalloproteinase 2 (gelatinase A	4,1
	435143 447497	R12375 AW167254	Hs.194500 Hs.205722		4.1
	456304	AI820973	113.603122	gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	4.1 4.1
75	427676	AA394062	Hs.300772	tropomyosin 2 (beta)	4.1
75	436608	AA628980		down syndrome critical region protein OS	4.1
	453331 420004	A1240665	LL +0.1000	ESTs	4.0
	412125	AW975532 Y17114	Hs.164039 Hs.73393	ESTs, Moderately similar to 138022 hypot eyes absent (Drosophila) homolog 4	4.0
00	426215	AW963419	Hs.155223		4.0 4.0
80	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA	4.0
	450581	AF081513	Hs.25195	TGF-beta 4	4.0
	415323 409893	BE269352 AW247090	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	4.0
	-03030	U11541030	Hs.57101	minichromosome maintenance deficient (S.	4.0

	432058	AW565996	Hs.130729	ESTs, Wealdy similar to ALU1_HUMAN ALU S	4.0
	444609	AW571659	Hs.278081	ESTs	4.0
	445666	R59960	Hs.282386	ESTs	4.0
_	437814	AI088192	Hs.135474	ESTs, Wealty similar to DOX9_HUMAN ATP-D	4.0
5	414948	C15240	Hs.182155	ESTs	4.0
	435542	AA687376		ESTs	4.0
	422564	AI148006	Hs.222120	ESTs	4.0
	449571	AW016812	Hs.200266	ESTs	4.0
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	4.0
10	458946	AA009716	Hs.42311	ESTs	4.0
	449655	AI021987	Hs.59970	ESTs	4.0
	426649	AI914936	Hs.97152	ESTs	4.0
	457292	AJ921270	Hs.281462	hypothetical protein FLJ14251	4.0
	440435	AL042201	Hs.21273	transcription factor NYD-sp10	4.0
15	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	4.0
-	420649	AI866964	Hs.124704	ESTs, Moderately similar to \$65657 alpha	4.0
	416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	4.0
	446291	BE397753	Hs.14623	interieron, gamma-inducible protein 30	3.9
	449256	AA059050	Hs.59847	ESTs	3.9
20	421637	AF035290	Hs.106300	Homo sepiens clone 23556 mRNA sequence	3.9
	456306	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.9
	438372	AI140189	Hs.123191	ESTs	3.9
	427375	AL035460	Hs.177536	metallocarboxypep6dase CPX-1	3.9
	415131	D61119	100.111000	gb:HUM158C118 Clontech human fetal brain	3.9
25	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	3.9
	424998	U\$8515	Hs.154138	chitinase 3-like 2	
	433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	3.9
	455104	BE064863	10.14142		3.9
	443426	AF098158	Hs.9329	gb:RC1-BT0313-110300-015-f06 BT0313 Homo chromosome 20 open reading frame 1	3.9
30	419594	AA013051	Hs.91417		3.9
50	417576	AA339449	Hs.82285	topoisomerase (DNA) II binding protein	3.9
	416857	AA188775		phosphoribosylglycinamide formyltransfer	3.9
	434784	AA549051	Hs.292453	ESTS	3.9
	438898		Hs.164007	ESTs	3.8
35		AIB19863	Hs.106243	ESTs	3.8
55	408102	U46351	Hs.621	lectin, galactoside-binding, soluble, 3	3.8
	422081	AW136820	Hs.196011	ESTs .	3.8
	411688	AW953440		gb:EST365510 MAGE resequences, MAGB Homo	3.8
	447343	AA256841	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	3.8
40	406395			Target Exon	3.8
40	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	3.8
	403696			C4001100":gi[5852342[gb]AAD54015.1] (AF0	3.8
	443740	R56434	Hs.21062	ESTs	3.8
	413076	U10564	Hs.75188	wee1 (S. pombe) homolog	3.8
45	409189	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	3.8
45	444326	A1939357	Hs.270710	ESTs	3.8
	436899	AA764852	Hs.291567	ESTs	3.8
	445075	AI651827	Hs.344767	ESTs	3.8
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	3.8
50	429163	AA884766		gb:am20a10.s1 Scares_NFL_T_GBC_S1 Homo s	3.8
50	416114	A1695549	Hs.183868	glucuronidase, beta	3.8
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	3.8
	446839	BE091926	Hs.16244	mitotic spindle colled-coll related prot	3.8
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	3.8
66	416664	H72780	Hs.20289	ESTs	3.8
55	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	3.8
	419735	AW750056	Hs.169577	Homo sapiens cDNA FLJ14743 fis, clone NT	3.8
	448275	BE514434	Hs.20830	kinesin-like 2	3.7
	405141	Y14443		zinc finger protein 200	3.7
40	41,1537	BE073250		gb:MR0-BT0551-060300-102-e05 BT0551 Homo	3.7
60	422648	D86983	Hs.118893	Melanoma associated gene	3.7
	449145	AJ832122	Hs.198408	ESTs	3.7
	428060	AA420618	Hs.249483	ESTs	3.7
	404584			Target Exon	3.7
	418596	AW976721	Hs.293327	ESTs	3.7
65	458072	AI890347	Hs.271923	Homo sapiens cONA: FLJ22785 fis, clone K	3.7
	445908	R13580	Hs.13436	Homo saplens clone 24425 mRNA sequence	3.7
	439979	AW600291	Hs.6823	hypothetical protein FiJ 10430	3.7
	431770	BE221880	Hs.268555	5-3 exoribonuclease 2	3.7
-	427809	M26380	Hs.180878	lipoprotein lipase	3.7
70	436674	AA725002	Hs.272018		3.7
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	3.7
	434467	BE552368	Hs.231853		3.7
	448048	BE281291	Hs.170408		3.7
-	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
75	402082			C18000743*:gij6678363 ref[NP_033416.1]1	3.7
	448019	AW947164	Hs.195641	ESTs, Moderately similar to 138022 hypot	3.7
	428873	AJ701609	Hs.98908	ESTs	3.7
	437323	AA371145	Hs.194397		3.7
	413095	AA494359	Hs.30715	potassium voltage-gated channel, isk-rel	3.7
80	425139	AW630488	Hs.25338	protesse, serine, 23	3.7
	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	3.7 3.7
	439574	A1459788	Hs.165190		3.7 3.7
	408829	NM_006042		heparan sulfate (glucosamine) 3-O-sulfot	3.7 3.7
					3.7

	407838	BE146411	Hs.40342	mulative and to	
	437748	AF234882	Hs.5814	putative nuclear protein suppression of turnorigenicity 7	3.7
	437470	AL390147	Hs.134742	hypothetical protein DKFZp\$470065	3.6 3.6
-	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	3.6
5	453438	AJ469935	Hs.22792	ESTs	3.6
	415024	AI983981	Hs.189114	ESTs	3.6
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	3.6
	441523	AW514263	Hs.301771	ESTs. Wealdy similar to ALUF_HUMAN !!!!	3.6
10	416427 448002	BE244050	Hs.79307	Rac/Cdc42 guarine exchange factor (GEF)	3.6
10	441352	Y15227 BE614410	Hs.20149 Hs.23044	deleted in lymphocytic leukernia, 1	3.6
	456534	X91195	Hs.100623	RAD51 (S. cerevisiae) hornolog (E coli Re phospholipase C, bela 3, neighbor pseudo	3.6
	402239			Target Exon	3.6 3.6
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.6
15	443715	AJ583187	Hs.9700	cyclin E1	3.6
	403011			ENSP00000215330*:Probable serine/threoni	3.6
	428403	A1393048	Hs.326159	leucine rich repeat (in FLII) interactin	3.6
	425202 409557	AW962282 BE182896	Hs.152049	ESTs, Wealdy similar to 138022 hypotheti	3.6
20	453948	AI970797	Hs.211193 Hs.64859	ESTs ESTs	3.6
	440225	BE295782	Hs.159	tumor necrosis factor receptor superfami	3.6
	425331	AW962128		gb:EST374201 MAGE resequences, MAGG Homo	3.6 3.6
	442326	H92962	Hs.124813	hypothetical protein MGC14817	3.6
25	437640	AA764893	Hs.272155	ESTs, Wealdy similar to I38022 hypotheti	3.6
25	424051	AL110203	Hs.138411	Homo saplens mRNA; cDNA DKFZp586J1922 (I	3.6
	406481 433835	AJ806185		Target Exon	3.6
	456052	BE311901	Hs.28935	gb:wf26a10.x1 Soares_NFL_T_GBC_S1 Homo s	3.6
	453857	AL080235	Hs.35861	gb:601142614F1 NIH_MGC_14 Homo sapiens c DKFZP586E1621 protein	3.6
30	439726	AW449893	Hs.293707	ESTs, Wealdy similar to I38598 zinc fing	3.5 3.5
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	3.5
	419402	268155	Hs.90291	laminin, beta 2 (laminin S)	3.5
	403108			ENSP00000241415":Hypothetical 67.7 kDa p	3.5
35	426509	M31166	Hs.2050	pentaxin-related gene, rapidly induced b	3.5
55	418883 432188	BE387036 AJ362952	Hs.1211 Hs.2928	acid phosphatase 5, tartrate resistant	3.5
	448789	BE539108	Hs.22051	solute carrier family 7 (cationic emino	3.5
	427299	AA830210	Hs.214263	hypothetical protein MGC15548 ESTs, Moderately similar to ALU1_HUMAN A	3.5 3.5
40	425212	AW962253	Hs.171618	ESTs	3.5 3.5
40	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.5
	442264	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	407253	AA411175	Hs.141939	ESTs, Moderately similar to \$65657 alpha	. 3.5
	457211 452682	AW972565 AA456193	Hs.32399	ESTs. Weakly similar to S51797 vasodilat	3.5
45	421247	BE391727	Hs.9071 Hs.102910	progestarone membrane binding protein	3.5
	418049	AA211467	Hs.190488	general transcription factor IIH, polype Homo saptens, Similar to nuclear localiz	3.5
	453792	AL134539	Hs.254129	KIAA1678	3.5 3.5
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	3.5
50	412014	AI620650	Hs.43761	ESTs, Wealty similar to A46010 X-linked	3.5
50	440370 407729	AA884000 T40707	Hs.8173	hypothetical protein FLJ 10803	3.5
	438527	AI969251	Hs.270862 Hs.115325	ESTS	3.5
	455648	BE064420	113.113023	RAB7, member RAS oncogene family-like 1 gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.5
	418630	Al351311	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	3.5 3.5
55	432242	AW022715	Hs.162160	ESTs, Weatly similar to ALU4_HUMAN ALU S	3.5
	424503	NM_002205	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	3.4
	449932	A1675444	Hs.263024	ESTs	3.4
	427700 403849	AA262294	Hs.180383	dual specificity phosphatase 6	3.4
60	429747	M87507	Hs.2490	Target Exon caspase 1, apoptosis-related cysteine pr	3.4
	451446	AJ826288	Hs.171637	hypothetical protein MGC2628	3.4
	434589	AF147363		gb:Homo sapiens full length insert cONA	3.4 3.4
	403361			NM_002210":Homo sapiens integrin, alpha	3.4
65	420841	Al625251	Hs.94037	hypothetical protein FLJ23053	3.4
UJ	438206 425295	AA780385	Hs.187885	ESTs	3.4
	411789	AA431366 AF245505	Hs.37251 Hs.72157	ESTs Addison	3.4
	440948	AW188311	Hs.128619	Adlican ESTs	3.4
=0	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	3.4 3.4
70	416821	AA436002	Hs.183161	ESTs	3.4
	459660	M79082		ESTs	3.4
	404209			Target Exon	3.4
	443950	NM_001425	Hs.9999	epithelial membrane protein 3	3.4
75	430694 425300	AA810624 AW501773	Hs.30936 Hs.270259	ESTs, Weakly similar to H2BH_HUMAN HISTO	. 3.4
	420300	AA258245	Hs.127573	ESTs Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.4
	458438	AJ141520	Hs.151464	ESTs, Wealdy similar to ALUC_HUMAN !!!!	3.4
	444911	U06117	Hs.250	xanthene dehydrogenase	3.4 3.4
80	421064	AI245432	Hs.101382	turnor necrosis factor, alpha-induced pro	3.4
80	441287	AW293132	Hs.131373	ESTs	3.4
	446960 405605	AW294936	Hs.156762	ESTs COMMISSIONERS AND ADDRESS OF THE PARTY	3.4
	433791	AA719352	Hs.112718	C2001342:gi]127814 sp[P26434 NAH4_RAT SO ESTs	3.4
			1-9-112710	LVIE	3.4

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	405238			Target Exon	3.4
	412986	X81120		cannabinoid receptor 1 (brain)	3.4
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	3.4
_	435523	T62849		membrane-spanning 4-domains, sublamily A	3.4
5	406739	AI566709	Hs.182426	ribosomal protein S2	3.4
	442710	AI015631	Hs.23210 Hs.280740	ESTs	3.4 3.4
	452526 456060	W38537 C14904	Hs.45184	hypothetical protein MGC3040 Homo sepiens cDNA FLJ12284 fis, clone MA	3.4
	435005	U80743	Hs.306094	trinucleotide repeat containing 12	3.4
10	421674	T10707	Hs.296355	hypothetical protein FLJ23138	3.4
	425242	D13635	Hs.155287	KIAA0010 gene product	3.4
	436805	AA731533	Hs.270751	ESTs	3.4
	418641	BE243138	Hs.86947	a disintegrin and metafloproteinase doma	3.4
15	430809	A1791150	Hs.262009	ESTs, Moderately similar to I38022 hypot	3.4
13	428878 413774	AA436884 AA131782	Hs.48926 Hs.182314	ESTs ESTs	3.3 3.3
	400533	74151102	113.102314	ENSP00000209376":PRED65 protein (Fragmen	3.3
	422448	AW372922	Hs.116774	integrin, alpha 1	3.3
	423905	AW579960	Hs.135150	tung type-I cell membrane-associated gly	3.3
20	430637	BE160081	Hs.256290	\$100 calcium-binding protein A11 (calgiz	3.3
	427899	AA829286	Hs.332053	serum amyloid A1	3.3
	434206	AW136973	Hs.180479	ESTs, Wealdy similar to S69890 mittogen i	3.3 3.3
	453387 436265	AI990741 AA731331	Hs.252809 Hs.190668	ESTs ESTs	3.3
25	412971	AA889628	Hs.35125	ESTS	3.3
	441701	AW339828	Hs.127497	ESTs	3.3
	418967	NM_001725	Hs.89535	bactericidal/permeability-increasing pro	3.3
	434577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fis, clone H	3.3
20	418216	AA662240	Hs.283099	AF15q14 protein	3.3
30	436137 428715	AI056769 AW293716	Hs.133512 Hs.53126	ESTs ESTs	3.3 3.3
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	3.3
	440074	AA863045	Hs.10669	ESTs, Wealdy similar to T00050 hypotheti	3.3
	405046			C3000978:gij9280045 dbjjBAB01579.1 (AB0	3.3
35	437815	AI823445	Hs.280699	ESTs	3.3
•	401272			C9000559*:gil12314195jemb[CAB99338.1] (A	3.3
	408896	AI610447	Hs.48778 Hs.2961	niban protein	3.3
	432343 407881	NM_002960 AW072003	Hs.40968	S100 catcium-binding protein A3 heparan sulfate (glucosamine) 3-O-sulfot	3.3 3.3
40	439978	BE139460	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	3.3
	421094	AW978202	Hs.289064	hypothetical protein FLJ22251	3.3
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	3.3
	446134	AW161234	Hs.13993	TBP-like 1	3.3
45	412281	AI810054	Hs.14119	ESTs	3.3
43	436282 452203	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	3.3
	421307	X57622 BE539976	Hs.103305	transporter 1, ATP-binding cassette, sub Homo sapiens mRNA; cDNA DKFZp43480425 (I	3.3 3.3
	409453	AJ458165	Hs.17296	hypothetical protein MGC2376	3.3
	411565	AW851728		gb:MR2-CT0222-011199-007-d06 CT0222 Homo	3.3
50	410422	AL042014	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	3.3
	450506	NM_004460		fibroblast activation protein, alpha	3.3
	451254	AI571016	Hs.172967		3.3 3.3
	423784 433325	AK000039 AW206986	Hs.132826 Hs.143905		3.3
55	419896	299362	14.140300	gb:HSZ99362 DXFZphamy1 Homo sapiens cDNA	3.3
•••	420552	AK000492	Hs.98808	hypothetical protein	3.3
	451778	AI826131	Hs.62954	ESTs, Wealdy similar to zinc finger prot	3.3
	427584	BE410293	Hs.179718		3.2
60	433507	AI817338	Hs.191791		3.2
OU	418661 440933	NM_001949 AI208217	Hs.1189 Hs.142879	E2F transcription factor 3 ESTs	3.2 3.2
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orotat	3.2
	404120	000020	10.2007	C5000537":gij3298595 gb AAC41376.1 (AF0	3.2
	453920	AJ133148	Hs.36602	I factor (complement)	3.2
65	437014	AA808757	Hs.222531		3.2
	424479	AF064238	Hs.149098		3.2
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	3.2
	425922 407304	AL157466 AA565832	Hs.162751 Hs.271649		3.2 3.2
70	411671	BE049094	113.27 1043	ESTs	3.2
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	3.2
	454765	AW819629		gb:RC5-ST0293-140200-014-H05 ST0293 Homo	3.2
	410407	X66839	Hs.63287	carbonic anhydrase IX	3.2
76	412490	AW803564	Hs.288850		3.2
75	434563	AW083994	Hs.9469	pleckstrin homology domain-containing, f	3.2
	417124 407378		Hs.25338 Hs.57776		3.2 3.2
	439764		Hs.22744		3.2
	445936		Hs.61478		3.2
80	446523	NM_003063		9 saroofipin	3.2
	406060			Target Exon	3.2
	432250		Hs.27417		3.2
	437269	AA334384	Hs.14942	0 ESTs	3.2

	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	3.2
	425146 438210	AW954627 AI825420	Hs.197824	gb:EST366697 MAGE resequences, MAGC Homo	3.2
	437698	R61837	Hs.7990	ESTs ESTs, Moderately similar to I84505 calci	3.2
5	444371	BE540274	Hs.239	forkhead box M1	3.2 3.2
	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	3.2
	445828	F05802	Hs.81907	ESTs	3.2
	450810	BE207588	Hs.334360	transforming growth factor beta 1 induce	3.2
	439533	W76021		gb:zd64c04.r1 Soares_fetal_heart_NbHH19W	3.2
10	418079	R40058	Hs.6911	ESTs	3.2
	418781	T41160	Hs.8404	ESTs	3.2
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	3.2 ·
	431319	AA873350	Hs.302232	ESTs .	3.2
15	445413 424947	AA151342 R77952	Hs.12677	CGI-147 protein	3.2
IJ	429490	AJ971131	Hs.23889	ESTs, Wealth similar to alternatively sp ESTs, Wealth similar to ALU7_HUMAN ALU S	3.2
	426765	AA743603	Hs.172108	nucleoporin 88kD	3.2 3.2
	419726	U50330	Hs.1274	bone morphogenetic protein 1	3.2
	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	3.1
20	439566	AF086387		gb:Homo sapiens full length insert cDNA	3.1
	452574	AF127481	Hs.301945	lymphoid blast crisis oncogene	3.1
	439753	BE262233	Hs.7423	hypothetical protein from EUROIMAGE 2168	3.1
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.1
25	439570	T79925	Hs.269165	ESTs, Wealdy similar to ALU1_HUMAN ALU S	3.1
23	443431	AI056847	Hs.20654	ESTs	3.1
	428289 415849	M26301 R20529	Hs.2253 Hs.6806	complement component 2	3.1
	419652	AL157485	Hs.91973	ESTs	3.1
	429500	X78565	Hs.289114	hypothetical protein hexabrachion (tenascin C, cytotactin)	3.1 3.1
30	457579	AB030816	Hs.36761	HRAS-like suppressor	3.1
	420579	AA278449	Hs.137429	ESTs	3.1
	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	3.1
	408247	AA053451	Hs.225632	leucine zipper protein 3	3.1
25	405183			NM_016358":Homo sapiens iroquois homeobo	3.1
35	420676	AJ434780	Hs.4248	vav 2 oncogene	3.1
	440286	U29589	Hs.7138	cholinergic receptor, muscarinic 3	3.1
	431176	AI026984	Hs.293662	ESTs	3.1
	417918 437945	AA209205 T78519	Hs.163754	hypothetical protein FLJ 12606	3.1
40	404632	170313		gb:yd68c08.r1 Soares fetal liver spieen NM_022490:Horno sapiens hypothetical prot	3.1 3.1
	428917	AA437337	Hs.16689	ESTs	3.1
	429940	W25215		gb:zb87a09.r1 Soares senescent fibroblas	3.1
	444018	AA448154		gb:zw82h09.r1 Soares_testis_NHT Homo sap	3.1
4.5	430701	AI760833	Hs.293971	ESTs	3.1
45	402229	8E262804		mitochondrial ribosomal protein S2	3.1
	454177	AW807321		gb:MR4-ST0062-240300-003-g05 ST0062 Homo	3.1
	400090	404046	11- 40440	Eos Control	3.1
	419326 435644	W94915 AA700867	Hs.42419 Hs.269659	ESTs ESTs	3.1
50	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	3.1
	458810	BE407125	Hs.231510	ESTs	3.1 3.1
	414403	AW969551	Hs.76064	ribosomal protein L27a	3.1
	449670	F07693	Hs.85603	Homo sepiens mRNA; cDNA DKFZp434K2172 (f	3.1
	403288			C1001737*:gi[7511201 pir][T27904 hypothe	3.1
55	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	3.1
	455899	BE155112		gb:PM1-HT0350-151299-003-a03 HT0350 Homo	3.1
	432044	AW972727		gb:EST384819 MAGE resequences, MAGL Homo	3.1
	443105 423789	X96753 AK002084	Hs.9004	chondroitin suffate proteoglycan 4 (mela	3.1
60	439538	AA837323	Hs.132851 Hs.56407	hypothetical protein FLJ11222 ESTs	3.1
	437681	AI207958	Hs.166556	Homo saplens, Similar to TEA domain fami	3.1 3.1
	433577	AW007080	Hs.284192	ESTs	3.1
	443021	AA388546	Hs.8904	lg superfamily protein	3.1
15	433894	AI907682	Hs.243293	ESTs	3.1
65	414884	R54418	Hs.183745	hypothetical protein FLJ 13456	3.1
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	3.1
	449162	AI632740	Hs.10476	ESTs	3.1
	417893	AA290605	Hs.190002		3.1
70	433578 438380	BE336886 T06430	Hs.3416 Hs.6194	adipose differentiation-related protein	3.0
	450756	AJ733488	Hs.144062	chondroitin suffate proteoglycan BEHAB/b ESTs	3.0
	422631	BE218919	Hs.118793		3.0 3.0
	414733	BE514535	Hs.77171	minichromosome maintenance deficient (S.	3.0
7.0	431019	NM_005249		forkhead box G18	3.0
75	434503	T96231	Hs.17762	ESTs	3.0
	455481	AW948317		gb:RC0-MT0015-280300-021-a09 MT0015 Homo	3.0
	427413	BE547647	Hs.177781		3.0
	414396	BE548266	Hs.76057	galactose-4-epimerase, UDP-	3.0
80	458760	AI498631	Hs.111334		3.0
-00	410555 411543	U92649 AW851248	Hs_64311	a disintegrin and metalloproteinase dorna gb:lL3-CT0220-160200-066-F01 CT0220 Homo	3.0
	435375	AI733610	Hs.187832	ESTs	3.0
	407047	X65965		gb:H.sapiens SOD-2 gene for manganese su	3.0 3.0
				A	3.0

	432065	AA401039	Hs.2903	protein phosphalase 4 (formerly X), cata	3.0
	443338	R99575	Hs.302908	ESTs	3.0
	433062	AK001757	Hs.281348	hypothetical protein FLJ10895	3.0
5	412135	AW895309	11- 00	gb:QV4-NN0038-300300-155-e07 NN0038 Homo	3.0
,	418669 449385	U85992 AI650471	Hs.87197	Human clone IMAGE:35527 unknown protein	3.0
	426384	AJ472078	Hs.347290 Hs.303662	ESTs	3.0
	436267	AW450938	Hs.180115	hypothetical protein FLJ13189 (FLJ13189) ESTs	3.0 3.0
	440388	AI693520	Hs.223000	ESTs	3.0
10	427235	Al126288	Hs.192232	ESTs	3.0
	420116	NM_013241	Hs.95231	FH1/FH2 domain-containing protein	3.0
	419764	BE262524	Hs.931B3	vasodilator-stimulated phosphoprotein	3.0
	405673 445921	M34996 AW015211	Hs.198253	major histocompatibility complex, class	3.0
15	427695	R88483	Hs.146181 Hs.172862	ESTs ESTs	3.0
	453324	W26592	Hs.232089	EST8	3.0
	404272			Target Exon	3.0 3.0
	428538	AA446440	Hs.98643	ESTs	3.0
20	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	3.0
20	444396 440483	T65213 AI200836	Hs.4257	ESTs	3.0
	429973	AI423317	Hs.150386 Hs.164680	ESTs ESTs	3.0
	450125	AA005418	Hs.158186	ESTS	3.0
	417409	BE272506	Hs.82109	syndecan 1	3.0 3.0
25	429569	AA454993	Hs.138343	ESTs, Wealdy similar to 178885 serine/th	3.0
	455778	BE088746		gb:CM2-BT0693-210300-123-d09 BT0693 Homo	3.0
	427954	J03060	Hs.247551	metaxin 1	3.0
	422418 427527	AK001383 AIB09057	Hs.116385	hypothetical protein FLJ10521	3.0
30	416677	T83470	Hs.293441 Hs.334840	immunoglobulin heavy constant mu	3.0
	451130	AI762250	Hs.345554	ESTs, Moderately similar to 178885 serin ESTs	3.0 3.0
	431431	AL096711	Hs.252953	Human DNA sequence from clone RP3-403A15	3.0
	425248	AW957442	Hs.252766	ESTs	3.0
35	422757	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	3.0
33	431836 416355	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	3.0
	426406	H49875 AI742501	Hs.268906 Hs.169756	ESTs	3.0
	419829	A1924228	Hs.115185	complement component 1, a subcomponent ESTs, Moderately similar to PC4259 femi	3.0
	412646	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmi	3.0 2.9
40	423869	BE409301	Hs.134012	C1g-related factor	2.9
	422710	AW936566	Hs.201876	ESTs	2.9
	445906	N28939	Hs.13434	Homo sapiens clone 24418 mRNA sequence	2.9
	429751 430413	M55210 AW842182	Hs.214982	laminin, gamma 1 (formerly LAMB2)	2.9
45	443433	R44743	Hs.241392 Hs.301667	small inducible cytokine A5 (RANTES) ESTs	2.9
	444145	BE153823	Hs.282385	ESTs. Weakly similar to 2004399A chromos	2.9
	425262	D87119	Hs.155418	GS3955 protein	2.9 2.9
	442476	AF069475		gb:AF069475 Homo sapiens astrocytoma lib	29
50	443361	A1792628	Hs.133273	ESTs	29
50	427144	X95097	Hs.2126	vasoactive intestinal peptide receptor 2	2.9
	415709 453385	AA649850 AW296101	Hs.278558 Hs.252806	ESTs	2.9
	442609	AL020996	Hs.8518	ESTs selenoprotein N	2.9
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit	2.9 2.9
55	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.9
	443502	AI074528	Hs.133949	ESTs	2.9
	444143	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm	2.9
	416308 447674	AW291942 BE270640	Hs.23628	3 beta-hydroxy-delta 5-C27-steroid oxido	2.9
60	408989	AW361666	Hs.19192 Hs.49500	cyclin-dependent kinase 2 KIAA0746 protein	29
	427418	AA402587	Hs.325520	LAT1-3TM protein	2.9 2.9
	408788	AL134947	Hs.213956	Homo sapiens BAC clone RP11-10205 from Y	2.9
	426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	2.9
65	403290	WC 4000		C10001011*:gi 4758212tref[NP_004411.1] d	2.9
05	430890 441217	X54232 Al922183	Hs.2699	glypican 1	2.9
	418287	A107331A	Hs.213246	ESTS	2.9
	443836	BE221613	Hs.140553	methionina aminopeptidase; elF-2-associa ESTs	2.9
	451527	AF022813	Hs.26518	transmembrane 4 superfamily member 7	2.9 2.9
70	418110	R43523	Hs.217754	hypothetical protein FLJ22202	2.9
	420886	AA805453		ESTs, Weakly similar to T29012 hypotheti	29
	439379	AA835002	Hs.125611	ESTs	2.9
	426197 406679	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	2.9
75	454120	AA070786 AB032990	Hs.40719	gb:zm66b07.r1 Stratagene neuroepithelium	2.9
	457244	AA581385	Hs.162473	hypothetical protein KIAA1164 ESTa, Wealdy similar to 138022 hypotheti	2.9
	432036	AF224266	Hs.272373	interleukin 20	2.9 2.9
	457364	AW971037		gb:EST383123 MAGE resequences, MAGK Homo	2.9 2.9
80	437860	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	29
80	453544	AA831785	Hs.171914	Homo sapiens cDNA FLJ14209 fis, clone NT	2.9
	454968 437528	AW849046	Ma 1003/-	gb:IL3-CT0214-150300-085-H08 CT0214 Homo	2.9
	437528 400850	N59646	Hs.169745	crumbs (Drosophila) homolog 1 Target Exon	2.9
				· or Bot CAUIT	2.9



	428896	AW291932	Hs.98936	ESTs	2.9
	426140 408872	AF131798 AH76139	Hs.343768	Homo sepiens clone 25119 mRNA sequence	2.9
	414799	A1752416	Hs.13291 Hs.77326	ESTs insufin-like growth factor binding prote	29 29
5	406646	M33600	Hs.308026	major histocompatibility complex, class	29
	416569	H64891		gh:yr68h03.r1 Soares fetal liver spleen	2.9
	439130 451433	AA306090 AA021140	Hs.124707 Hs.269265	ESTs ESTs, Wealthy similar to A46010 X-linked	2.9
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	29 29
10	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.9
	420172 442485	AA601122	Hs.95655	secreted and transmembrane 1	2.9
	416505	BE092285 H66470	Hs.29724 Hs.16004	hypothetical protein FLJ13187 ESTs	29 29
	415198	AW009480	Hs.943	natural killer cell transcript 4	29
15	420674	NM_000055	Hs.1327	butyrylcholinesterese	29
	452139 447499	AA099969 AW262580	Hs.16331 Hs.147674	Homo sapiens cDNA: FLJ21482 fis, ctone C protocadherin beta 16	2.8
	411373	BE326276	Hs.8861	ESTs	28 28
20	456816	AK001509	Hs.144391	hypothetical protein FLJ 10647	2.8
20	414232 416188	W86946 BE157260	Hs.238246 Hs.79070	hypothetical protein FLJ22479	2.8
	447733	AF157482	Hs.19400	v-myc avian myelocytomatosis viral oncog MAD2 (mitotic arrest deficient, yeast, h	2.8 2.8
	438524	AA889055	Hs.123468	ESTs	2.8
25	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	2.8
23	408715 424028	AI567839 AF055084	Hs.151714 Hs.153692	Homo sapiens mRNA for KIAA1769 protein, Homo sapiens cDNA FLJ14354 fis, clone Y7	2.8
	421679	AJ475110	Hs.203933	ESTs	2.8 2.8
	450651	W79000	Hs.44545	ESTs, Wealdy similar to 834087 hypotheti	2.8
30	452785 432842	AL359942 AW674093	Hs.296434 Hs.334822	erythroid differentiation and denucleati	2.8
	403291	7111074030	15.554022	hypothetical protein MGC4485 Target Exon	2.8 2.8
	453096	AW294631	Hs.11325	ESTs	2.8
	422545 440296	X02761 D30829	Hs.287820	fibronectin 1	2.8
35	427154	AL137262	Hs.160610 Hs.325630	splicing factor profine/glutamine rich (hypothetical protein MGC4289	2.8 2.8
	422282	AF019225	Hs.114309	apolipoprotein L	2.8
	434868	R50032	Hs.159263	collegen, type VI, alpha 2	2.8
	414727 437437	BE456904 AA226869	Hs.190162	gb:hz28f03.x1 NCI_CGAP_GC6 Homo sepiens hypothetical protein DKFZp762L0311	2.8
40	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.8 2.8
	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	2.8
	444006 448432	BE395085 AI783588	Hs.10088	type I transmembrane protein Fn14	2.8
	453682	179703	Hs.208575	ESTs gb:yd71e08.r1 Soares fetal liver spieen	2.8 2.8
45	447527	AI702896	Hs.42091	ESTa	2.8
	418557 409157	BE140602	Hs.245645	ESTs	2.8
	457653	AA064631 AI820719	Hs.154662	gb:zf72c03.s1 Soares_pineal_gland_N3HPG OnaJ (Hsp40) homolog, subfamily A, membe	2.8 2.8
50	456908	AI953671	Hs.220994	hypothetical protein FLJ14129	2.8
50	439220	AW295340	Hs.130417	ESTs, Weakly similar to Z195_HUMAN ZINC	2.8
	418312 ,454581	AW972468 AW809189	Hs.170307	Ral guanine nucleotide exchange factor R gb:MR4-ST0118-261099-012-e10 ST0118 Homo	28
	419169	AW851980	Hs.262346	ESTs, Weakly similar to \$72482 hypotheti	2.8 2.8
55	400645	4144554656		Target Exon	2.8
"	413951 441360	AW051200 AI091713	Hs.75640 Hs.106597	natriuretic peptide precursor A Homo sapiens, Similar to RIKEN cDNA 1110	2.8 2.8
	404150		1.5.100331	Target Exon	2.8
	402936	******		ENSP00000217246*:DJ803K15.1 (novel prote	2.8
60	454457 439544	AW753456 W26354	Hs.28891	gb:QV2-CT0261-261099-011-d11 CT0261 Homo	2.8
	403969		1420031	hypothetical protein FLJ11360; artemis p ENSP0000034663:Zinc finger protein 131	2.8 2.8
	447183	AI554733	Hs.173182	ESTs	2.8
	446566 426141	H95741 C05886	Hs.17914 Hs.293972	membrane-spanning 4-domains, subfamily A ESTs	2.8
65	440148	AW014231	Hs.90790	Homo sapiens cDNA: FL122930 fis, clone K	2.8 2.8
	430335	D80007	Hs.239499	KIAA0185 protein	2.8
	447071 428899	AW236867 AA744610	Hs.244376		2.8
	400658	~~~~	Hs.194431	palladin ENSP00000237081*:KIAA1217 PROTEIN (FRAGM	28 28
70	403942			Target Exon	2.8
	420565	AI806770	Hs.30258	ESTs	2.8
	409734 456645	8E151564 AF227156	Hs.56155 Hs.110103	hypothetical protein RNA polymerase I transcription factor RR	2.8
~~	401841		10103	NM_015113:Homo sapiens KtAA0399 protein	2.8 2.8
75	447247	AW369351	Hs.287955	Homo sapiens cDNA FL113090 fis, clone NT	2.8
	450150 409154	A1754391 U72882	Hs.23510 Hs.50842	Kruppel-like factor 12	2.8
	410267	AW978005	Hs.12600	interferon-induced protein 35 N-ethylmalelmide-sensitive factor attach	2.8 2.8
80	448224	R48700	Hs.20733	Homo sapiens cDNA: FLJ22356 fis, clone H	28
ου	410268 447512	AA316181 AW958148	Hs.61635 Hs.129454	six transmembrane epithelial antigen of	28
	417749	U09196	Hs.82520	ESTs polymerase (DNA-directed), delta 4	2.8 2.8
	415293	R49462	Hs.106541	EST8	2.8

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	416207	NM_014745	Hs.79077	Homo sapiens, clone MGC:2908, mRNA, comp	2.8
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	2.8
	425128	BE561929	Hs.154718	turnor protein D52-fike 2	2.7
5	444491	AI151091	Hs.270714	EST ₅	2.7
3	428311	NM_005651	Hs.183671 Hs.301865	Typtophan 2,3-dioxygenase	27
	430377 417944	NM_001922 AU077196	Hs.82985	dopachrome tautomerase (dopachrome delta collagen, type V, alpha 2	2.7 2.7
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	27
	438138	R98299	Hs.177502	ESTs	2.7
10	425421	L11669	Hs.157145	tetracycline transporter-like protein	2.7
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	2.7
	451748	AK001612	Hs.26962 Hs.25614	Homo sepiens cDNA FLJ10750 fis, clone NT	2.7
	452085 405941	AW239140	113.23014	ESTs, Wealdy similar to PC4396 mucin 3 T Target Exon	2.7 2.7
15	417395	BE564245	Hs.82084	Integrin beta 3 binding protein (beta3-e	27
	449667	AB023227	Hs.23860	KIAA1010 protein	2.7
	428808	AA436007	Hs.188780	EST8	2.7
	425843	BE313280	Hs.159627	death associated protein 3	2.7
20	438025 400924	AW501360	Hs.258910	ESTs	2.7 2.7
20	412898	AJ129903	Hs.74669	Target Exon vesicle-associated membrane protein 5 (m	2.7
	413834	BE295896	Hs.224179	ESTs. Weakly similar to I38022 hypothesi	2.7
	453785	AJ368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.7
25	406736	Al254733	Hs.182426	ribosomal protein S2	2.7
25	414280	BE410769	Hs.75873	zyxin	2.7
	434203 442621	BE262677	Hs.283558	hypothetical protein PRO1855	2.7 2.7
	414591	A1004333 A1888490	Hs.130553 Hs.55902	ESTs, Weakly similar to ALUA_HUMAN !!!! ESTs, Weakly similar to ALUB_HUMAN ALU S	2.7
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	2.7
30	416784	AA334592	Hs.79914	lumican	2.7
	413851	AW897510	Hs.137387	ESTs	2.7
	451767	AI625014	Hs.187328	ESTs	2.7
	44 1668 435664	AI611973 AI032087	Hs.136313	ESTs	27
35	435046	AA662772	Hs.269819 Hs.174330	ESTs ESTs, Wealdy similar to ALU1_HUMAN ALU S	2.7 2.7
55	439467	AW292275	Hs.158365	ESTs	2.7
	441329	AI203575	Hs.46821	hypothetical protein FLJ20086	2.7
	426925	NM_001196	Hs.315689	Homo sepiens cDNA: FLJ22373 fls, clone H	2.7
40	427241	AA399988	Hs.112087	Human DNA sequence from clone RP11-530N1	2.7
40	449919 458070	AI674685	Hs.200141	ESTs CSTs Workly similar to 139500 size fee	2.7 2.7
	444794	AW503578 AI419991	Hs.209406 Hs.145225	ESTs, Weathly similar to 138600 zinc fing ESTs	. 27
	410781	AI375672	Hs.165028	EST\$	27
	449520	R34993	Hs.226666	ESTs, Moderately similar to 154374 gene	2.7
45	439481	AF086294	Hs.125844	ESTs	2.7
	401702			NM_001171*:Homo sapiens ATP-binding cass	2.7
	432890 435545	NM_014442 AA687415	Hs.279751 Hs.28107	sialic acid binding tg-like lectin 8	2.7 2.7
	416422	H60457	rs.20101	ESTs ESTs, Moderately similar to ZN91_HUMAN Z	27
50	429415	NM_002593	Hs.202097	procollagen C-endopeptidase enhancer	2.7
	420982	AW576160	Hs.100729	KIAAD692 protein	2.7
	431421	AW969118	Hs.108144	ESTs. Wealty similar to unnamed protein	2.7
	444168	AW379879	11. 000010	gb:RC1-HT0256-081199-011-f01 HT0256 Homo	2.7
55	419964 424480	AA811657 AA341442	Hs.220913 Hs.205299	ESTs ESTs	2.7 2.7
"	436314	A1983409	Hs.189226		27
	405516			ENSP00000200457*:Thyroid receptor intera	2.7
	449340	AW235786	Hs.195359		2.7
60	457876	AJ821940		ESTs, Moderately similar to ALU8_HUMAN A	2.7
60	423799 422551	AW026300 AW967284	Hs.132906	19A24 protein gb:EST379359 MAGE resequences, MAGJ Homo	2.7 2.7
	404592	A11501204		NM_022739":Homo saplens E3 ublquitin lig	2.7
	424200	AA337221		gb:EST41944 Endometrial turnor Homo sapie	2.7
	428612	AA770001	Hs.188778		2.7
65	446139	H77395	Hs.39749	ESTs	2.7
	440478	AJ733047	Hs.130005		27
	429612 422530	AF062649 AW972300	Hs.252587 Hs.118110		2.7 2.7
	423713	AW754182		gb:RC2-CT0321-131199-011-c01 CT0321 Home	2.7
70	402032			ENSP00000251056":Plasma membrane calcium	27
	424186	AI536021	Hs.288706		2.7
	402799			Target Exon	2.7
	423352		Hs.193576		2.7
75	412021 458617	AW885592 Z25900	Hs.18724	gb:RC4-QT0071-090300-011-g11 QT0071 Homo Homo sapiens mRNA; cDNA DKFZp564F093 (fr	2.7 2.7
, ,	404170		rts. 10724	NM_000636":Homo sapiens superoxide dismu	2.7
	410886			gb:MR4-ST0121-141099-010-G06_1 ST0121 Ho	2.7
	414988	C17535		gb:C17535 Human placenta cDNA (TFujiwara	2.7
80	450325		Hs.26289		2.7
δŪ	458918		Hs.25269		2.7
	405760 406789			Target Exon ribosomal protein L29	2.7 2.7
	424586			gb:EST51529 Gall bladder II Homo sepiens	27

	400000	V13107			
	400335 435065	Y13187 8E064391	Hs.248068	Homo sapiers dmd gene, Intron 11	27
	419373	NM_003244	Hs.90077	gb:RC4-BT0310-110300-015-b08 BT0310 Homo	2.7
	406785	AA588061	113.50011	TG-interacting factor (TALE family homeo	2.7
5	433006	BE242758	Hs.190223	gb:nk10d03.s1 NCI_CGAP_Co2 Homo sapiens ESTs, Moderately similar to T29285 hypot	27
-	428690	AI948490	Hs.98765	ESTs	2.7 2.7
	432692	AW974944	Hs.200577	ESTs	2.7
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	2.7
10	452811	AA937079	Hs.118983	hypothetical protein FLJ12150	2.6
10	457035	AA398074	Hs.119143	ESTs, Moderately similar to KIAA1513 pro	26
	427725	U66839	Hs.180533	mitogen-activated protein kinase kinase	26
	433681 423748	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fs, clone NT	2.6
	422764	AI149048 AI767727	Hs.30211 Hs.47522	hypothetical protein FLJ22313	2.6
15	403431	701121	113.47322	ESTs Target Exon	2.6
	439332	AW842747	Hs.300870	Homo sapiens mRNA; cDNA DKFZp\$47M072 (fr	26
	412749	AA378417	Hs.74564	signal sequence receptor, beta (transloc	2.6 2.6
	409703	NM_006187	Hs.56009	2-5-oligoadenylate synthetase 3 (100 k	26
20	405717			CX000838:gl]10092633pef]NP_055314.1 pu	2.6
20	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cO	26
	414039	M83221	Hs.858	v-rel avian reticuloendotheliosis viral	26
	452683	AI089575	Hs.9071	progesterone membrane binding protein	2.6
	447587 408605	AW292139 AF025374	Hs.115789 Hs.46465	ESTS	26
25	407103	AA424881	Hs.256301	T-cell, immune regulator 1 hypothetical protein MGC13170	2.6
•	427395	AW298741	Hs.97861	ESTs, Moderately similar to 138022 hypot	2.6 2.6
	435113	AA665469	Hs.117136	ESTs	2.6
	419015	T79262	Hs.14463	ESTs	2.6
20	427648	AI376722	Hs.180062	proteasome (prosome, macropain) subunit,	2.6
30	453707	AW003879	Hs.126522	Homo saplens, clone MGC:16722, mRNA, com	2.6
	411927	BE274009	Hs.772	glycogen synthase 1 (muscle)	2.6
	404053	44460034	11- 2022	Target Exon	2.6
	415069 449625	AA159831 NM_014253	Hs.29286	ESTs, Weakly similar to 149636 DNA-bindi	2.6
35	438033	T26483	Hs.6059	odz (odd Oz/ten-m, Drosophila) homolog 1	2.6
-	451593	AF151879	Hs.26706	EGF-containing fibulin-like extracellula CGI-121 protein	26
	435828	AA700705	Hs.13852	ESTs	26 26 .
	443753	AW367578	Hs.134749	ESTs	2.6
40	416097	BE387371	Hs.118964	hypothetical protein FLJ20085	2.6
40	413986	243567		gb:HSC1FC021 normalized infant brain cDN	2.6
	439755	AW748482	Hs.77873	B7 homolog 3	2.6
	408371	AF161545	Hs.44439	hypothetical protein	2.6
	445658	AI469062	Hs.172660	ESTs	2.6
45	438166 449426	N30158 T92251	Hs.122645 Hs.198882	ESTs ESTs	2.6
	422605	H16646	Hs.118666	hypothetical protein PP591	2.6
	415788	AW628686	Hs.78851	KIAA0217 protein	2.6 2.6
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.5
	400295	W72838		Al905687:IL-8T095-190199-019 BT095 Homo	2.6
50	441128	AA570256		ESTs, Wealdy similar to T23273 hypotheti	2.6
	420372	AW960049	Hs.293660	Homo sapiens, clone IMAGE:3535476, mRNA,	2.6
	428977	AK001404	Hs.194698	cyclin B2	26
	424278 445211	AK000723 BE045601	Hs.144517	hypothetical protein FLJ20716	2.6
55	412715	NM_000947	Hs.118248 Hs.74519	ESTs, Weakly similar to YC18_HUMAN HYPOT	2.6
-	417838	R24713	Hs.22514	primase, polypeptida 2A (58kD) ESTs	2.6
	420670	AW973577		ESTS	2.6 2.6
	403267			Target Exon	2.6
60	454354	AW389896		gb:RC4-ST0173-191099-032-e12 ST0173 Homo	2.6
60	452903	AJ953425	Hs.345291	ESTs, Weakly similar to 138022 hypotheti	2.6
	427830	AA416598	Hs.98233	ESTs	2.6
	435953 430744	A1767087	Hs.114142	ESTs	2.6
	413335	AA485229 AI613318	Hs.105649 Hs.48442	ESTs ESTs	2.6
65	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	2.6
	431865	AA521106	Hs.136375	ESTs. Weakly similar to S65824 reverse t	2.6 2.6
	434274	AA528539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	26
	447854	AW138454	Hs.11594	ESTs	2.6
70	412799	AJ267608		gb:aq91h03.x1 Stanley Frontal SB pool 1	26
70	455409	AW936832		gb:PM2-DT0023-050400-003-h03 DT0023 Homo	2.6
	408212	AA297567	Hs.43728	hypothetical protein	2.6
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	2.6
	443539 434898	AJ076182 AW500458	Hs.134074	ESTs, Moderately similar to ALUS_HUMAN A	2.6
75	438118	AW753311	Hs.29956 Hs.346690	KIAA0450 protein ESTs	2.6
	431786	AW452784	Hs.220718	ESTs	2.6
	421689	N87820	Hs.106826	KIAA1696 protein	2.6
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	2.6 2.6
00	424684	AW752714	Hs.5174	ribosomal protein S17	2.6
80	439823	AW665287	Hs.124514	ESTs	2.6
	411962	AA099050		gb:zk85d12.r1 Soares_pregnant_uterus_NbH	2.6
	445774 400492	AI254165	Hs.339968	ESIS	26
				C10001573°:gi]7302749[gb]AAF57827.1 (AE	2.6
				0.40	

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	450625	AW970107	No 2075	gb:EST382188 MAGE resequences, MAGK Homo	2.6
	426931 440131	NM_003416 AI023425	Hs.2076 Hs.222225	zinc finger protein 7 (KOX 4, clone HF.1	2.6
	438525	AW368528	Hs.100855	ESTs ESTs	26
5	412247	AF022375	Hs.73793	vascular endothelial growth factor	26 26
-	406662	X62006	Hs.172550	polypyrimidine tract binding protein (he	2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
	402260			NM_001436":Homo sapiens fibrillarin (FBL	2.6
- ^	429599	AAB06106	Hs.123664	ESTs	2.6
10	429562	AJ732767	Hs.158101	Homo sapiens cDNA FLJ14673 fis, clone NT	2.6
	432527	AW975028	Hs.102754	ESTs	2.6
	434420	AA688278	Hs.194864	hypothetical protein FLJ22578	2.6
	452732	BE300078	Hs.80449	Horno sapiens, clone IMAGE:3535294, mRNA,	2.6
15	424408	AI754813	Hs.146428	collagen, type V, atpha 1	2.6
13	413151	H47969 N39535	Hs.141971	ESTs. Weakly similar to ALU1_HUMAN ALU S	2.6
	416244 403104	W33232	Hs.32748	ESTS	2.6
	400780			C8000064*:gi[10432393 emb CAC10283.1] (A	2.6
	433009	AA761668		NM_007325*:Homo sapiens glutamate recept gb:nz24c08.s1 NCI_OGAP_GCB1 Homo sapiens	2.6
20	424090	X99699	Hs.139262	XIAP associated factor-1	2.6
	403212	,00000	10.103202	NM_019595:Homo saptens intersectin 2 (IT	2.6 2.6
	407855	R54126	Hs.40500	similar to S. cerevisiae RER1	2.6
	406849	AA454809	Hs.172928	collagen, type I, alpha 1	2.6
	443462	AJ064590	Hs.171176	ESTs	2.6
25	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrota	2.6
	450089	AJ681883	Hs.209546	ESTs, Weakly similar to 2109260A B cell	26
	419571	AW674962	Hs.91148	protein kinase 02	2.6
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	2.6
20	444881	A1623288	Hs.192805	ESTs	2.6
30	420658	AW965215	Hs.130707	ESTs	2.6
	437634	AW293046	Hs.255158	ESTs .	2.6
	426894	AI204209	Hs.143911	ESTs	2.6
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	2.6
35	434171	BE247688	Hs.347349	KIAA0948 protein	2.6
رر	410174	AA306007	Hs.59461	DKFZP434C245 protein	2.6
	427245	AA421022	Hs.97739	ESTs	2.5
	437085 400362	AA743935	Hs.202329	ESTs	2.5
	452221	AF068294 C21322	Hs.272414 Hs.288057	Homo sapiens HDCMB45P mRNA, partial cds	2.5
40	439079	AF085937	Hs.38348	hypothetical protein FLJ22242	2.5
,,,	437287	AA748180	Hs.159346	ESTs	25
	411852	AA528140	Hs.107515	hypothetical protein FLJ21369	2.5
	427824	AA406245	Hs.24895	ESTs, Wealdy similar to T00329 hypotheti ESTs	2.5
	435177	AI018174	Hs.42938	ESTs	2.5
45	449433	AI672096	Hs.9012	ESTs, Wealdy similar to \$26650 DNA-bindi	2.5
	447853	A1434204	Hs.164285	ESTs, Weakly similar to AFG1_YEAST AFG1	2.5 2.5
	416704	H77795	Hs.39785	ESTs	2.5
	401696			Target Exon	2.5
C A	445677	H96577	Hs.6838	ras homotog gene family, member E	2.5
50	413840	AI301558	Hs.146381	RNA binding motil protein, X chromosome	2.5
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	2.5
	420289	N55394	Hs.96398	8-oxoguanine DNA glycosylase	2.5
	421848	X15880	Hs.108885	collagen, type VI, alpha 1	2.5
55	421234	AA907153	Hs.190060	ESTs	2.5
J)	414598	AI094221	Hs.135150	tung type-I cell membrane-associated gly	2.5
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	2.5
	458199 433523	AW136417 H29882		hypothetical protein FLJ 14464	2.5
	429125	AA446854	Hs.271004	ESTs Misself similar to 120022 has all all	2.5
60	418399	AF131781	Hs.84753	ESTs, Weakly similar to 138022 hypotheti	25
	404748		113,04133	hypothetical protein FLJ12442 ENSP0000238177":Similar to kynurenine 3	2.5
	413507	BE145360	Hs.190064	ESTs, Weakly similar to I38022 hypotheti	25
	418886	AA993982	Hs.130858	ESTs	2.5 2.5
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	2.5 2.5
65	452367	U71207	Hs.29279	eyes absent (Orosophila) homolog 2	2.5
	436258	AW867491	Hs.107125	plasmalemma vesicle associated protein	2.5
	459527	AW977558	Hs.291735	ESTs, Weakly similar to 178885 serine/th	2.5
	450543	Al394037	Hs.170296	Homo sapiens cDNA: FLJ22090 fis, clone H	2.5
70	434818	AA650097	Hs.5996	ESTs	2.5
70	444534	AW271626	Hs.42294	ESTs	2.5
	452113	AJ859393		gb:wm11a02.x1 NCI_CGAP_Ut4 Homo sapiens	2.5
	429115	AA446728	Hs.289020	Homo sapiens cDNA FLJ14098 fis, clone MA	2.5
	434012	AA621425	Hs.186256	ESTs	2.5
75	447143	AW292408	Hs.152290	ESTs, Highly similar to JC2463 vasoactiv	2.5
13	449505	AI653006	Hs.195374	ESTs	2.5
	419817	AA743434	Hs.193778	ESTs	2.5
	457986	AA781745	Hs.126920	Horno sapiens, clone IMAGE:4299555, mRNA,	2.5
	431454	AW975980	Hs.292918	ESTs	2.5
80	425018 427513	BE245277	Hs.154196	E4F transcription factor 1	2.5
	441318	AJ476318 AJ078234	Hs.192480 Hs.176130	ESTs SSTs	2.5
	424830	AW270580		ESTs	2.5
	414271	AK000275	Hs.189311 Hs.75871	ESTs, Wealdy similar to putative p150 [H protein kinase C binding protein 1	2.5
			0011	Protein unesa o enemiA hatati I	2.5

	446089	AI860021	Hs.345028	ESTs. Moderately similar to A47582 B-cel	2.5
	415983	AJ436798	Hs.117078	Homo sepiens cDNA: FLJ23028 fis, clone L	2.5
	408292	AW178363		gb:RC3-HT0105-010999-002-H06 HT0105 Homo	
	446862	AV660697	Hs.282700	ESTs	2.5
5	448970	AW138582	13.202100		25
•	459200	Y09306	Ma 20140	gb:UI-H-BI1-acw-a-06-0-UI.s1 NCI_CGAP_Su	2.5
			Hs.30148	homeodomain-interacting protein kinase 3	2.5
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	2.5
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10	441255	R06350	Hs.171635	ESTs .	2.5
	441627	AA947552	Hs.58086	branched chain aminotransferase 1, cytos	2.5
	438714	AA814859	Hs.294112	ESTs	2.5
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	418291	BE300369	Hs.289038	hypothetical protein MGC4126	
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	416845	H95279	Hs.293788	gb:yu20h02.s1 Soares letal liver spleen	2.5
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20	444884	Al201094	Hs.148540	ESTs	2.5
	440826	AW383518	Hs.346256	ESTs. Moderately similar to ALU2_HUMAN A	2.5
	431374	BE258532	Hs.251871	CTP synthase	25
	458093	AJ207768	Hs.343628	sialyttransferase 4B (beta-gatactosklase	2.5
	422484	AA568770	Hs.123158	Homo sapiens cDNA FLJ12830 fis, clone NT	2.5
25	442804	AW300118	Hs.131257	ESTs	25
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	451350	AI791447		gb:ni13a05.y5 NCI_CGAP_Co4 Homo saplens	2.5
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	442085	AA975688	Hs.159955	ESTa	2.5
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	2.5
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	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	2.5
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	450683	H43540	Hs.25292	ribonuclease HI, targe subunit	2.5
	407198	H91679		gb:yv04a07.s1 Soares fetal liver spieen	25
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75	409449	H11341	Hs.13366	Homo sepiens cDNA: FLJ23567 fis, clone L	2.5
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	TABLE 1	4B:			
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Unique Eos probeset identifier number Gene cluster number Genbank accession numbers Pkey: CAT number: Accession:

80

Pkey CAT Number Accession 408292 1050507_1 AW178363 AW846011 AW845964 AW845988 AW845977 AW846002



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30	Pkey:		ninua number en	responding to an Eos probeset
30	Ref:			The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et at." refers to the publication entitled "The DNA
	1001.			n chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
	Strand:			nd from which exons were predicted.
	Nt_positio			le positions of predicted exons.
35	III. positio		audica madelos	a positions of productor oxions.
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	403267	7887182	Plus	116078-121895
65	403288	8081479	Plus	133763-133899, 135813-135958
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	403349	8569773	Minus	167815-168374
	403361	8570313	Minus	112496-112687
70	403431	7139839	Plus	56509-56860
	403481	9965004	Plus	93496-93633
	403696	3135242	Minus	143467-143634
	403790	8084957	Minus	87826-87947,89835-90002
76	403849	7708855	Plus	95043-96519
75	403942	7711825	Minus	99606-99757
	403961	7596976	Minus	110393-110603
	403959	8569909	Plus	31237-31375,32405-32506
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	404209	5006246		11247-11514
	404272	9885189	Plus	83207-83355,84358-84496,90519-90720,91371-91447

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	404584	9857511	Plus	138551-139153
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5	404532	9796668	Plus	45096-45229
	404748	7263437	Plus	11446-11591
	404891	7329392	Plus	84974-85125
	405046	7596829	Minus	4373-4528
	405141	8980911	Ptus	99861-100054
10	405183	7209940	Plus	12335-12653
	405238	7249119	Minus	51728-51838
	405348	2914717	Minus	43310-43462
	405516	9454624	Plus	112707-112876,113676-113854
	405558	1521110	Plus	4502-4644,5983-6083
15	405605	5836195	Minus	117070-117270
	405717	9588573	Plus	11275-11973
	405760	6066938	Minus	37424-38045
	405863	7657810	Plus	49410-49620
	405941	6758796	Plus	2798-3444
20	406060	6899623	Minus	20339-20746
	406290	5686274	Plus	8711-9358
	406395	9256242	Minus	20805-20960
	406478	9857502	Plus	68314-68523,68853-68950
25	406481	9864741	Minus	91439-91579

TABLE 15A: ABOUT 1033 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT TISSUES
Table 15A lists about 1033 genes up-regulated in glioblastoma compared to normal normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03
GeneChip array such that the ratio of "average" glioblastoma to "average" normal tissues was greater than or equal to 3.0. The "average" glioblastoma level was set to the 85° percentite amongst various brain tumors. The "average" normal tissues level was set to the 85° percentite amongst various non-matignant adult tissues. In order to remove gene-specific before one-specific hybridization, the 10° percentite value amongst the various non-matignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pier:

Unique Eos probeset Identifier number
Exacon:
Expender Accession number, Genbank accession number
UnigenelD:
Unique en umber
Unique en umber
Unique en en title
Unique gene title
Ratio of GLIOBLASTOMA to NORMAL ADULT TISSUES 30

35

40	Pkey	ExAcon	UnigenelD	Unigene Title	RI
40	427343	A1880044	Hs.176977	protein kinase C binding protein 2	60.5
	431917	D16181	Hs.2868	peripheral myelin protein 2	54.9
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	53.1
	428321	AI699994	Hs.2868	peripheral myelin protein 2	49.6
4.0	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	45.4
45	435147	AL133731	Hs.4774	Homo saplens mRNA; cDNA DKFZp761C1712 (f	43.9
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	42.7
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	42.3
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	39.1
	430838	N46664	Hs.169395	hypothetical protein FLJ12015	37.9
50	417183	R52089	Hs.172717	ESTs	37.6
	426325	D28114	Hs.169309	myelin-associated oligodendrocyte basic	36.5
	425088	AA663372	Hs.169395	hypothetical protein FLJ12015	34.3
	429007	D80642		gb:HUM092E098 Human fetal brain (TFujiwa	33.9
	449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	33.9
55	423849	AL157425	Hs.133315	Homo sepiens mRNA; cDNA DKFZp761J1324 (f	32.7
	429276	AF058085	Hs.198612	G protein-coupled receptor 51	32.3
	413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	29.0
	450133	AW969769	Hs. 105201	ESTs	27.9
	412733	AA984472	Hs.74554	KIAA0080 protein	27.6
60	425842	AL587490 ·	Hs.159623	NK-2 (Drosophila) homotog B	27.3
	415829	AB013805	Hs.80220	catenin (cadherin-associated protein), d	27.1
	424140	248051	Hs.141308	myelin oligodendrocyte glycoprotein	25.2
	402604			Target Exon	24.3
	437204	AL110216	Hs.22826	ESTs, Weakly similar to IS5214 salivary	24.3
65	422656	AI870435	Hs.1569	LIM homeobox protein 2	23.6
	447359	NM_012093	Hs.18268	adenylate kinase 5	23.3
	436878	BE465204	Hs.47448	ESTs	22.9
	435708	AI362949	Hs.75169	ESTs	22.9
70	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	22.7
70	439239	A1031540	Hs.235331	ESTs	22.4
	409395	U46745	Hs.336678	dystrobrevin, atoha	22.2
	425799	T08133	Hs.182906	Homo sagiens mRNA for KIAA1872 protein.	21.9
	425057	AA826434	Hs.1619	achaete-scute complex (Orosophila) homol	21.3
~~	444378	R41339	Hs.47860	neurotrophic tyrosine kinase, receptor,	21.2
75	444513	AL120214	Hs.7117	glutamate receptor, ignotropic, AMPA 1	21.0
	419078	M93119	Hs.89584	insulinoma-essociated 1	21.0
	425048	H05468	Hs.164502	ESTs	20.9
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	19.3
00	423853	AB011537	Hs.133466	slit (Drosophila) homolog 1	19.3
80	418110	R43523	Hs.217754	hypothetical protein FLJ22202	19.2
	447004	AW296968	Hs.157539	ESTs	18.6
	439415	F05538	Hs.4273	ESTs	18.6
	441497	R51064	Hs.23172	ESTs	

	425523	AB007948	Hs.158244	KIAA0479 protein	18.3
	413597	AW302885	Hs.117183	ESTs	18.2
	433551	AI985544	Hs.12450	protocadherin 9	17.7
5	428392	H10233	Hs.2265	secretory granula, neuroendocrine protei	17.3
5	453642	A1370936	Hs.34074	dipeptidylpeptidase VI	17.3
	418338	NM_002522	Hs.84154	neuronal pentraxin I	17,1
	437268	A1754847	Hs.227571	regulator of G-protein signalling 4	16.8
	408604	D51408	Hs.21925	ESTs	16.6
10	424581	M52062	Hs.150917	catenin (cadherin-associated protein), a	15.6
10	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (C/EBP),	16.5
	448302	AJ480208	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	16.4
	429466	M85835	Hs.12827	ESTs	16.3
	441350 448672	A8020690	Hs.7782	paraneoplastic antigen MA2	15.9
15	448743	AI955511	Hs.225106	ESTs	15.8
13	415910	AB032962	Hs.21896	KIAA1136 protein	15.7
	441285	U20350 NM_002374	Hs.78913 Hs.167	chemoline (C-X3-C) receptor 1	15.3
	431019	NM_005249	Hs.2714	microtubule-associated protein 2	15.2
	431941	AK000106	Hs.272227	forkhead box G1B Homo sepiens cDNA FLJ20099 fis, clone CO	14.8
20	433800	AI034361	Hs.135150		14.3
	416370	N90470	Hs.203697	lung type-I cell membrane-associated gly ESTs, Weakly similar to 138022 hypotheti	14.3
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	14.1
	444471	AB020684	Hs.11217	KIAA0877 protein	14.0
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	13.9 13.8
25	448595	AB014544	Hs.21572	KIAA0644 gene product	13.6
	441440	AI807981	Hs.30495	ESTs	13.6
	428982	NM_005097	Hs.194704	leucine-rich, glioma inactivated 1	13.5
	424790	AL119344	Hs.13326	ESTs, Wealty similar to 2004399A chromos	13.3
20	459516	AI049662	Hs.245858	EST	13.2
30	421264	AL039123	Hs.103042	microtubula-associated protein 18	13.2
	428342	AI739168		Homo sapiens cDNA FLJ13458 fs, clone PL	13.1
	408562	A1436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	12.9
	412959	D87458	Hs.75090	KIAA0282 protein	12.9
25	439199	R40373	Hs.26299	ESTs	12.8
35	423419	R55336	Hs.23539	ESTs	12.5
	445495	BE622641	Hs.38489	ESTs, Weakly similar to 138022 hypotheti	12.4
	415849	R20529	Hs.6806	ESTs	12.4
•	452372	A1885742	Hs.228474	ESTs	12.4
40	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	12.3
40	426344	H41821	Hs.322469	transcriptional activator of the c-los p	12.2
	415734	NM_014747	Hs.78748	KIAA0237 gene product	12.1
	426269 444119	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	12.1
	409049	R41231 AI423132	Hs.184261	ESTs, Weakly similar to T26686 hypotheti	12.0
45	434277	X77748	Hs.146343 Hs.3786	ESTs	11.9
	427897	NM_017413	Hs.303084	glutamate receptor, metabotropic 3	11.9
	453941	U39817	Hs.36820	apelin; peptide ligand for APJ receptor	11.8
	424120	T80579	Hs.290270	Bloom syndrome ESTs	11.8
	418738	AW388533	Hs.6682	solute carrier family 7, (cationic amino	11.7 11.7
50	411305	BE241596	Hs.69547	myelin basic protein	11.7
	424945	AJ221919		hypothetical protein FLJ10582	11.6
	449539	W80363	Hs.58446	ESTs	11.5
	409638	AW450420	Hs.21335	ESTs	11.5
	441016	AW138653	Hs.25845	ESTs .	11.4
55	429037	XB1895	Hs.194765	H.sapiens GENX-5624 mRNA, 3" UTR	11.3
	407034	U84540		gb:Human dystrobrevin isoform DTN-3 (DTN	11.2
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	11.2
	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	11.2
60	424432	AB037821	Hs.146858	protocadherin 10	11.1
UU	424893 425649	AW295112	Hs.153648	Homo sapiens cDNA FLJ13303 fis, clone OV	11.1
	438380	U30930	Hs.158540	UDP glycosyltransferese 8 (UDP-galactose	11.1
	423678	T06430	Hs.6194	chondroitin sulfate proteoglycen BEHAB/b	11,1
	446692	AW963357 Z44514	Hs_7847	ESTs .	10.7
65	430691	C14187	Un 102620	Homo sapiens mRNA for KIAA1763 protein,	10.7
~~	428728	NM_016625	Hs.103538	ESTS	10.7
	427701	AA411101	Hs.191381 Hs.243886	hypothetical protein	10.6
	431988	AC002302	Hs.77202	nuclear autoantigenic sperm protein (his protein kinase C, beta 1	10.6
	433896	AW294729	Hs.274461	ESTs	10.5
70	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (I	10.5
_	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	10.4
	445041	T64183	Hs.282982	solute certier	10.3
	445782	AI553048	Hs.144006	ESTs	10.3 10.2
	451952	AL120173	Hs.301663	ESTs .	10.2 10.2
75	446711	AF169692	Hs.12450	protocadherin 9	10.1
	438054	AA776626	Hs.169309	EST6	10.1
	443785	AW449952	Hs.190125	basic-helix-loop-helix-PAS protein	10.1
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	10.0
00	419863	AW952691	Hs.93485	Homo sepiens mRNA; cDNA DKFZp761D191 (fr	10.0
80	416857	AA188775	Hs.292453	ESTs	10.0
	435191	R15912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	10.0
	419271	N34901	Hs.238532	ESTs	9.9
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	9.9



	415293	R49462	Hs.106541	ESTs	9.9
	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	9.8
	452526 427304	W38537	Hs.280740	hypothetical protein MGC3040	9.8
5	420547	AA761526 AF155140	Hs.163853 Hs.98738	ESTs .	9.7
3	421659	NM_014459	Hs.106511	gonadotropin-regulated testicular RNA he	9.6
	426847	S78723	Hs.298623	protocedherin 17 5-hydroxytryplamine (serotonin) receptor	9.6
	429656	X05608	Hs.211584	neurofilament, tight polypeptide (68kD)	9.6 9.5
	447101	N72185	Hs.44189	ESTs	9.5
10	442613	AID04002	Hs.130522	Kv channel-interacting protein 1	9.5
	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	9.5
	445102	AW204610	Hs.22270	ESTs	9.5
	435793	AB037734	Hs.4993	KIAA1313 protein	9.5
15	437948	AA772920	Hs.303527	ESTs	9.5
15	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	9.4
	415170	R44386	Hs.164578	ESTs	9.3
	415486 435501	H12214 AW051819	Hs.13284	ESTs. Weakly similar to 2109260A B cell	9.2
	415072	AL110370	Hs.129908 Hs.79000	KIAA0591 protein growth associated protein 43	9.2
20	442910	Al365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	9.2
	438080	AA777381	Hs.291530	ESTs, Wealty similar to ALUC_HUMAN !!!!	9,1 9,1
	425187	AW014486	Hs.22509	ESTs	9.1
	424028	AF055084	Hs.153692	Homo sapiens cONA FLJ14354 fis, clone Y7	9.0
25	430091	AB032958	Hs.233023	KIAA1132 protein	9.0
25	427540	R12014	Hs.20976	ESTs	9.0
	447198	D61523	Hs.283435	ESTs	9.0
	449611	A1970394	Hs.197075	ESTs	8.9
	444124	R43097	Hs.6818	ESTs	8.9
30	451996 45404B	AW514021 H05626	Hs.245510	ESTs	8.8
20	412266	N59006	Hs.6921 Hs.26133	ESTs ESTs	8.8
	433597	AA708205	Hs.100343	ESTs	8.8
	447342	Al199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	8.7 8.6
	450154	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	8.6
35	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyl	8.5
	423135	N67655	Hs.26411	ESTs	8.5
	418097	R45137	Hs.21868	ESTs	8.4
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	8.4
40	419721	NM_001650	Hs.288650	aquaporin 4	8.4
40	449300	A1656959	Hs.346514	ESTs	8.4
	436954 425354	AA740151 U62027	Hs.130425	ESTs	8.3
	424997	AL138167	Hs.155935	complement component 3a receptor 1	8.3
	442710	AI015631	Hs.96920 Hs.23210	ESTs ESTs	8.3
45	449625	NM_014253	75.23210	odz (odd Oz/ten-m, Drosophila) homolog 1	8.2
	451625	R56793	Hs.106576	elanine-glyoxyfata aminotransferase 2-li	8.2 8.2
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	8.D
	449605	AW138581	Hs.198416	ESTs	8.0
50	407886	AW969688	Hs.100826	ESTs	8.0
50	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	7.9
	429946	R49390	Hs.254129	KIAA1678	7.9
	400293	N51002	Hs.306480	Homo sapiens mRNA; cDNA DKFZp761E2112 (f	7.9
	455601 409799	AI368680 D11928	Hs.816	SRY (sex determining region Y)-box 2	7.9
55	415279	F04237	Hs.76845 Hs.1447	phosphoserine phosphatase-like	7.8
	429918	AW873986	Hs.119383	glial fibrillary acidic protein ESTs	7.8
	449433	AI672096	Hs.9012	ESTs, Wealthy similar to \$26650 DNA-bindi	7.8 7.8
	422411	AW749443	Hs.22511	ESTs	7.7
60	448902	245998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp76111912 (f	7.7
60	452355	N54926	Hs.29202	G protein-coupled receptor 34	7.7
	447414	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	7.7
	407168	R45175	Hs.117183	ESTs	7.6
	448555	AI536697	Hs.159863	ESTs	7.6
65	428536 408947	AI143139 AL080093	Hs.2288	visinin-like 1	7.6
0.5	420352	U79734	Hs.49117 Hs.97206	Homo saplens mRNA; cDNA DKFZp564N1662 (f	7.6
	435624	AF218942	Hs.24889	huntingtin interacting protein 1 formin 2	7.6
	440105	AA694010	Hs.6932	Homo saplens clone 23809 mRNA sequence	7.6
	412068	S72043	Hs.73133	metaflothionein 3 (growth inhibitory fac	7.6 7.6
70	445568	H0091B	Hs.268744		7.5
	417160	N76497	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	7.5
	423361	AW170055	Hs.47628	ESTs	7.5
	456965	AW131888	Hs.172792	ESTs. Weakly similar to hypothetical pro	7.5
75	458332	AI000341	Hs.220491	ESTs	7.4
15	409902	AI337658	Hs.156351	EST8	7.3
	448321	NM_005883	Hs.20912	adenomatous polyposis coli like	7.3
	420345 402855	AW295230	Hs.25231	ESTS	7.3
	424481	R19453	Hs.1787	NM_001839*:Homo saplens calponin 3, acid	7.2
80	425741	AF052152	Hs.159412	proteolipid protein 1 (Pelizaeus-Merzbac Homo sepiens clone 24828 mRNA sequence	7.2 7.2
	448986	H42169	Hs.347310	hypothetical protein FLJ14627	7.2
	415651	AI207162	Hs.3815	stathmin-fike-protein RB3	7.2
	412709	AL022327	Hs.74518	KIAA0027 protein	7.1

	451521	A1879148	Hs.26770	fatty acid blinding protein 7, brain	7.1
	445745	AB007924	Hs.13245	KIAAD455 gene product	7.1
	439451 418030	AF085270 BE207573	Hs.278554	heterochromatin-like protein 1	7,1
5	400292	AA250737	Hs.83321 Hs.72472	neuromedin 8	7.1
_	407748	AL079409	Hs.38176	BMP-R1B KIAA0606 protein; SCN Circadian Oscillat	7.1
	440435	AL042201	Hs.21273	transcription factor NYD-sp10	7.0
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	7.0 7.0
10	417417	F05745	Hs.89512	ATPase, Ca transporting, plasma membrane	7.0
10	440152	AB002376	Hs.7006	KIAA0378 protein	7.0
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	7.0
	454293	H49739	Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	7.0
	447197 426814	R36075 AF036943	No 473510	gb:yh88b01.s1 Soares placenta Nb2HP Homo	7.0
15	416836	D54745	Hs.172619 Hs.80247	myelin transcription factor 1-Bus	6.9
	447350	Al375572	Hs. 172634	cholecystokinin ESTs	6.9
	440074	AA863045	Hs.10669	ESTs. Weakly similar to T00050 hypotheti	6.9
	436039	AW023323	Hs.121070	ESTs	6.9 6.9
20	444398	T65213	Hs.4257	ESTs	6.9
20	425234	AW152225	Hs.165909	ESTs, Wealdy similar to 138022 hypotheti	6.9
	438330	AW450572	Hs.257316	ESTs	6.8
	410305	AF030409	Hs.62185	solute carrier family 9 (sodium/hydrogen	6.B
	421141 412788	AW117261	Hs.125914	ESTs	6.7
25	411078	AA120960 AJ222020	Hs.198416 Hs.182364	ESTs Composition	6.7
	443455	AB001025	Hs.9349	CocoaCrisp ryanodine receptor 3	6.7
	448769	N66037	Hs.38173	ESTs	6.7
	441523	AW514263	Hs.301771	ESTs, Wealty similar to ALUF_HUMAN !!!!	6.7 6.7
20	414214	D49958	Hs.75819	glycoprotein M6A	6.6
30	439845	AL355743	Hs.56663	Homo saplens EST from clone 41214, full	6.6
	437036	AI571514	Hs.133022	ESTs	6.6
	429239 434164	AA448419	Hs.45209	ESTs	6.6
	412155	AW207019 R38167	Hs.148135	serine/threonine kinase 33	6.6
35	452834	AI638627	Hs.12449 Hs.105685	Homo sapiens transmembrane protein HTMP1 KIAA1688 protein	6.5
	441916	AA993571	Hs.129075	ESTs .	6.5
	451516	AI800515	Hs.12024	ESTs	6.5 6.5
	434808	AF155108	Hs.256150	Homo saplens, Similar to RIKEN cDNA 2810	6.5
40	452461	N78223	Hs.108106	transcription factor	6.5
40	450375	AA009647		a disintegrin and metalloproteinase doma	6.4
	434811	AW971205	Hs.114280	ESTs	6.4
	424624 429250	AB032947	Hs.151301	Ca2+dependent activator protein for secr	6.4
•	414245	H56585 BE148072	Hs.198308	tryptophan rich basic protein	6.3
45	433447	U29195	Hs.75850 Hs.3281	WAS protein family, member 1	6.3
	424922	BE386547	Hs.217112	neuronal pentraxin II hypothetical protein MGC10825	6.3
	426919	AL041228		ELAV (embryonic lethal, abnormal vision,	6.3 6.3
	411411	AA345241	Hs.55950	ESTs, Wealdy similar to KIAA1330 protein	6.3
50	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	6.2
30	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	6.2
	433929 423346	Al375499	Hs.27379	ESTs	6.2
	448148	AI267677 NM_016578	Hs.127416 Hs.20509	synaptojanin 1	6.2
	412140	AA219691	Hs.73825	HBV pX associated protein-8 RAB6 interacting, kinesin-like (rabkines	6.2
55	409731	AA125985	Hs.56145	Onymosin, beta, Identified in neuroblast	6.2
	420608	BE548277	Hs.103104	ESTs	6.2 6.2
	424085	NM_002914	Ha.139226	replication factor C (activator 1) 2 (40	6.2
	422175	N79885	Hs.6382	ESTs. Highly similar to T00391 hypotheti	6.1
60	428845 439274	AL157579	Hs.153610	KIAA0751 gene product	6.1
00	447499	AF086092 AW262580	Hs.48372 Hs.147674	ESTs	8.1
	425977	R15138	Hs.165570	protocadherin beta 16	6.1
	453924	R49295	Hs.24886	Homo sapiens clone 25052 mRNA sequence ESTs	6.1
	449340	AW235786	Hs.195359	hypothetical protein MGC10954	6.1 6.1
65	420077	AW512260	Hs.87767	ESTs	6.1
	431721	AB032996	Hs.268044	KIAA1170 protein	6.1
	433701	AW445023	Hs.15155	ESTs	6.1
	430968 429469	AW972830	11- 07	gb:EST384925 MAGE resequences, MAGL Horno	6.1
70	456723	M64590 Z43902	H\$.27	glycine dehydrogenase (decarboxylating;	6.1
	448681	AL109781	Hs.4748 Hs.21754	adenylate cyclase activating polypeptide Homo sapiens mRNA full length insert cDN	6.0
	429900	AA460421	Hs.30875	ESTs	6.0
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALUS_HUMAN A	6.0 6.0
75	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	6.0
75	448243	AW369771	Hs.52620	integrin, beta 8	6.0
	415427	BE244050	Hs.79307	Rac/Cdc42 guarine exchange factor (GEF)	6.0
	419704 436936	AA429104	Hs.45057	ESTs	6.0
	428409	AL134451 AW117207	Hs.197478	ESTs EST-	6.0
80	433244	AB040943	Hs.98523 Hs.271285	ESTs KIAA1510 protein	6.0
	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cON	6.0
	408096	BE250162	Hs.83765	dihydrofotate reductase	6.0 6.0
	419929	U90268	Hs.93810	cerebral cavernous matformations 1	6.0

	422544 413627	AB018259	Hs.118140	KIAA0716 gene product	6.0
	413627	BE 182082 H66373	Hs.246973 Hs.5856	ESTs	6.0
	410366	AI267589	Hs.302689	ESTs, Highly similar to bA393J16.3 [H.sa hypothetical protein	6.0 6.0
5	429183	AB014604	Hs.197955	KIAA0704 protein	5.9
	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DXFZp564B083 (tr	5.9
	441102	AA973905		intermediate fitament protein syncollin	5.9
	448533	ALT 19710	Hs.21365	nucleosome assembly protein 1-like 3	5.9
10	407182	AA312551	Hs.230157	ESTS	5.9
10	437372 433523	AA323968	Hs.283631	hypothetical protein DKFZp547G183	5.9
	444165	H29882 AL137443	Hs.10441	ESTs hypothescal protein FLJ11236	5.9
	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	5.9 5.9
	420156	AW449258	Hs.6187	ESTs	5.9
15	422864	AA318323	Hs.12827	gb:EST20390 Retina II Homo sapiens cDNA	5.8
	446727	AB011095	Hs.16032	KIAA0523 protein	5.8
	448543	AW897741	Hs.21380	Homo saplens mRNA; cDNA DKFZp586P1124 (I	5.8
	430132 425782	AA204686 U66468	Hs.234149	hypothetical protein FLJ20647	5.8
20	419629	AB020695	Hs.159525 Hs.91662	cell growth regulatory with EF-hand doma KIAA0888 protein	5.8
	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	5.8 5.8
	407608	AA663559	Hs.279789	histone deacetylase 3	5.8
	414737	AI160386	Hs.125087	ESTs	5.8
25	432154	AI701523	Hs.112577	ESTs	5.8
23	410099 411379	AA081630 A/816344	U- 17554	KIAA0036 gene product	5.8
	440492	R39127	Hs.12554 Hs.21433	ESTs, Wealdy similar to NPL4_HUMAN NUCLE hypothetical protein DKFZp547J036	5.8
	424560	AA158727	Hs.150555	protein predicted by clone 23733	5.7 5.7
	419498	AL036591	Hs.20887	hypothetical protein FLJ10392	5.7
30	436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	5.7
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (5.7
	419088 436109	AI538323 AA922153	Hs.52620	integrin, beta 8	5.7
	428588	F12101	Hs.132760 Hs.185701	hypothetical protein MGC15729 Homo sapiens mRNA full length insert cDN	5.7 5.7
35	451752	AB032997	Hs.26966	KIAA1171 protein	5.7
	413492	D87470	Hs.75400	KIAA0280 protein	5.7
	414683	S78296	Hs.76888	hypothetical protein MGC12702	5.6
	418079	R40058	Hs.6911	ESTs	5.6
40	445873 437034	AA250970 AA742643	Hs.251946	poly(A)-binding protein, cytoplasmic 1-4 gb:ny91c01.s1 NCI_CGAP_GCB1 Homo sepiens	5.6
	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo segien	5.6 5.6
	452785	AL359942	Hs.296434	erythroid differentiation and denucleati	5.6
	408081	AW451597	Hs.167409	ESTs	5.6
45	436887	AW953157	Hs. 193235	hypothetical protein DKFZp547D155	5.6
73	413589 418506	AW452631 AA084248	Hs.313803 Hs.85339	ESTs, Highly similar to AF157833 1 noncl	5.6
	433556	W56321	Hs.111460	G protein-coupled receptor 39 calcium/calmodufin-dependent protein kin	5.6 5.5
	448299	AA497044	Hs.20887	hypothetical protein FLJ 10392	5.5
50	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	5.5
50	447773	AI423930	Hs.36790	ESTs, Weakly similar to putative p150 (H	5.5
	422421 453128	AA325138 AW026516	Hs.235873	hypothetical protein FLJ22672	5.5
	453220	AB033089	Hs.31791 Hs.32452	acylphosphatase 2, muscle type Homo sapiens mRNA for KIAA1263 protein,	5.5
	440866	A1703103	Hs.271360	hypothetical protein MGC16275	5.5 5.4
55	428976	AL037824	Hs.194695	ras homolog gene family, member I	5.4
	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	5.4
	452799	AI948829	Hs.213786	ESTs	5.4
	429038 445255	AL023513 NM_014841	Hs.194766 Hs.12477	seizure related gene 6 (mouse)-like	5.4
60	424332	AA338919	Hs.101615	synaptosomal-associated protein, 91 kDa ESTs	5.4 5.4
	440210	AW674562	Hs.125296	ESTs	5.4
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	5.4
	448935	AL078596	Hs.22591	nuclear receptor subfamily 2, group E, m	5.4
65	452786 408790	R61362 AW580227	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	5.4
05	423476	AL035633	Hs.47860	neurotrophic tyrosine kinase, receptor,	5.4
	448507	AL133109	Hs.21333	Human DNA sequence from ctone RP5-1046G1 Homo saplens mRNA; cDNA DKFZp566N1047 (f	5.4
	419683	AA248897	Hs.48784	ESTs	5.4 5.4
~^	407728	AW071502	Hs.175931	ESTs	5.4
70	453313	BE005771	Hs.153746		5.4
	422094	AF129535	Hs.272027	F-box only protein 5	5.4
	452856 434792	AF034799 AA649253	Hs.30881 Hs.132458	protein tyrosine phosphatase, receptor t	5.4
_	412190	R16180	Hs.274461		5.4
75	425588	F07396	Hs.46627	EST4	5.3 5.3
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	5.3
	429698	A1685086	Hs_26339	ESTs, Weakly similar to S21348 probabte	5.3
	424458	M29273	Hs.1780	myelin associated glycoprotein	5.3
80	446997 427302	AA383439 AA400540	Hs.16758 Hs.135282	Spir-1 protein	5.3
	439607	BE540565	Hs.159460		5.3 5.3
	448499	BE613280	Hs.77550	hypothetical protein MGC1780	5.3
	410037	AB020725	Hs.58009	KIAA0918 protein	5.3
				0.40	

	451407	AA131376	Hs.343809	fibroblast growth factor 128	5.3
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	5.3
	428784	Y12851	Hs.193470	purinergic receptor P2X, tigand-gated to	5.3
5	418512	AW498974		diacylglycerol kinase, zeta (104kD)	5.3
,	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	5.3
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	5.2
	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	5.2
	404819	AA380153		NM_002688*:Homo saplens peanut (Orosophi	5.2
10	426503	AA380153		gb:EST93093 Skin turnor I Homo sapiens cD	5.2
10	405348 431552	AJ815863	LL 150072	C7001664:gi 12698061 db BAB21849.1 (AB	5.2
	418677	S83308	Hs.259873	axonal transport of synaptic vesicles	5.2
	427250	R35941	Hs.87224	SRY (sex determining region Y)-box 5	5.2
	428037	N47474	Hs.25418	ESTs	5.2
15	445740	T78281	Hs.69230 Hs.13226	potassium Intermediate/smail conductance	5.2
	430130	AL137311	Hs.234074	Homo sepiens clone 25181 mRNA sequence	5.2
	423859	BE409301	Hs.134012	Homo sapiens mRNA; cDNA DKFZp761G02121 (5.2
	416220	N49776	Hs.170994	C1q-related factor hypothetical protein MGC10946	5.2
	457005	AJ007421	Hs.172597	sal (Drosophila)-like 3	5.2
20	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.1
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	5.1 5.1
	410631	AA086469	Hs.47171	ESTs Consequence paraceas (55720	5.1
	414821	M63835	Hs.77424	Fc tragment of IgG, high affinity ta, re	5.1
	420133	AA426117	Hs.155543	ESTs	5.1
25	453884	AA355925	Hs.35232	KIAA0186 gene product	5.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	5.1
	414727	BE466904	Hs.190162	gb:hz28f03.x1 NCI_CGAP_GC6 Homo sapiens	5.1
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	5.1
20	437387	AI198874	Hs.28847	AD026 protein	5.0
30	400533			ENSP00000209376":PRED65 protein (Fragmen	5.0
	430979	AI479755	Hs.129010	ESTs	5.0
	448944	AB014605	Hs.22599	etrophin-1 interacting protein 1; activi	5.0
	444600	R41398	Hs.6996	ESTs	5.0
35	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	5.0
33	428878	AA436884	Hs.48926	ESTs	5.0
	444670	H58373	Hs.332938	hypothetical protein MGC5370	5.0
	440471	AAB86146	Hs.307944	ESTs	5.0
	410434 441390	AF051152	Hs.63668	toll-like receptor 2	5.0
40	448765	Al692560 R15337	Hs.131175	ESTS	4.9
10	422263	AA307639	Hs.21958	Homo sapiens mRNA; cONA DKFZp547D086 (fr	4.9
	431117	AF003522	Hs.129908 Hs.250500	KIAA0591 protein	4.9
	407235	D20569	Hs.169407	delta (Drosophila)-like 1	4.9
	417404	NM_007350	Hs.82101	SAC2 (suppressor of actin mutations 2, y	4.9
45	448548	R13209	Hs.21413	pleckstrin homology-like domain, family	4.9
	420092	AA814043	Hs.88045	solute carrier family 12, (potassium-chi ESTs	4.9
	449571	AW016812	Hs.200266	ESTs	4.9 4.9
	412811	H06382		ESTs	4.9 .
	409100	H98216	Hs.42245	ESTs, Moderately similar to 138022 hypot	4.9
50	403142			NM_002706*:Homo sapiens protein phosphat	4.9
	414300	Al304870	Hs.188680	ESTs	4.9
	436607	AW661783	Hs.211061	ESTs	4.9
	431553	X78075	Hs.2799	cartilage linking protein 1	4.9
66	449328	AI962493	Hs.345303	ESTs	4.9
55	420805	L10333	Hs.99947	reticulon 1	4.9
	421688	AK000307	Hs.106825	hypothetical protein FLJ20300	4.9
	452898	AA814497	Hs.78792	ESTs	4.9
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	4.9
60	432328	AI572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	4.9
50	408453 428841	AI369838 AI418430	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	4.8
	416439	AA180363	Hs.104935	ESTs	4.8
	447458	AI741082	Hs.118769 Hs.158961	ESTs CCT-	4.8
	429433	AA452899	Hs.213586	ESTS	4.8
65	409746	NM_004794	Hs.56294	ESTs, Weakly similar to KIAA1353 protein	4.8
	436511	AA721252	Hs.291502	RAB33A, member RAS oncogene family ESTs	4.8
	443392	AI055821	Hs.293420	ESTs	4.8
	423600	AI633559	Hs.310359	ESTS	4.8 4.8
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	
70	414706	AW340125	Hs.76989	KIAA0097 gene product	4.8 4.8
	407385	AA610150	Hs.272072	ESTs, Weakly similar to 138022 hypotheti	4.B
	439340	AB032436	Hs.6535	brain-specific Na-dependent inorganic ph	4.7
	427624	AA406245	Hs.24895	ESTs	4.7
25	413248	T64858	Hs.21433	hypothetical protein DKFZp547J036	4.7
75	408670	AF160967	Hs.45784	potassium large conductance calcium-acti	4.7
	440491	R35252	Hs.130558	ESTs, Wealthy similar to 2109260A B cell	4.7
	411555	AF113537	Hs.70669	HMP19 protein	4.7
	430471	AF064845	Hs.241523	hypothetical protein FLJ10142	4.7
80	413530	AA130158	Hs.19977	ESTs, Moderately similar to ALUB_HUMAN A	4.7
οU	445900	AF070526	Hs.125036	Homo sapiens clone 24787 mRNA sequence	4.7
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	4.7
	459527	AW977556	Hs.291735	ESTs, Weakly similar to 178885 serine/th	4,7
	453096	AW294631	Hs.11325	ESTs	4.7

	400125	0.2000	11- 242502		
	409125 428001	R17258 H97428	Hs.343567 Hs.219907	exonal transport of synaptic vesicles ESTs, Moderately similar to Transforming	4.7 4.7
	410276	A1554545	Hs.68301	Engiopoietin-2	4.7
5	421637	AF035290	Hs.106300	Homo sapiens clone 23556 mRNA sequence	4.7
10	421633 440052	AF121860 AI633744	Hs.106260	sorting nextn 10	4.7
	439566	AF086387	Hs.195648	ESTs, Weakly similar to I38022 hypotheti gb:Homo saplens full length insert cDNA	4.7 4.7
	432890	NM_014442	Hs.279751	siafic acid binding Ig-like lectin 8	4.6
	402145	*******		Target Exon	4.6
	409892 458760	AW956113 AJ498631	Hs.7149 Hs.111334	gb:EST368183 MAGE resequences, MAGD Homo	4.6
	453362	H14988	Hs.107375	ferritin, light polypeptide ESTs	4.6 4.6
	436734	AI937612	Hs.273758	hypothetical protein FLJ23112	4.6
15	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	4.6
	409041 428832	AB033025 AA578229	Hs.50081 Hs.324239	Hypothetical protein, XP_051850 (KIAA119 ESTs, Moderately similar to ZN91_HUMAN 2	4.6
	423770	AW976766	Hs.132776	Homo sapiens cDNA FLJ 10077 fis, clone HE	4.6 4.6
	410264	AK001853	Hs.61508	Homo sapiens cDNA FLJ10991 fis, clone PL	4.6
20	429149 437762	AW193360 T78028	Hs.197962	ESTs, Wealdy similar to I38022 hypotheti	4.6
	439249	AF086060	Hs.154679 Hs.170053	synaptotagmin I G-protein coupled receptor 88	4.6 4.6
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	4.6
	425256	BE297611	Hs.155392	collapsin response mediator protein 1	4.6
25	415257 428186	F03016 AW504300	Hs.27513 Hs.295605	ESTs	4.6
	458814	Al498957	Hs.170861	mannosidase, alpha, class 2A, member 2 ESTs. Weakly similar to Z195_HUMAN ZINC	4.6 4.6
	451320	AW118072		diacylglycerol kinase, zeta (104kD)	4.5
	424998 422709	U58515 AA315331	Hs.154138	chitinase 3-like 2	4.5
30	420578	AA813546	Hs.153485 Hs.99034	ESTs GTP-binding protein Rho7	4.5 4.5
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	4.5
	457465	AW301344	Hs.122908	DNA replication factor	4.5
	427712 444656	Al368024 Al277924	Hs.283696 Hs.145199	ESTs ESTs	4.5
35	413409	AI638418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	4.5 4.5
	429399	AA452244	Hs.16727	ESTs	4.5
	450639	AI703186	Hs.277174	ESTs	4.5
	452106 424240	AJ141031 AB023185	Hs.21342 Hs.143535	ESTs calcium/calmodulin-dependent protein kin	4.5 4.5
40	433009	AA761668	12.14000	gb:nz24c08.s1 NCI_CGAP_GC81 Homo sapiens	4.5
	446657	AJ335191	Hs.260702	ESTs, Weakly similar to 2109260A B cell	4.5
	428189 423178	AA424030 AI033140	Hs.46627 Hs.124983	ESTS	4.5
	445133	AW157646	Hs.198689	Homo sapiens mRNA; cDNA DKFZp564C142 (fr ESTs	4.5 4.5
45	418771	AA807881	Hs.25329	ESTs	4.4
	438456	AA913381	Hs.20594	ESTs	4.4
	410386 413834	W26187 BE295896	Hs.3327 Hs.224179	Homo sapiens cONA: FLJ22219 fis, clone H ESTs, Weakly similar to I38022 hypotheti	4.4
	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	4.4 4.4
50	420560	AW207748	Hs.59115	ESTs	4.4
	439662 408577	H97552 H50572	Hs.269060 Hs.19515	ESTs ESTs, Highly similar to NRG3_HUMAN PRO-N	4.4
	445034	AW293376	Hs.143659	ESTS	4.4 4.4
55	402605			Target Exon	4.4
33	426271 457561	AF026547 AA331517	Hs.169047 Hs.286055	chondraitin sulfate proteoglycan 3 (neur	4.4
	430676	AF084866	FIS.200033	chimerin (chimaerin) 2 gb:Homo sapiens envelope protein RIC-3 (4.4 4.4
	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.4
60	452752 439108	AW044058	Hs.33578	KIAA0820 protein	4.4
00	405819	AW163034	Hs.6467	synaptogyrin 3 NM 002578-Moreo explore n21 /CDY-N153 and	4.4
	446544	AI631932	Hs.7047	NM_002578:Homo sapiens p21 (CDKN1A)-acti ESTs, Weakly similar to Unknown [H.sapie	4.4 4.4
	412530	AA756268	Hs.266273	hypothetical protein FLJ13346	4,4
65	420871 408622	AA702972 AA056060	Hs.65300 Hs.202577	ESTs	4.4
	429269	AA449013	Hs.99203	Homo sepiens cDNA FLJ12166 fis, clone MA ESTs	4.4
	427463	AA442224	Hs.97900	ESTs	4.3 4.3
	425402	AI215881	Hs.24970	ESTs. Weakly similar to B34323 GTP-bindi	4.3
70	412046 427194	Y07847 AA399018	Hs.73088 Hs.250835	RAS-related on chromsome 22 ESTs	4.3
	437834	AA769294	Hs.283854	gb:nz35g03.s1 NCI_CGAP_GC81 Homo saplens	4.3 4.3
	409172	299399	Hs.122593	EST8	4.3
	409953 426968	AA332277	Hs.57691	cadherin 18, type 2	4.3
75	452092	U07616 BE245374	Hs.173034 Hs.27842	amphiphysin (Stiff-Mann syndrome with br hypothetical protein FLJ11210	4.3
	438458	AW975186		gb:EST387294 MAGE resequences, MAGN Homo	4.3 4.3
	446936	H10207	Hs.47314	ESTs .	4.3
	433932 424800	AW954599 AL035588	Hs.169330		4.3
80	421988	AW450481	Hs.153203 Hs.161333		4.3 4.3
	442832	AW206560	Hs.253569	ESTs	4.3
	416586	D44843	Hs.14144	secreted modular calcium-binding protein	4.2
	408369	R38438	Hs.182575	solute carrier family 15 (H7?? transport	4.2

	450530	NM_006668	Hs.25121	cytochrome P450, subfamily 46 (cholester	4.2
	449318	AW236021	Hs.78531	Homo saplens, Similar to RIKEN cONA 5730	4.2
	438624	AA889055	Hs.123468	ESTs	4.2
•	421027	AA761198	Hs.55254	ESTs .	4.2
5	417632	R20855	Hs.5422	glycoprotein M6B	4.2
	419412	AW161058	Hs.90297	synuclein, beta	4.2
	430228	AW950939	Hs.6382	ESTs, Highly similar to T00391 hypotheti	4.2
	450813	AJ739625	Hs.203376	ESTs	4.2
10	412505	AA974491	Hs.21734	ESTs	4.2
10	440158	AA868507	Hs.126141	ESTs	4.2
	441707	R42637	Hs.21963	hypothetical protein DKFZp761B0514	4.2
	438703	AI803373	Hs.31599	ESTs	4.2
	444127	N63620	Hs.13281	ESTs	4.2
15	447397	BE247676	Hs.18442	E-1 enzyme	4.2
IJ	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	4.2
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	4.2
	416871	H98716 Al669535	Hs.40369	gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	4.2
	408838 425287		Hs.155524	ESTS	4.2
20	404584	R88249	ns.133324	peanut (Drosophila)-like 2	4.2
20	436035	AA703679	Hs.106999	Target Exon	4.2
	409091	AW970386	Hs.269423	ESTs, Wealthy similar to SYT5_HUMAN SYNAP	4.2
	437117	AL049256	Hs.122593	ESTs ESTs	4.2
	429643	AA455889	Hs.167279	FYVE-linger-containing Rab5 effector pro	4.2
25	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	4.2
	408177	AJ241733	Hs.43871	ESTs	4.2
	438875	AA827840	Hs.189059	ESTs	4.2 4.2
	447877	AJ435184	Hs.164252	ESTs	4.2
	415402	AA164687	Hs.177576	mannosyl (alpha-1,3-)-glycoprotein beta-	4.2
30	434859	BE255080	Hs.299315	collapsin response mediator protein-5; C	4.2
	449714	AB033015	Hs.23941	KIAA1189 protein	4.2
	427315	AA179949	Hs.175563	Homo saplens mRNA; cDNA DKFZp564N0763 (f	4.2
	404541			NM_030795:Homo sapiens stathmin-like 4 (4.1
	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fis, clone PL	4.1
35	422374	AW732869	Hs.1519	protein kinase, cAMP-dependent, regulato	4.1
	422253	W81526	Hs.118329	ESTs. Moderately similar to GAD_HUMAN GA	4.1
	440483	AJ200836	Hs.150386	ESTs	4.1
	429421	AL031658		Hurnan DNA sequence from done RP1-310013	4.1
40	432882	NM_013257	Hs.279696	serum/glucocorticold regulated kinase-li	4,1
40	424001	W87883	Hs.137476	paternally expressed 10	4.1
	422170	AI791949	Hs.112432	anti-Mullerian hormone	4.1
	445292	AV653264	Hs.13982	Homo sapiens cDNA FLJ14666 fis, clone NT	4.1
	450407	NM_000810	Hs.24969	gamma-aminobutyric acid (GABA) A recepto	4,1
45	429401	AW296102	Hs.99272	ESTs, Weakly similar to S32567 A4 protei	4.1
43	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	4.1
	415796	R87548	Hs.78854	ATPase, Na? transporting, beta 2 polypep	4.1
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.1
	457211 416547	AW972565	Hs.32399	ESTs. Weakly similar to S51797 vasocilat	4.1
50	412777	H62914 Al335773	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	4.1
20	445225	AJ216555	Hs.270123	ESTs	4,1
	408926	AF217525	Hs.202398 Hs.49002	ESTs	4.1
	417873	BE266659	Hs.293659	Down syndrome cell adhesion molecule	4.1
	443301	AJ733614	Hs.220587	Homo sapiens, Similar to RIKEN cDNA A430 ESTs, Moderately similar to ALU5_HUMAN A	4.1
55	429281	AA830856	Hs.29808	Homo saplens cDNA: FLJ21122 fis, clone C	4.1 4.1
	448966	AW372914	Hs.66149	phosphoinositol 3-phosphate-binding prot	4.1
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.1
	417355	D13168	Hs.82002	endothelin receptor type B	4.1
60	410359	R38824	Hs.106313	ESTs	4,1
60	426529	AF090100	Hs.170241	Homo sapiens clone IMAGE 23915	4.1
	433323	AA805132	Hs.159142	ESTs	4.1
	434933	R91095	Hs.4276	KIAA1701 protein	4.1
	453331	AJ240665		ESTs	4.1
65	422661	NM_014700	Hs.119004	KIAA0665 gene product	4.1
03	424726	AK001007	Hs.138760	Homo sapiens cDNA FLJ10145 fis, clone HE	4.0
	415805	F13271	Hs.79981	Human clone 23560 mRNA sequence	4.0
	441797	A1936933	Hs.214635	ESTa	4.0
	424282	R76421	Hs.135694	ESTS	4.0
70	407792	AI077715	Hs.39384	putative secreted ligand homologous to I	4.0
, 0	425390	AI092634 A 1243396	Hs.156114	protein tyrosine phosphatase, non-recept	4.0
	435312 424635	AJ243396	Hs.4865	voltage-gated sodium channel beta-3 subu	4.0
	423279	AA420687 AW959861	Hs.115455 Hs.290943	Homo sapiens cONA FLJ14259 fis, clone PL	4.0
	444001	AVV959881 AI095087		ESTS	4.0
75	410768	AF038185	Hs.152299 Hs.66187		4.0
	426413	AA377823	13.0010/	Homo sapiens clone 23700 mRNA sequence	4.0
	450581	AF081513	Hs.25195	gb:EST90805 Synovial sercoma Homo saplen TGF-beta 4	4.0
	435854	AJ278120	Hs.4996		4.0
	433615	AA732982	Hs.269607	putative ankyrin-repeat containing prote ESTs, Weakly similar to ALU1_HUMAN ALU S	4.0
80	432058	AW665996	Hs.130729	ESTs, Weakly similar to ALUI_HUMAN ALU S	4.0
	439774	AL360257	Hs.213493		4.0
	445668	R59960	Hs.282386	ESTs	4.0 4.0
	450582	Al339732		G-rich RNA sequence binding factor 1	4.0
					7.0

	437814	AI088192	Hs.135474	ESTA WASHINGTON TO POVO LUMAN APO O	
	451468	AW503398	Hs.293663	ESTs, Weakly similar to DDX9_HUMAN ATP-D	4.0
	449277	AA001064	Hs.43670	ESTs, Moderately similar to I38022 hypot ESTs	4.0
	440553	AA889416	Hs.344043	Homo saplens cDNA FLJ14459 fls, clone HE	4.0 4.0
5	445888	AF070564	Hs.13415	Homo sapiens clone 24571 mRNA sequence	4.0
_	420111	AA255652		gb:zs2th11.r1 NCI_CGAP_GCB1 Homo sepiens	4.0
	407198	H91679		gb:yv04a07.s1 Soares total liver spleen	4.0
	422564	AI148006	Hs.222120	ESTs	4.0
• •	443992	AW022228	Hs.322922	ESTS	4.0
10	435542	AA687376		ESTs .	4.0
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	4.0
	437748	AF234882	Hs.5814	suppression of turnorigenicity 7	4.0
	439285	AL133916		hypothetical protein FLJ20093	4.0
15	449655	AI021987	Hs.59970	ESTs	4.0
13	458435	A1418718	Hs.144121	ESTs. Weakly similar to T45916 hypotheti	4.0
	412659 423905	AW753865	Hs.74376	olfactomedin related ER localized protei	4.0
	432683	AW579960 AW995441	Hs.135150 Hs.10475	lung type-I cell membrane-associated gly	4.0
	410765	AI694972	Hs.66180	ESTs nucleosome assembly protein 1-like 2	4.0
20	420649	AJ866964	Hs.124704	ESTs, Moderately similar to S65657 alpha	4.0
	450927	AI807804	Hs.134342		4.0 4.0
	448985	AA324885	Hs.22777	carbonic anhydrase XI	4.0
	415406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	4.0
	412754	AW160375	Hs.74565	emyloid beta (A4) precursor-like protein	3.9
25	416340	N31772	Hs.79226	fasciculation and elongation protein zet	3.9
	428862	NM_000345	Hs.2316	SRY (sex determining region Y)-box 9 (ca	3.9
	413554	AA319145	Hs.75426	secretogranin II (chromogranin C)	3.9
	419687	A1638859	Hs.227699	ESTs, Wealthy similar to T2D3_HUMAN TRANS	3.9
20	453438	AJ469935	Hs.22792	ESTs	3.9
30	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.9
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	3.9
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	3.9
	41 1666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	3.9
35	439935	S75105	Hs.8358	glutamate receptor, lonotropic, kainate	3.9
22	459278	AW294559	Hs.34054	Home sapiens cDNA: FLJ22488 fis, clone H	3.9
	432809	AA565509	Hs.131703	ESTs	3.9
	450568 413951	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	3.9
		AW051200	Hs.75640	natriuretic peptide precursor A	3.9
40	435743 447937	T66881 AL109716	Hs.12952	ESTs	3.9
40	417576	AA339449	Hs.20034	Homo sapiens mRNA full length insert cDN	3.9
	448526	AB028945	Hs.82285 Hs.21361	phosphoribosylghycinamide formyltransfer	3.9
	445890	AF055019	Hs.21906	KIAA1023 protein	3.9
	425241	AA324624	Hs.155247	Homo sapiens clone 24570 mRNA sequence	3.9
45	417333	AL157545	Hs.173179	aldolase C, fructose-bisphosphate bromodomain and PHD finger containing, 3	3.8
	435832	AA425688	Hs.41641	Bruno (Drosophila) -like 4, RNA binding	3.8 3.8
	410592	R94088	Hs.43569	ESTs	3.8
	443361	AJ792628	Hs.133273	ESTs	3.8
~ ^	403696			C4001100":gi[5852342]gb]AAD54015.1] (AF0	3.8
50	437756	AA767537	Hs.197096	ESTs	3.8
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	3.8
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	3.8
	425652	AB021742	Hs.322431	neurogenic differentiation 2	3.8
55	437449	AL390153	Hs.208339	Homo sapiens mRNA; cDNA DKFZp752G113 (fr	3.8
"	421040	AA715026	Hs.135280	ESTs	3.8
	454171 443740	AW854832	U- 34884	gb:QV2-CT0261-201099-011-05 CT0261 Homo	3.8
		R56434	Hs.21062	ESTs	3.8
	441558 423175	AI611973 W27595	Hs.136313 Hs.347310	ESTS	3.8
60	457183	H91882	Hs.118569	hypothetical protein FLJ14627	3.8
- •	438142	T90309	Hs.269651	DvI-binding protein IDAX (inhibition of ESTs	3.8
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	3.8
	436899	AA764852	Hs.291567	ESTs	3.8 3.8
	456497	AW967956	Hs.123648	ESTs. Weakly similar to AF108460 1 utimu	3.8
65	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	3.8 3.8
	413199	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	3.8
	410711	AB002316	Hs.65746	KIAA0318 protein	3.8
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	3.8
70	438944	AA302517	Hs.92732	KIAA1444 protein	3.8
70	445078	AI869975	Hs.4775	junctophilin 3	3.8
	424330	AW073953	Hs.333396		3.8
	439099	AB037800	Hs.6462	protein kinase C and casein kinase subst	3.8
	449444	AW818435	Hs.23590	solute carrier family 16 (monocarboxylic	3.8
75	411252	AB018549	Hs.6932B	MD-2 protein	3.7
75	448275	BE514434	Hs.20830	kinesin-like 2	3.7
	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	3.7
	400777	41666 104		NM_007325*:Homo sapiens glutamate recept	3.7
	419586	A1088485	Hs.144759		3.7
80	458072	AI890347	Hs.271923		3.7
30	445908	R13580	Hs.13438	Homo sepiens clone 24425 mRNA sequence	3.7
	448451 430183	AW015994	Hs.345433		3.7
	430147	BE010038 R60704	U. 024404	gb:PM3-BN0176-100400-001-g04 BN0176 Homo	3.7
	-30147	1400704	Hs.234434	hairy/enhancer-of-split related with YRP	3.7

	458912	AJ911066		ESTs	3.7
	428110	AI312485	Hs.138294	ESTs, Moderately similar to Z195_HUMAN Z	3.7
	448048	BE281291	Hs.170408	ESTs, Moderately similar to A47582 B-cel	3.7
5	442326 422798	H92962 R92347	Hs.124813 Hs.34574	hypothetical protein MGC14817	3.7
-	428873	Al701609	Hs.98908	ESTs, Weakly similar to ALUI_HUMAN ALU S ESTs	3.7 3.7
	438208	ALD41224	Hs.65379	ESTs	3.7
	414040	N58513	Hs.32171	ESTs .	3.7
10	407846 408829	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	3.7
10	425010	NM_006042 T16837	Hs.48384 Hs.4241	heparan suffate (glucosamine) 3-O-suffot ESTs	3.7 3.7
	427209	H06509	Hs.92423	KIAA1566 protein	3.7
	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	3.6
15	410126	BE169274		KIAA0036 gene product	3.6
13	426646 418329	AA382787 AW247430	Hs.122713 Hs.84152	ESTs	3.6
	419390	AJ701162	Hs.90207	cystathionine-beta-synthase hypothetical protein MGC11138	3.6 3.6
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	3.6
20	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	3.6
20	448425 423611	AI500359 AB011163	Hs.346112 Hs.129908	ESTs	3.6
	438831	BE263273	Hs.6439	KIAA0591 protein synapsin II	3.6 3.6
	419235	AW470411	Hs.288433	neurotrimin	3.6
25	451027	AW519204	Hs.40808	ESTs	3.6
25	428483 424947	AI908539	Hs.184592	KIAA0344 gene product	3.6
	404150	R77952		ESTs, Wealthy similar to atternatively sp Target Exon	3.6
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.6 3.6
20	443715	AI583187	Hs.9700	cyclin E1	3.6
30	435910	AI084152	Hs.21782	ESTs, Wealthy similar to ALU7_HUMAN ALU S	3.6
	418064 432488	BE387287 AA551010	Hs.83384 Hs.216640	S100 catclum-binding protein, beta (neur ESTs	3.6
	431342	AW971018	Hs.21659	ESTs	3.6 3.6
25	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.6
35	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRN	3.6
	448448 447818	NM_014954 W79940	Hs.21239 Hs.21906	KIAA0985 protein Homo sapiens clone 24670 mRNA sequence	3.6
	445105	AF238869	Hs.283955	Homo sapiens clone GLSH-2 similar to gli	3.6 3.6
40	409557	BE182896	Hs.211193	ESTs	3.6
40	425202	AW962282	Hs.152049	ESTs, Wealdy similar to I38022 hypotheti	3.6
	451734 425331	NM_006176 AW962128	Hs.26944	neurogranin (protein kinase C substrate,	3.6
	412799	A1267606		gb:EST374201 MAGE resequences, MAGG Homo gb:aq91h03.x1 Stanley Frontal SB pool 1	3.6 3.6
	435040	AI932350	Hs.152825	ESTs	3.6
45	434149	Z43829	Hs.244624	hypothetical protein MGC5469	3.6
	415709 424051	AA649850	Hs.278558	ESTs	3.6
	437640	AL110203 AA764893	Hs.138411 Hs.272155	Homo sapiens mRNA; cDNA DKFZp586J1922 (f ESTs, Wealdy similar to I38022 hypotheti	3.6 3.6
	445953	AI612775	Hs.145710	ESTs	3.6
50	449256	AA059050	Hs.59847	ESTs .	3.6
	424687 409327	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.6
	417675	L41162 AI808607	Hs.53563 Hs.3781	collagen, type IX, alpha 3 similar to murine leucine-rich repeat pr	3.6
	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-ti	3.6 3.6
55	443912	R37257	Hs.184780	ESTS	3.6
	424572	M19650	11. 440000	2,3-cyclic nucleotide 3' phosphodieste	3.5
	424899 439726	AL119387 AW449893	Hs.119062 Hs.293707	ESTs Workly similar to 129609 vian for	3.5
	416490	AF090116	Hs.79348	ESTs, Weakly similar to 138598 zinc fing regulator of G-protein signatting 7	3.5 3.5
60	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	3.5
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.5
	407624 419038	AW157431 AW134924	Hs.248941 Hs.190325	ESTs ESTs	3.5
	451489	NM_005503		amyloid beta (A4) precursor protein-bind	3.5 3.5
65	428242	H55709	Hs.2250	leukemia Inhibitory factor (cholinergic	3.5
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	3.5
	435575 424340	AF213457	Hs.44234	triggering receptor expressed on myeloid	3.5
	425790	AA339036 AW136286	Hs.7033 Hs.288446	ESTs ESTs	3.5 3.5
70	432188	Al362952	Hs.2928	solute carrier family 7 (cationic amino	3.5
	453898	AW293483	Hs.255205	KIAA1853 protein	3.5
	434784	AA649051	Hs.164007		3.5
	452449 425212	AW068658 AW962253	Hs.20943 Hs.171618	ESTs ESTs	3.5
75	407253	ANY302253 AA411175	Hs.141939		3.5 3.5
	418049	AA211467	Hs.190488	Homo sapiens, Similar to nuclear localiz	3.5
	421247	BE391727	Hs.102910	general transcription factor IIH, potype	3.5
	459311 439450	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	3.5
80	435545	R51613 AA687415	Hs.125304 Hs.28107	ESTs ESTs	35
	445729	H21066	Hs.13223	Homo sepiens mRNA full length insert cON	3.5 3.5
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	3.5
	412590	AL134388	Hs.135033	ESTs, Weakly similar to 138022 hypotheti	3.5

				•	
	438527	AI969251	Hs.115325	RAS7, member RAS oncogene family-like 1	3.5
	441111	AI806867	Hs.126594	ESTs	3.5
	418630	AI351311	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	3.5
5	439920	H05430	Hs.288433	neurotrimin	3.5
3	421268	AI126821	Hs.30514	ESTs	3.5
	432022 412719	AL162042	Hs.272348	Homo sepiens mRNA; cONA DKFZp761L1212 (1	3.5
	435092	AW016610 AL137310	Hs.816 Hs.4749	EST8	3.5
	414178	AW957372	Hs.46791	Homo sepiens mRNA; cDNA DKF2p761E13121 (3.5
10	437252	AI433833	Hs. 164159	ESTs, Wealdy similar to I38022 hypotheti ESTs, Wealdy similar to ALU1_HUMAN ALU S	3.5
	452108	AW135982	Hs.203013	hypothetical protein FLJ12748	3.5 3.4
	421183	AL135740	Hs.102447	TSC-22-like	3.4
	441834	AL138034	Hs.7979	KIAA0736 gene product	3.4
	413812	AW188687	Hs.44748	ESTs	3.4
15	449932	AI675444	Hs.263024	ESTs	3.4
	447067	R42098	Hs.21964	ESTs	3.4
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.4
	447028	AJ973128	Hs.167257	brain link protein-1	3.4
20	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	3.4
20	418358	L02840	Hs.84244	potassium voltage-gated channel, Shab-re	3.4
	417084	H08370	Hs.33067	ESTs	3.4
	444534	AW271626	Hs.42294	EST8	3.4
	440700 436637	AW952281	Hs.296184	guanine nucleotide binding protein (G pr	3,4
25	412820	A1783629 BE001238	Hs.26766	ESTs	3.4
~-	428138	AA773842	Hs.293799	gb:CM3:BN0075-240200-101-d11 BN0075 Homo ESTs	3.4
	453033	AA325869	Hs.31463	KIAA0281 gene product	3.4 3.4
	453305	R39224	Hs.267997	EHM2 gene	3.4
	459660	M79082		ESTs	3.4
30	418821	AA435002	Hs.183161	ESTs	3.4
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	437085	AA743935	Hs.202329	ESTs	3.4
35	419852	AW\$03756	Hs.286184	hypothetical protein dJ551D2.5	3.4
33	430694	AA810624	Hs.30936	ESTs, Weakly similar to H2BH_HUMAN HISTO	3.4
	441287	AW293132	Hs.131373	EST8	3.4
	425870 443672	R13406	Hs.56782	ESTs	3.4
	448044	AA323362 AI458682	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	3.4
40	405238	A1430002		gbtk13e01.x1 NCI_CGAP_Lu24 Homo sepiens	3.4
٠٠.	440404	AJ0158B1	Hs.324527	Targel Exon mitochondrial ribosomal protein \$5	3.4 3.4
	453590	AF150278	Hs.33578	KIAA0820 protein	3.4
	450756	A1733488	Hs.144062	ESTs	3.4
	404283			ENSP00000244751*:Copine-like protein KIA	3.4
45	423257	AW161039	Hs.125878	synapsin (I)	3.4
	432149	AW614326	Hs.133483	ESTs, Weakly similar to T34549 probable	3.4
	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	3.4
	422809	AK001379	Hs.121028	hypothetical protein FLJ 10549	3.4
50	420050	AL118615	Hs.94653	neurochondrin	3.4
50	431789	H19500	Hs.269222	milogen-activated protein kinase 4	3.4
	408601	U47928	Hs.86122	protein A	3.4
	453740 449919	AL120295	Hs.311809	ESTs, Moderately similar to PC4259 femi	3.4
	426380	A1674585 A1291267	Hs.200141	ESTs	3.4
55	408554	AAB36381	Hs.149990 Hs.315111	ESTs nuclear receptor co-repressor/HDAC3 comp	3.4
-	443257	AI334040	Hs.11614	HSPC065 protein	3.3
	432731	R31178	Hs.287820	fibronectin 1	3.3 3.3
	421679	AJ475110	Hs.203933	ESTs	3.3
~~	453169	AB037815	Hs.32156	KIAA1394 protein	3.3
60	437397	AA349847	Hs.4221	hypothetical protein DKFZp761H039	3.3
	443310	BE552018	Hs.133152	EST:	3.3
	423169	BE047009	Hs.21837	ESTs, Wealthy similar to KIAA0927 protein	3.3
	433657	AJ244368	Hs.8124	PH domain containing protein in retine 1	3.3
65	408449	NM_004408	Hs.166161	dynamin 1	3.3
03	417402	8E503227	Hs.134759	ESTs	3.3
	416677	T83470	Hs.334840	ESTs, Moderately similar to 178885 serin	3.3
	439753 455646	BE262233	Hs.7423	hypothetical protein from EUROIMAGE 2168	3.3
	450337	BE054420 A1693256	Hs.202427	gb:RC4-BT0311-241199-012-c08 BT0311 Hamo ESTs	3.3
70	423420	AI571364	Hs.128382		3.3
. •	433236	NM_004296	Hs.3221	Homo sapiens mRNA; cDNA DKFZp76111224 (f regulator of G-protein signalfing 6	3.3 3.3
	417868	A1078534	Hs.122592	ESTs	3.3 3.3
	438207	AA334774	Hs.12845	hypothetical protein MGC13159	3.3
-	441607	NM_005010	Hs.7912	neuronal cell adhesion motocule	3.3
75	449249	T52285	Hs.193115		3.3
	418216	AA682240	Hs.283099		3.3
	456060	C14904	Hs.45184	Homo sapiens cDNA FLJ12284 ffs, clone MA	3.3
	449145	AJ632122	Hs.198408	ESTs	3.3
80	415101	R45531	Hs.144534		3.3
30	401272	41530000		C9000559*:gij12314195 emb CAB99338.1 (A	3.3
	420297	A1628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	419991 443761	AJ000098 AI525743	Hs.94210	eyes absent (Drosophila) homolog 1	3.3
	773101	MULLITAD	Hs.345187	ESTs	3.3

			475700	MA A A MAN	
	427317 426920	AB028955 AA393351	Hs.175780 Hs.132121	KIAA1032 protein ESTs	3.3 3.3
•	433894	AI907682	Hs.243293	ESTS	3.3
	454253	AV660717	Hs.47144	DKFZP586N0819 protein	3.3
5	419647	AA348947	Hs.91816	hypothetical protein	3.3
	439978	BE139460	Hs.124673	Homo sepiens cDNA FLJ11477 fis, clone HE	3.3
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	3.3 3.3
	428670 435375	AA431682 AJ733610	Hs.134832 Hs.187832	ESTs ESTs	3.3
10	419043	T19167	Hs.89566	ets variant gene 1	3.3
	403341		14.00000	Target Exon	3.3
	436282	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	3.3
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	3.3
1.5	456209	W60633	Hs.297792	ESTs	3.3
15	438810	AW897846	Hs.6421	hypothetical protein OKFZp761N09121	33
	411565 418203	AW851728 X54942	Hs.83758	gb:MR2-CT0222-011199-007-d06 CT0222 Homo CDC28 protein kinase 2	3.3 3.3
	451254	AJ571016	Hs.172967	ESTs	3.3
	435056	AW023337	Hs.5422	glycoprotein M6B	3.3
20	433842	AJ652156	Hs.26346	ESTs	3.3
	433325	AW206986	Hs.143905	ESTs	3.3
	451066	A1758660	Hs.206132	ESTS	3.3
	436114 421688	AA778232 AB011156	Hs.19515 Hs.106794	ESTs, Highly similar to NRG3_HUMAN PRO-N KIAA0584 protein	3.3 3.3
25	429228	AI553633	Hs.326447	ESTS .	3.3
	450325	AI935962	Hs.26289	ESTs	3.3
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	3.3
	451778	AJ826131	Hs.62954	ESTs. Wealdy similar to zinc finger prot	3.3
20	435977	AL138079	Hs.5012	brain-specific membrane-anchored protein	3.2
30	450475 418661	AW805634 NM_001949	Hs.205015 Hs.1189	ESTs	3.2 3.2
	436480	AJ271643	Hs.87469	E2F transcription factor 3 putative acid-sensing ion channel	3.2
	407332	AI801565	Hs.200113	Homo sapiens cDNA FLJ11379 fls, clone HE	3.2
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	3.2
35	409248	AB033035	Hs.51965	KIAA1209 protein	3.2
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	3.2
	434834 450358	AF156774 AB010098	Hs.324020 Hs.24907	1-acytglycerol-3-phosphate O-acytransfe coronin, actin-binding protein, 28	3.2 3.2
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	3.2
40	405239	U89281	15200015	oxidative 3 alpha hydroxysteroid dehydro	3.2
	407304	AA565832	Hs.271649	gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens	3.2
	451697	AW449774	Hs.296380	POM (POM121 rat homolog) and ZP3 fusion	3.2
	435071	D60683	Hs.35495	ESTs	3.2
45	420352	BE258835	U- 1440E7	gb:601117374F1 NIH_MGC_16 Homo sapiens c	3.2 3.2
45	412193 442320	AI684467 AI287817	Hs.144057 Hs.129636	ESTs ESTs	3.2
	407378	AA299264	Hs.57776	ESTs, Moderately similar to (38022 hypot	3.2
	414528	AA148950	Hs.188836		3.2
	439764	T26535	Hs.22744	hypothetical protein MGC13105	3.2
50	410425	BE278367	Hs.63510	KIAA0141 gene product	3.2
	429876	AB028977	Hs.225974		3.2 3.2
	427627 439039	R87582 A1656707	Hs.179915 Hs.48713	guanine nucleotide blinding protein (G pr ESTs	3.2
	447925	AW292271	Hs.250718		3.2
55	447714	AW296313	Hs.255537		3.2
	434574	AI424458	Hs.33470	ESTs	3.2
	437269	AA334384	Hs.149420		3.2
	416845 452234	H95279 AW084176	Hs.293788 Hs.223298		3.2 3.2
60	440274	R24595	Hs.7122	scrapie responsive protein 1	3.2
•	437698	R61837	Hs.7990	ESTs, Moderately similar to 184505 calci	3.2
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.2
	445828	F05802	Hs.81907	ESTs	3.2
65	423779	AW071837	Hs.57971	ESTs	3.2
ŲJ	403790 453792	AL134539	Hs.254129	NM_001334*:Homo sapiens cathepsin O (CTS) KIAA1678	3.2 3.2
	428167	AA770021	Hs. 16332	ESTs	3.2
	445413	AA151342	Hs.12677	CGI-147 protein	3.2
~~	415314	N88802	Hs.5422	glycoprotein MGB	3.2
70	425115		Hs.123956		3.2
	432625		Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	412420 422772		Hs.73853 Hs.12022	bone morphogenetic protein 2 B KIAA0749 protein	3.1 3.1
	437414				3.1
75	427961				3.1
-	435256	AF193766	Hs.13872	cytokina-lika protein C17	3.1
	428966		Hs.19468		3.1
	413995				3.1
80	443431		Hs.20654		3.1 3.1
50	414217 419617		Hs.27989 Hs.91622		3.1
	444326		Hs.27071		3.1
	436315				3.1

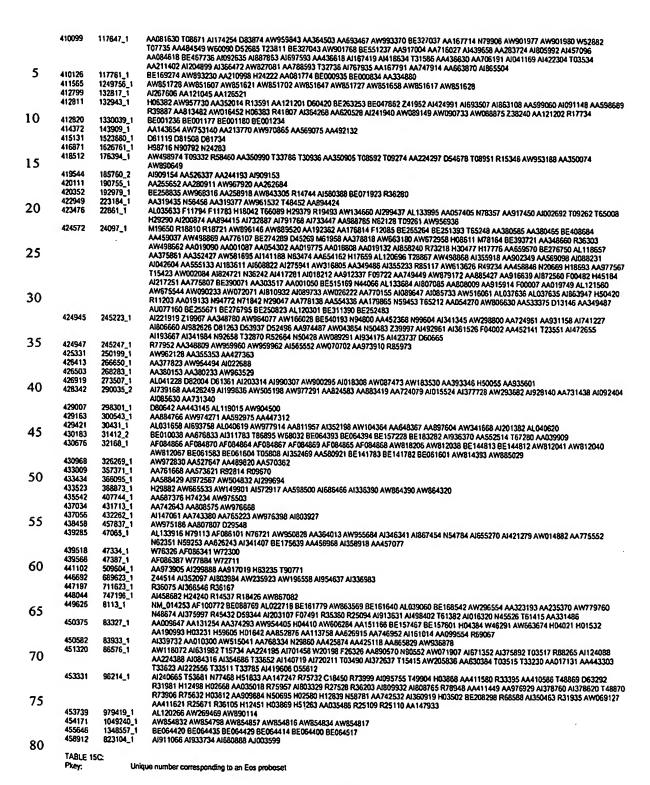
Pkey CAT Number Accession

PCT/US02/29560

	446131	NM_000929	Hs.290	phospholipase A2, group V	3.1
	423858	AL137326	Hs.133483	Homo saplens mRNA; cDNA DXFZp43480650 (f	3.1
	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	3.1
5	432682	AI376400	Hs.159588	ESTs	3.1
,	450661 417636	AW952160 R08916	Hs.83849 Hs.191212	ESTs ESTs	3.1 3.1
	417918	AA209205	Hs. 163754	hypothetical protein FLJ12606	3.1
	454032	W31790	Hs.194293	ESTs, Wealthy similar to 154374 gene NF2	3.1
10	443150	AJ034467	Hs.34650	ESTs	3.1
10	404532			NM_022490:Homo sepiens hypothetical prot	3.1
	425537	AB007913	Hs.158291	KIAA0444 protein	3.1
	437162 400090	AW005505	Hs.5464	thyroid hormone receptor coactivating pr Eos Control	3.1 3.1
	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	3.1
15	422949	AA319435		gb:EST21657 Adrenal gland turnor Homo sap	3.1
	448750	U95020	Hs.21903	calcium channel, voltage-dependent, beta	3.1
	433560 433042	AI925195	Hs.130891	hypothetical protein MGC4400	3.1
	449722	AW193534 BE280074	Hs.281895 Hs.23960	Homo sapiens cDNA FLJ11660 fls, clone HE cyclin B1	3.1 3.1
20	425480	AB023198	Hs.158135	KIAA0981 protein	3.1
-	449670	F07693	Hs.85603	Homo sapiens mRNA; cDNA DKFZp434K2172 (f	3.1
	452619	AWZ98597	Hs.61884	Horno sapisns, clone IMAGE:4298026, mRNA,	3.1
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	3.1
25	405605 417565	AI203405	Hs.47831	C2001342gi 127814 sp P26434 NAH4_RAT SO ESTs	3.1 3.1
	439538	AA837323	Hs.56407	ESTs	3.1
	414117	W88559	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	3.1
	430818	AJ311928	Hs.348156	gb:qo89h04.x1 NCI_CGAP_IGd5 Homo sapiens	3.1
30	408508 414884	AI806109 R54418	Hs.135736	KIAA1580 protein	3.1
50	439963	AW247529	Hs.183745 Hs.6793	hypothetical protein FLI 13456 platelet-activating factor acetylhydrola	3.1 3.1
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	3.1
	417169	R13550	Hs.246773	ESTs	3.1
35	450202	AW969756	Hs.34145	ESTs, Wealdy similar to 849647 GTP-bindi	3.1
33	428060 430526	AA420615 AF181862	Hs.249483 Hs.242407	ESTS	3.1
	421458	NM_003654		G protein-coupled receptor, family C, gr carbohydrate (keratan suffate Gal-6) suf	3.1 3.1
	429163	AA884766		gb:arn20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.0
40	428180	A1129767	Hs.182874	guanine nucleotide binding protein (G pr	3.0
40	422631 433290	BE218919 R20077	Hs.118793 Hs.302185	hypothetical protein FLJ10688	3.0
	412507	L36645	Hs.73964	Homo sapiens clone 23618 mRNA sequence EphA4	3.0 3.0
	415827	H17462	Hs.23079	ESTs	3.0
45	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	3.0
43	457358 441732	AJ479755 AW298818	Hs.129010 Hs.127341	ESTs ESTs	3.0
	459318	NM_000038		gb:Homo sapiens adenomatosis polyposis c	3.0 3.0
	426384	A1472078	Hs 303662	hypothetical protein FLJ13189 (FLJ13189)	3.0
50	436267	AW450938	Hs.180115	EST8	3.0
50	450650 414865	T65617 AA157155	Hs.101257 Hs.274414	hypothetical protein MGC3295	3.0
	459080	AW192083	Hs.290855	hypothetical protein FLJ14457 ESTs	3.0 3.0
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.0
55	432593	AW301003	Hs.51483	ESTs, Weakly similar to hypothetical pro	3.0
33	443753 445921	AW367578	Hs.134749	ESTs	3.0
	427695	AW015211 R88483	Hs.146181 Hs.172862	ESTs ESTs	3.0 3.0
	438283	Al458931	Hs.37282	ESTs	3.0
60	453324	W26592	Hs.232089	ESTs	3.0
60	421094	AW978202	Hs.289064	hypothetical protein FLJ22251	3.0
	433434 452850	AA588429 H23230	Hs.22481	gb:no22b03.s1 NCI_CGAP_Pr22 Homo sepiens	3.0
	416658	U03272	Hs.79432	ESTs, Moderately similar to A46010 X-lin fibrillin 2 (congenital contractural ara	3.0 3.0
	429569	AA454993	Hs.138343	ESTs, Wealthy similar to 178885 serine/th	3.0
65	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	3.0
	443833	AL031290	Hs.9654	similar to pregnancy-associated plasma p	3.0
	433229 429046	AB040925 X57436	Hs.91625 Hs.194772	KIAA1492 protein	3.0
	431431	AL096711	Hs.252953		3.0 3.0
70	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.0
	423165	AI937547	Hs.124915	hypothetical protein MGC2601	3.0
	440261	M81886	Hs.7117	glutamate receptor, ionotropic, AMPA 1	3.0
	441364 437058	AW450466 AI147061	Hs.126830	ESTs, Weakly similar to YD38_YEAST HYPOT gb:ok33a11.s1 Soares_NSF_F8_9W_OT_PA_P_S	3.0
75	429168	AA984682	Hs.146589	ESTs, Weakly similar to JC5238 galactosy	3.0 3.0
_	453739	AL120266		ESTs	3.0
	TABLE	160-			
	TABLE 1 Pkey:		iqua Fos ombo	set identifier number	
80	CAT num	nber: Go	ene chuster num	ber	
	Accessio	on: Ge	inbank accessi	on numbers	

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	Ref:	Sequ	ience source. T	he 7 digit numbers in this column are Genbank Ide	ntifier (GI) numbers.	*Dunham, et al.* refers to the publication entitled "The DNA
	Character (sequ	ence of human	chromosome 22" Dunham, et al. (1999) Nature 402		
_	Strand: Nt_position			I from which exons were predicted. positions of predicted exons.		
5	-					
	Pkey 400533	Ref 6981826	Strand	Nt_position		
	400533	8131663	Minus Plus	277132-277595 70745-71121		
	401272	9797373	Minus	98374-98509		
10	402145	8018280	Plus	113086-114800		
	402604 402605	9909420 9909420	Plus	20393-20767		
	402855	9662953	Minus Minus	47680-47973 59763-59909		
	403142	9444521	Plus	89286-90131		
15	403341	8569175	Phys	30699-30910		
	403696 403790	3135242 8084957	Minus Minus	143467-143634 87826-87947,89835-90002		
	404150	7534008	Plus	165811-165943		
	404283	2276311	Minus	99460-99564		
20	404541	8318559	Plus	103456-103664		
	404584 404632	9857511 9796668	Plus Plus	138651-139153		
	404819	4678240	Plus	45096-45229 16223-16319,16427-16513,16736-16859,16941-	17075.17170-17287.1	7389-17529 18261-18357 18443-18578
	405238	7249119	Minus	51728-51836		7555-17520,10201-10021,10440-10070
25	405239	7249119	Plus	144345-144464,144690-144836,151750-151883,	152407-152484	
	405348 405605	2914717	Minus	43310-43462		
	405819	5836195 4007557	Minus Plus	117070-117270 2830-2967		
••				2000-2001		
30						
	Table 164	A: ABOUT 85	GENES UP-R	EGULATED IN GUOBLASTOMA MULTIFORMA C	OMPARED TO NOR	MAL CENTRAL NERVOUS SYSTEM ous system (CNS). These were selected from 59680 probesets on
						ster than or equal to 3.0. The "average" GBM level was set to the
ā.c	85th percer	ntile amongst v	rarious GBM tun	nors. The "average" normal CNS tissue level was a	set to the 85" percent	le amongst vrious CNS tissues. In order to remove gene-specific
35			-spacific hybridi	zation, the 10th percentile value amongst various or	on-malignant tissues v	was subtracted from both the numerator and the denominator before
	Pkey:	ras evaluated.	nua Eas probas	et identifier number		
	ExAcon:			n number, Genbank accession number		
40	Unigenet): Uni	gene number			
40	Unigene T		gene gene title	TO		
	R1:	Rai	IO OI GLIUBLAS	TOMA MULTIFORMA to CNS		
	Pkey	ExAcon	UnigeneiD	Unigene Title	•	RI
45	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,		47.2
45	422737	M26939	Hs.119571			44.9
	423961 433001	D13566 AF217513	Hs.136348 Hs.279905	periostin (OSF-2os) clone HQ0310 PRO0310p1		33.3 25.9
	449539	W80383	Hs.58446	ESTs		25.8
50	417308	H60720	Hs.81892	KIAA0101 gene product		23.3
50	424800	AL035588	Hs.153203	MyoD family inhibitor		23.0
	414825 431941	X06370 AK000106	Hs.77432 Hs.272227	epidermal growth factor receptor (avian Homo sapiens cDNA FLJ20099 fis, clone CO		19.6 18.7
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11		17.8
66	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2		17.8
55	428330 417130	L22524 AW276858	Hs.2256	matrix metalloproteinase 7 (matrilysin,		17.7
	414217	A1309298	Hs.81256 Hs.279898	S100 calcium-binding protein A4 (calcium Homo sapiens cDNA: FLJ23165 fis, clone L		17.5 17.0
	428242	H55709	Hs.2250	teukernia inhibitory factor (cholinergic		15.9
60	425397	J04088	Hs.156346	topoisomerase (DNA) Il alpha (170kO)		15.6
60	424835 408243	AA420687 Y00787	Hs.115455			15.2
	422672	X12784	Hs.624 Hs.119129	Interleukin 8 collegen, type IV, alpha 1	1	14,7 14,7
	434078	AW880709				14.6
65	409799	D11928	Hs.76845	phosphoserine phosphatase-like		14.2
03	414761 442432	AU077228 BE093589	Hs.77256	enhancer of zeste (Drosophila) homolog 2		14.2
	446584	U53445	Hs.38178 Hs.15432	downregulated in ovarian cancer 1		14.1
	444969	AJ203334	Hs.160628			13.5
70	430691	C14187	Hs.103538			12.9
70	426075 445101	AW513691			,,	12.4
	441269	T75202 AW015206	Hs.12314 Hs.178784	Homo sapiens mRNA; cDNA DKFZp586C1019 ESTs	(I	12.1 11.9
	417426	NM_00229		laminin, beta 1		11.9
26	430132	AA204886	Hs.234149	hypothetical protein FLJ20647		11.8
75	422163	AF027208				11.3
	411411 449722	AA345241 BE280074	Hs.55950 Hs.23960	ESTs, Weakly similar to KIAA1330 protein cyclin B1		11.3
	436291	BE568452				11.2 11.0
00	435020	AW505076	Hs.301855			10.9
80	412140	AA219691		RAB6 interacting, kinesin-like (rabkines		10.9
	419239 417043	AA468183 NM_00436		Homo sapiens cONA: FLJ23241 fis, clone C collagen, type VI, atpha 3		10.6
	413929	BE501689		collagen, type VI, arpha 3 collagen, type IV, alpha 2		10.6 10.6
					50	· ***
				7	3U	

	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	10.6
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	10.4
	406972 412986	M32053 X81120	Hs.75110	gb:Human H19 RNA gene, complete cds. cannabinoid receptor 1 (brain)	10.4 10.3
5	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	10.3
	449611	A1970394	Hs.197075	ESTs	10.1
	427581	NM_014788	Hs.179703	KIAA0129 gene product	10.1
	431512 429183	BE270734 AB014504	Hs.2795 Hs.197955	lactate dehydrogenase A KIAA0704 protein	9.9 9.8
10	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	9.7
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	9.7
	433800 433647	A1034361	Hs.135150	lung type-I cell membrane-associated gly	9.7
	414622	AA603367 AI752666	Hs.222294 Hs.76669	ESTs nicotinamide N-methyttransferase	9.7 9.5
15	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	9.3
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	9.3
	409902 450375	A1337658 AA009647	Hs.156351	ESTs a disintegrin and metalloproteinase doma	9.3 9.2
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	9.1
20	442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	9.1
	452461 434846	N78223 AW295389	Hs.108106 Hs.119768	transcription factor	9.1
	422158	L10343	Hs.112341	ESTs protease inhibitor 3, skin-derived (SKAL	9.1 9.0
25	425187	AW014485	Hs.22509	ESTs	9.0
25	443247 458079	BE614387 AI796870	Hs.333893	c-Myc target JPO1	8.7
	410276	AI554545	Hs.54277 Hs.68301	ONA segment on chromosome X (unique) 992 angiopoietin-2	8.7 8.6
	402855			NM_001839*:Homo sapiens calponin 3, acid	8.6
30	439710	AF086543		gb:Homo saplens full length insert cDNA	8.6
50	411968 410102	AJ207410 AW248508	Hs.69280 Hs.279727	Homo sapiens, clone (MAGE:3636299, mRNA, ESTs; homologue of PEM-3 (Ciona savignyi	8.6 8.6
	436895	AF037335	Hs.5338	carbonic anhydrase XII	8.6
	418203	X54942	Hs.83758	CDC28 protein kinase 2	B.6
35	416892 425234	L24498 AW152225	Hs.80409 Hs.165909	growth arrest and DNA-damage-inducible,	8.5
55	449961	AW265634	Hs.133100	ESTs, Wealdy similar to I38022 hypotheti ESTs	8.5 8.5
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	8.4
	417061 453884	A1675944 AA355925	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	8.3
40	424085	NM_002914	Hs.36232 Hs.139226	KIAA0186 gene product replication factor C (activator 1) 2 (40	8.3 8.2
	419938	AU076772	Hs.1279	complement component 1, r subcomponent	8.1
	411078	AJ222020	Hs.182364	CocoaCrisp	8.1
	406850 447726	AI624300 AL137638	Hs.172928 Hs.19368	collagen, type 1, alpha 1 matriin 2	8.0 8.0
45	439999	AA115811	Hs.6838	ras homotog gene family, member E	8.0
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural are	7.9
	439451 458814	AF086270 AI498957	Hs.278554 Hs.170861	heterochromatin-fike protein 1 ESTs, Weakly similar to Z195_HUMAN ZINC	7.9
	447004	AW296968	Hs.157539	ESTS. WELLOW SINES BY 2193_HOMON ZINC	7.9 7.9
50	436140	W87355	Hs.269587	ESTs	7.9
	436607 422809	AW661783 AK001379	Hs.211061 Hs.121028	ESTS .	7.8
	440052	AJ633744	Hs.195648	hypothetical protein FLI10549 ESTs, Wealdy similar to I38022 hypotheti	7.7 7.7
86	422106	D84239	Hs.111732	Fc fragment of IgG binding protein	7,7
55	418113 410286	AI272141 AI739159	Hs.83484 Hs.61898	SRY (sex determining region Y)-box 4	7.7
	424687	J05070	Hs.151738	DKFZP586N2124 protein matrix metalloproteinase 9 (gelatinase B	7.7 7.6
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	7.6
60	421988 452620	AW450481 AA436504	Hs.161333	ESTS	7.6
-	453941	U39817	Hs.119286 Hs.36820	ESTs Bloom syndrome	7.6 7.5
	416737	AF154335	Hs.79691	LIM domain protein	7.5
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	7.5
65	418400 437036	BE243026 AJ571514	Hs.301989 Hs.133022	KIAA0246 protein ESTs	7.5 7.5
	421899	AJ011895	Hs.109281	Nef-associated factor 1	7.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.4
	427528 427871	AU077143 AW992405	Hs.179565 Hs.59622	minichromosome maintenance deficient (S. Homo sapiens, clone IMAGE:3507281, mRNA,	7.4 7.3
70	448935	AL078596	Hs.22591	nuclear receptor subfamily 2, group E, m	7.3
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	7.3
	449571 427899	AW016812 AA829286	Hs.200266 Hs.332053	ESTs serum emyloid A1	7.3 7.1
	447458	A1741082	Hs.158961	ESTs	7.3 7.3
75	430630	AW269920	Hs.2621	cystatin A (stefin A)	7.2
	411252 432731	AB018549 R31178	Hs.69328 Hs.287820	MD-2 protein	7.2
	454117	BE410100	Hs.287820 Hs.40368	fibronectin 1 adaptor-related protein complex 1, sigma	7.2 7.2
90	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	7.2
80	428728	NM_016625		hypothetical protein	7.1
	416111 432281	AA033813 AK001239	Hs.79018 Hs.274263	chromatin assembly factor 1, subunit A (hypothetical protein FLJ10377	7.1 7.1
	410434	AF051152	Hs.63668	toll-like receptor 2	7.1

	420018	U56387	Hs.94376	and the second of the second o	
	418293	A1224483	Hs.16063	proprotein convertase subtilisin/kexin t hypothetical protein FLJ21877	7.1
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	7.1 7.0
_	445900	AF070526	Hs.125036	Homo saptens clone 24787 mRNA sequence	7.0 7.0
5	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	7.0
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	7.0
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	6.9
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	6.9
10	424381	AA285249	Hs.146329	protein kinase Chk2	6.9
10	410064	X53416	Hs.195464	filamin A, alpha (actin-binding protein-	6.9
	415682 421977	AI347128	Hs.191870	ESTs	6.9
	429447	W94197 AW812452	Hs.110165 Hs.83286	ribosomal protein L26 homolog	6.8
	423198	M81933	Hs.1634	ESTs, Wealthy similar to S14747 sphingomy cell division cycle 25A	6.8
15	413627	BE182082	Hs.246973	ESTs	6.8 6.8
	412777	AI335773	Hs.270123	ESTs	6.8
	409829	M33552	Hs.56729	lymphocyte-specific protein 1	6.8
	451129	BE072681		gb:RC2-BT0548-200300-012-e09 BT0548 Homo	6.8
20	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	6.7
20	446131	NM_000929	Hs.290	phospholipase A2, group V	6.7
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	6.7
	420311 425202	AW445044 AW962282	Hs.38207	Human DNA sequence from done RP4-530I15	6.7
	408161	AW952912	Hs.152049 Hs.300383	ESTs, Weakly similar to 138022 hypotheti	6.7
25	440704	M69241	Hs.162	hypothetical protein MGC3032 insufin-like growth factor binding prote	6.7
	407182	AA312551	Hs.230157	ESTs	6.7 6.7
	445837	AI261700	Hs.145544	ESTs	6.6
	433376	AJ249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	6.6
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	6.6
30	447439	AA313565	Hs.145020	ESTs. Wealthy similar to KIAA1205 protein	6.5
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	6.5
	450506	NM_004460		fibroblast activation protein, alpha	6.5
	432593	AW301003	Hs.51483	ESTs, Wealdy similar to hypothetical pro	6.5
35	418054 452799	NM_002318 AI948829	Hs.83354	lysyl oxidase like 2	6.5
55	446657	Al335191	Hs.213786 Hs.260702	ESTs Mindle similar to 24000504 P. and	6.5
	424247	X14008	Hs.234734	ESTs, Wealdy similar to 2109260A B cell	6.4
	443884	N20617	Hs.194397	lysözyme (renal amytoidosis) leptin receptor	6.4 6.4
	420560	AW207748	Hs.59115	ESTs	6.4
40	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	6.3
	420649	AI866964	Hs.124704	ESTs, Moderately similar to S65657 alpha	6.3
	457465	AW301344	Hs.122908	DNA replication factor	6.3
	440332	AI218517	Hs.188051	ESTs	6.3
45	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	6.3
43	413063	AL035737	Hs.75184	chilinase 3-like 1 (cartilage glycoprote	6.2
	448275 440286	BE514434	Hs.20830	kinesin-like 2	6.2
	439518	U29589 W76326	Hs.7138	cholinergic receptor, muscarinic 3	6.2
	412567	AI750979	Hs.74034	gb:zd60d04.r1 Soares_fetal_heart_NbHH19W Homo sapiens cione 24651 mRNA sequence	6.1
50	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	6.1 6.1
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	6.1
	428450	NM_014791	Hs.184339	KIAA0175 gene product	6.0
	412125	Y17114	Hs.73393	eyes absent (Orosophila) homotog 4	6.0
66	413786	AW613780	Hs.13500	ESTs	6.0
55	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	5.9
	400419 408380	AF084545		Target	5.9
	426108	AF123050 AA522037	Hs.44532	diubiquitin	5.9
	414774	X02419	Hs.166468 Hs.77274	programmed cell death 5	5.9
60	437695	AA769202	Hs.192142	plasminogen activator, urokinase ESTs	5.9 5.8
_	409463	AI458165	Hs.17296	hypothetical protein MGC2376	5.8 5.8
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	5.8
	443731	AI083928	Hs.145418	ESTs	5.8
65	405558			Target Exon	5.8
U.S	422094	AF129535	Hs.272027	F-box only protein 5	5.8
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	5.8
	425882 412471	U83115 M83193	Hs.161002 Hs.73946	absent in melanoma 1	5.8
	429149	AW193360		endothelial cell growth factor 1 (plate)	5.8
70	436827	H72187	Hs.197952 Hs.5322	ESTs, Weakly similar to 138022 hypothesi guanine nucleotide binding protein (G pr	5.8
-	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	5.7 5.7
	414053	BE391635	Hs.75725	transgelin 2	5.7
	435805	AA731533	Hs.270751	ESTs	5.7 5.7
75	442201	AW516704	Hs.208726	ESTs .	5.7
75	453361	AA035197	Hs.107375	ESTs	5.6
	429083	Y09397	Hs.227817	BCL2-related protein A1	5.6
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	5.6
	423081 407013	AF262992 U35637	Hs.123159	sperm essociated antigen 4	5.6
80	406478	44444		gb:Human nebulin mRNA, partial cds	5.5
	435937	AAB30893	Hs.119769	Target Exon ESTs	5.5
	453362	H14988	Hs.107375	ESTs	5.5 5.5
	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 ffs, clone PL	5.5 5.5
				•	



	440043				
	442547	AA306997	Hs.217484	ESTs, Weatly similar to ALU1_HUMAN ALU S	5.5
	443883 429643	AA114212 AA455889	Hs.9930	serine (or cysteine) proteinase inhibito	5.5
	407862	BE548267	Hs.167279 Hs.337986	FYVE-finger-containing Reb5 effector pro	5.5
5	407624	AW157431	Hs.248941	Homo sapiens cDNA FLJ10934 fls, clone OV ESTs	5.4 5. 4
_	448769	N66037	Hs.38173	ESTs	5.4
	417124	BE122762	Hs.25338	ESTS	5.4
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	5.4
	457292	AF921270	Hs.281462	hypothetical protein FLJ14251	5.3
10	418596	AW976721	Hs.293327	ESTs	5.3
	410295	AA741357	Hs.5174	midogen (enactin)	5.3
	433323	AA805132	Hs.159142	ESTs	5.3
	412326	R07566	Hs.73817	small inducible cytoldine A3 (homologous	5.3
15	418830	AI351311	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	5.3
1.5	420075 427676	AF142482 AA394062	Hs.203846 Hs.300772	TEA domain family member 3	5.2
	407729	T40707	Hs.270862	tropomyosin 2 (beta) ESTs	5.2
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	5.2 5.2
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	5.2
20	433556	W56321	Hs.111460	catclum/catmodulin-dependent protein kin	5.2
	424998	U58515	Hs.154138	chitinase 3-like 2	5.2
	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	5.2
	445118	AI208762	Hs.345572	ESTs	5.2
25	408523	AW833259	Hs.314287	ESTs	5.2
23	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	5.2
	449300 429732	AJ656959 U20158	Hs.346514 Hs.2488	ESTs	5.2
	423757	AL049337	Hs.132571	lymphocyte cytosofic protein 2 (SH2 doma	5.2
	439570	T79925	Hs.269165	Homo sapiens mRNA; cDNA DKFZp564P016 (fr ESTs, Weatly similar to ALU1_HUMAN ALU S	5.1
30	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	5.1 5.1
	443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	5.1
	421247	BE391727	Hs.102910	general transcription factor (IH, polype	5.1
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	5.1
25	419968	X04430	Hs.93913	interleukin 6 (Interferon, beta 2)	5.0
35	424009	F11690		gb:HSC30D041 normalized infant brain cDN	5.0
	418283	579895	Hs.83942	cathensin K (pychodysostosis)	5.0
	429469	M54590	Hs.27	glycine dehydrogenase (decarboxylating;	5.0
	417404 408829	NM_007350 NM_006042	Hs.82101	plackstrin homology-like domain, family	. 5.0
40	418097	R45137	Hs.48384 Hs.21868	heparan sulfate (glucosamine) 3-O-sulfot ESTs	5.0
,,,	453331	AI240665	ris.21000	ESTs	5.0
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	4.9 4.9
	426044	AA502490	Hs.170290	ESTs .	4.9
4 ~	444161	N52543	Hs.142940	ESTs	4.9
45	428227	AA321649	Hs.2248	small inducible cytokine subfamily 8 (Cy	4.9
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU \$	4.9
	447752	M73700	Hs.105938	tactotransferrin	4.9
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	4.9
50	402274 444656	AI277924	11- 445400	C19000498:gij4567179jgbjAAD23607.1jAC00	4.9
50	422087	X58968	Hs.145199 Hs.111301	ESTS	4.9
	443744	AI084326	Hs.271548	matrix metalloproteinase 2 (gelatinase A ESTs, Weakly similar to 178885 serine/th	4.9
	416871	H98716	113.27 1340	gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	4.9 4.9
	409112	BE243971	Hs.50849	quinone axidoreductase homolog	4.8
55	403481			Target Exon	4.8
	443740	R56434	Hs.21062	ESTs	4.8
	435005	U80743	Hs.306094	trinucleotide repeat containing 12	4.8
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Horno s	4.8
60	451418	BE387790	Hs.25369	hypothetical protein FLJ20287	4.8
50	428403 430968	AI393048 AW972830	Hs.326159	leucine rich repeat (in FLII) interactin	4.8
	425212	AW962253	Hs.171618	gb:EST384925 MAGE resequences, MAGL Homo ESTs	4.8
	409205	A1952884	Hs.14832	ESTs, Moderately similar to unnamed prot	4.8
	431176	AI026984	Hs.293662	ESTs	4.8 4.8
65	420092	AA814043	Hs.88045	ESTs	4.8
	437834	AA769294	Hs.283854	gb:nz36g03.s1 NCI_CGAP_GC81 Homo sapiens	4.8
	432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens	4.8
	403011			ENSP00000215330":Probable serine/threoni	4.7
70	405348	004504		C7001664:gi[12698061 db BAB21849.1 (AB	4.7
70	447072	D61594	Hs.17279	tyrosylprotein sulfotransferasa 1	4.7
	443318 421027	AI051603 AA761198	Hs.133141		4.7
	449318	AW236021	Hs.55254 Hs.78531	ESTs Homo sapiens, Similar to RIKEN cONA 5730	4.7
	429170	NM_001394		dual specificity phosphatase 4	4.7
75	411852	AA528140	Hs.107515		4.7 4.7
-	450166	AA429504		ESTs	4.7
	438456	AA913381	Hs.20594	ESTs	4.7
	446839	BE091926	Hs.16244	mitotic spindle colled-coil related prot	4.7
80	438527	Al969251	Hs.115325	RAB7, member RAS oncogene family-like 1	4.7
φU	458946	AA009716	Hs.42311	ESTs	4.7
	454860	AW835767	14- 450	gb:QV4-LT0016-240200-110-b08 LT0016 Hamo	4.7
	424736 443426	AF230877 AF098158	Hs.152701		4.7
	T-3720	VL 030 130	Hs.9329	chromosome 20 open reading frame 1	4.6

	422648	D66983	Hs.118893	Melanoma associated gene	4.6
	431319	AA873350	Hs.302232	ESTs	4.6 4.6
	445666	R59960	Hs.282386	ESTs	4.6
•	415406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	4.6
5	422887	AI751848	Hs.49215	ESTs	4.6
	422938 405141	NM_001809	Hs.1594	centromere protein A (17kD)	4.6
	440210	Y14443 AW874562	Hs.125296	zinc finger protein 200 ESTs	4.6
	432527	AW975028	Hs.102754	ESTs	4.6 4.6
10	439726	AW449893	Hs.293707	ESTs, Weakly similar to 138598 zinc fing	4.6
	435143	R12375	Hs. 194600	ESTs	4.6
	422170	AJ791949	Hs.112432	anti-Mullerian hormone	4.6
	452874	AK001061	Hs.30925	hypothetical protein FLJ 10199	4.6
15	408996 412568	AI979168 AI878826	Hs.344096	glycoprotein (transmembrane) nmb	4.6
	426215	AW963419	Hs.74034 Hs.155223	caveolin 1, caveolae protein, 22kD stanniocatoin 2	4.5
	413076	U10564	Hs.75188	wee1 (S. pombe) homolog	4.5 4.5
	456759	BE259150	Hs.127792	delta (Drosophila)-lika 3	4.5
20	419735	AW750056	Hs.169577	Homo sapiens cDNA FLJ14743 fis, clone NT	4.5
20	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	4.5
	441217	AI922183	Hs.213245	ESTs	4.5
	435542 440435	AA687376 AL042201	Hs.21273	ESTs	4.5
	400288	X06256	Hs.149609	transcription factor NYD-sp10 Integrin, alpha 5 (fibronectin receptor,	4.5
25	416114	AI595549	Hs.183868	glucuronidase, beta	4.5 4.5
	437323	AA371145	Hs. 194397	leptin receptor	4.5
	425139	AW630488	Hs.25338	protease, serine, 23	4.5
	423678	AW963357	Hs.7847	ESTs	4.5
30	403961 443462	A1064600	Lts 474470	Target Exon	4.5
50	418483	AI064690 W26076	Hs.171176 Hs.221847	ESTs ESTs	4.5
	428873	AI701609	Hs.98908	ESTs	4.5 4.5
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	4.5
25	408298	AI745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	4.5
35	449145	AI632122	Hs.198408	ESTs .	4.4
	439574 423905	A1469788	Hs.165190	ESTs	4.4
	453387	AW579960 AI990741	Hs.135150 Hs.252809	lung type-I cell membrane-associated gly ESTs	4.4
	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	4.4
40	433507	AI817338	Hs.191791	ESTs	4.4
	448048	BE281291	Hs.170408	ESTs, Moderately similar to A47582 8-cel	4.4
	421064	AJ245432	Hs.101382	turnor necrosis factor, alpha-induced pro	4.4
	402604	2500000		Target Exon	4.4
45	445291 424503	BE397753 NM_002205	Hs.14623 Hs.149609	interferon, garma-inducible protein 30	4.4
15	423600	AI633559	Hs.310359	integrin, alpha 5 (fibronectin receptor, ESTs	4.4
	403361	1000000	13.310033	NM_002210*:Homo sapiens integrin, stpha	4.4 4.4
	408432	AW195262		gb:xn67b05.x1 NCI_CGAP_CML1 Homo sepiens	4.4
50	424489	T48851	Hs.274470	D-siglec precursor,	4.3
50	442264	AJ278777	Hs.263455	ESTs. Wealdy similar to ALU1_HUMAN ALU S	4.3
	447247 417018	AW369351 M16038	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.3
	414020	NM_002984	Hs.80887 Hs.75703	v-yes-1 Yamaguchi sarcoma viral related	4.3
	439566	AF086387	NS.73703	small inducible cytokine A4 (homologous gb:Homo sapiens full length insert cDNA	4.3 4.3
55	425242	D13635	Hs.155287	KIAA0010 gene product	4.3
	423529	T87318	Hs.120411	ESTA	4.3
	439538	AA837323	Hs.56407	ESTs	4.3
	453682 425259	T79703 AL049280	14.455000	gb:yd71e08.r1 Soares fetal liver spleen	4.3
60	417918	AA209205	Hs.155397 Hs.163754	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.3
	426649	AJ914936	Hs.97152	hypothetical protein FLJ12606 ESTs	4.3 4,3
	438875	AA827640	Hs. 189059	ESTs	4.3
	445868	BE169357	Hs.207428	ESTs	4.3
65	426509	M31166	Hs.2050	pentaxin-related gene, rapidly induced b	4.3
Ų,	409893 432058	AW247090	Hs.57101	minichromosome maintenance deficient (S.	4.3
	430694	AW665996 AA810624	Hs.130729 Hs.30936	ESTs. Weakly similar to ALU1_HUMAN ALU S	4.3
	441523	AW514263	Hs.301771	ESTs, Weakly similar to H2BH_HUMAN HISTO ESTs, Weakly similar to ALUF_HUMAN !!!!	4.3
70	443950	NM_001425	Hs.9999	epithelial membrane protein 3	4.2 4.2
70	419896	Z99362		gb:HSZ99362 DKFZphamy1 Homo sapiens cDNA	4.2
	452994	AW962597	Hs.31305	KIAA1547 protein	4.2
	420841	AI625251	Hs.94037	hypothetical protein FLJ23053	4.2
	441255 416426	R06350 AA180256	Hs.171635	ESTs	4.2
75	411789	AF245505	Hs.210473 Hs.72157	Homo sepiens cDNA FLJ14872 fis, clone PL Adlican	4.2
-	409638	AW450420	Hs.21335	ESTs	4.2
	439192	AW970536	Hs.105413		4,2 4,2
	440684	AI253123	Hs.127356	ESTs, Highly similar to \$21424 nestin (H	4.2
80	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	4.2
50	432343 401454	NM_002960	Hs.2961	S100 calcium-binding protein A3	4.2
	431770	BE221880	Hs.268555	NM_014226*:Homo sapiens renal tumor anti	4.2
	442326	H92962	Hs.124813	5-3' expribonuclease 2 hypothetical protein MGC14817	4.2
				Hypothesia protein mary 14017	4.2

	419402	Z68155	Hs.90291	Aminin hata 2 (lambia C)	4.2
	435703	AW630133	Hs.83313	taminin, beta 2 (laminin S) GK003 protein	4.2
	444609	AW571659	Hs.278081	ESTs	4.2
5	404407		.:	Target Exon	4.2
3	450581 407838	AF081513 8E146411	Hs.25195	TGF-bela 4	4.2
	410407	X66839	Hs.40342 Hs.63287	putative nuclear protein carbonic anhydrase IX	4.1 4.1
	418883	BE387036	Hs.1211	acid phosphatese 5, tartrate resistant	4.1
10	438898	AI819863	Hs.106243	ESTs	4.1
10	421674	T10707	Hs.295355	hypothetical protein FLJ23138	4.1
	445921 453055	AW015211 AW291438	Hs.148181 Hs.31917	ESTS	4.1 4.1
	413450	Z99716	Hs.75372	Homo sapiens, clone MGC:9658, mRNA, comp N-acetytgalactosaminidase, atpha-	4.1
	427463	AA442224	Hs.97900	ESTs	4.1
15	450639	AI703188	Hs.277174	ESTs ,	4.1
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formytransfer	4.1
	437269 415688	AA334384 AA166963	Hs.149420	ESTs gb:zo86d01.s1 Stratagens ovarian cancer	4.1 4.1
	414300	Al304870	Hs.188680	ESTs	4.1
20	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	4.1
	415024	AI983981	Hs.189114	ESTs	4.1
	408102	U46351	Hs.621	tectin, galactoside-binding, soluble, 3	4.1
	448019 451433	AW947164 AA021140	Hs.195641 Hs.269265	ESTs, Moderately similar to 138022 hypot	4.1 4.1
25	446523	NM_003063	Hs.334629	ESTs, Weakly similar to A46010 X-linked sarcolipin	4.1
	427700	AA262294	Hs.180383	dual specificity phosphatase 6	4.1
	402239			Target Exon	4.1
	423713	AW754182	U- 425474	gb:RC2-CT0321-131199-011-c01 CT0321 Homo	4.1
30	437814 414948	AI088192 C15240	Hs.135474 Hs.182155	ESTs, Wealdy similar to DDX9_HUMAN ATP-D ESTs	4.1 4.0
-	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	4.0
	427375	AL035460	Hs.177536	metallocarboxypeptidase CPX-1	4.0
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	4.0
35	449655	AI021987	Hs.59970	ESTs	4.0
55	439978 432842	BE139460 AW674093	Hs.124673 Hs.334822	Homo saplens cDNA FL111477 fis, clone HE hypothetical protein MGC4485	4.0 4.0
	422282	AF019225	Hs.114309	spolipoprotein L	4.0
	452574	AF 127481	Hs.301946	lymphoid blast crisis oncogene	4.0
40	449256	AA059050	Hs.59847	ESTs	4.0
40	453385 443715	AW296101 AI583187	Hs.252806	ESTs	4.0
	451778	AJ826131	Hs.9700 Hs.62954	cyclin E1 ESTs, Wealdy similar to zinc finger prot	4.0 4.0
	441287	AW293132	Hs.131373	ESTs	4.0
	418661	NM_001949	Hs.1189	E2F transcription factor 3	4.0
45	420894	AA744597	Hs.88854	ESTs	4.0
	454120 441627	AB032990 AA947552	Hs.40719	hypothetical protein KIAA1164	4.0
	453948	A1970797	Hs.58086 Hs.64859	branched chain aminotransferase 1, cytos ESTs	4.0 4.0
	444170	AW813879	Hs.102408	ESTs	4.0
50	427221	L15409	Hs.174007	von Hippel-Lindau syndrome	4.0
	418821	AA436002	Hs.183161	ESTs	4.0
	418216 435106	AA662240 AA100847	Hs.283099 Hs.5978	AF15q14 protein ESTs, Highly similar to AF174600 1 F-box	4.0 4.0
	430890	X54232	Hs.2699	glypican 1	3.9
55	429490	AI971131	Hs.23889	ESTs, Wealthy similar to ALU7_HUMAN ALU S	3.9
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	3.9
	438265 407304	AA731331 AA565832	Hs.190668 Hs.271649	ESTS	3.9
	433244	AB040943	Hs.271285	gb:nj32b03.s1 NCI_CGAP_AA1 Homo saplens KIAA1510 protein	3.9 3.9
60	446960	AW294936	Hs.156762	ESTs	3.9
	406627	T64904	Hs.163780	ESTs	3.9
	420552	AK000492	Hs.98806	hypothetical protein	3.9
	402082 419594	AA013051	Hs.91417	C18000743*:gi[6678363 ref NP_033416.1 t topoisomerase (DNA) II binding protein	3.9 3.9
65	448966	AW372914	Hs.88149	phosphoinositol 3-phosphate-binding prot	3.9
	427527	AI809057	Hs.293441	immunoglobulin heavy constant mu	3.9
	422564	Al148006	Hs.222120	ESTs	3.9
	418781 431820	T41160 AW410408	Hs.8404	ESTs	3.9
70	413095	AA494359	Hs.271167 Hs.30715	L-pipecolic acid oxidase potassium voltage-gated channel, lsk-rel	3.9 3.9
•	430637	BE160081	Hs.256290		3.9
	443539	AJ076182	Hs.134074	ESTs, Moderately similar to ALUS_HUMAN A	3.9
	422173	BE385828	Hs.250619		3.9
75	433388 403849	AJ432672	Hs.288539		3.8
	406646	M33600	Hs.308026	Target Exon major histocompatibility complex, class	3.8 3.8
	445075	AI651827	Hs.344767		3.8
	420004	AW975532	Hs.164039	ESTs, Moderately similar to 138022 hypot	3.8
80	449670	F07693	Hs.85603	Homo sapiens mRNA; cDNA DKFZp434K2172 (1	3.8
50	424479 449625	AF064238 NM_014253	Hs.149098	smoothelin odz (odd Oz/ten-m, Drosophila) homolog 1	3.8 3.8
	418641	BE243136	Hs.86947	a disintegrin and metalloproteinase doma	3.8
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.8

	403000				
	427286 453920	AW732802 Al133148	Hs.2132 Hs.36602	epidermal growth factor receptor pathway	3.8
	453857	AL080235	Hs.35861	I factor (complement) DKFZP586E1621 protein	3.8 3.8
	406872	AI760903		gb.wi09h08.x1 NCI_CGAP_CLL1 Homo sapiens	3.6
5	403696			C4001100*:gij5852342 gb AAD54015.1 (AF0	3.8
	417791	AW965339	Hs.111471	ESTs	3.8
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	3.8
	404209 431454	AW975980	Hs.292918	Target Exxon ESTs	3.8 3.8
10	410422	AL042014	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	3.8
	406739	A1566709	Hs.182426	ribosomal protein S2	3.8
	450810	BE207588	Hs.334360	transforming growth factor beta 1 induce	3.8
	457876	AI821940		ESTs, Moderately similar to ALU8_HUMAN A	3.8
15	435718	R06569	Hs.269534	ESTS	3.8
13	429716 442710	R25685 A1015631	Hs.211933 Hs.23210	collagen, type XIII, alpha 1 ESTs	3.8 3.8
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	3.8
	419764	BE262524	Hs.93183	vasodilator-stimulated phosphoprotein	3.8
20	436674	AA725002	Hs.272018	low molecular mass ubiquinone-binding pr	3.8
20	408896	AI610447	Hs.48778	niban protein	3.8
	425300	AW601773	Hs.270259	ESTS	3.8
	432886 424090	BE159028 X99699	Hs.279704 Hs.139262	chromatin accessibility complex 1 XIAP associated factor-1	3.8 3.7
	420202	AL036557	Hs.95910	putative lymphocyte G0/G1 switch gene	3.7
25	427584	BE410293	Hs.179718	v-myb avlan myeloblastosis viral oncogen	3.7
	420579	AA278449	Hs.137429	ESTs	3.7
	405038	Y14443	41- 425022	zinc finger protein 200	3.7
	412590 406714	AL134388 Al219304	Hs.135033 Hs.266959	ESTs, Wealdy similar to I38022 hypotheti	3.7
30	412014	AI620650	Hs.43761	hemoglobin, gamma G ESTs, Weakly similar to A46010 X-finked	3.7 3.7
-	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	3.7
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	3.7
	408955	BE315170	Hs.8087	Target CAT	3.7
35	441362	BE614410	Hs.23044 Hs.182314	RAD51 (S. cerevisiae) homolog (E coli Re	3.7
ננ	413774 440225	AA131782 BE295782	Hs.159	ESTs tumor necrosis factor receptor superfami	3.7 · 3.7
	414528	AA148950	Hs.188836	ESTs	3.7
	436137	AI056769	Hs.133512	ESTs	3.7
40	414733	BE514535	Hs.77171	minichromosome maintenance deficient (S.	3.7
40	406785	AA588061	11- 400000	gb:nk10d03.s1 NCI_CGAP_Co2 Homo sapiens	3.7
	443361 434868	AI792628 R50032	Hs.133273 Hs.159263	ESTs	3.7
	409557	BE182896	Hs.211193	collagen, type VI, aipha 2 ESTs	3.7 3.7
	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.7
45	427695	R88483	Hs.172862	ESTS	3.7
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.6
	437916 434563	8E566249 AW083994	Hs.20999 Hs.9469	hypothetical protein FLJ23142	3.6
	444371	BE540274	Hs.239	pteckstrin homology domain-containing, f forkhead box M1	3.6 3.6
50	437816	AJ823445	Hs.280599	ESTs	3.6
	405605			C2001342:gij127814jspjP26434jNAH4_RAT SO	3.6
	444794	AI419991	Hs.145225	ESTs	3.6
	430540 429747	AW245422	Hs.106357	Homo sapiens cDNA: FLJ22105 fis, clone H	3.6
55	453785	M87507 Al368236	Hs.2490 Hs.283732	caspase 1, apoptosis-related cysteine pr ESTs, Moderately similar to ALU1_HUMAN A	3.6 3.6
	403267	, 4000000	12.200102	Target Exon	3.6
	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	3.6
	447497	AW167254	Hs.205722	ESTs	3.6
60	428600 428715	AW863261 AW293716	Hs.242413	hypothetical protein DKFZp434K1421	3.6
00	416097	BE387371	Hs.53126 Hs.118964	ESTs hypothetical protein FLJ20085	3.6 3.6
	453438	Al469935	Hs.22792	EST8	3.6
	427299	AA830210	Hs.214263		3.6
45	434577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fis, clone H	3.6
65	452785	AL359942	Hs.296434	erythroid differentiation and denucleati	3.6
	434467 435523	BE552368 T62849	Hs.231853 Hs.11090		3.6
	418287	AI872319	Hs.78935	membrane-spanning 4-domains, subfamily A methionine aminopeptidase; etF-2-associa	3.6 3.6
	422156	N34524	***************************************	gb:yy56d10.s1 Soares_multiple_sclerosis_	3.6
70	441224	AU076964	Hs.7753	catumenin	3.6
	458072	A1890347	Hs.271923		3.6
	435677 433325	AA694142 AW206986	Hs.293726		3.6
	420683	AA830168	Hs.143905 Hs.271305		3.6 3.6
75	443206	AB011420	Hs.9075	serine/threonine kinase 17a (apoptosis-i	3.6
	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	3.6
	404584			Target Exon	3.5
	428311	NM_005651			3.5
80	425922 415131	AL157466 D61119	Hs.162751	Homo sapians mRNA; cDNA OKFZp761E2423 (f gb:HUM158C11B Clontech human fetal brain	3.5 3.5
	412971	AA889628	Hs.35125	ESTs	3.5
	451593	AF151879	Hs.26706	CGI-121 protein	3.5
	416427	BE244050	Hs.79307	Rac/Cdc42 guaraine exchange factor (GEF)	3.5

	427809	M26380	Hs.180878	Epoprotein lipase	
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine or	3.5
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	3.5
-	445936	BE543594	Hs.61478	hypothetical protein FLJ22329	3.5 3.5
5	411537	BE073250		9b:MR0-BT0551-060300-102-e05 RT0551 Homo	3.5
	432250	AA452088	Hs.274170	Opa-Interacting protein 2	3.5
	458438	Al141520	Hs.151464	ESTs, Wealty similar to ALUC_HUMAN (!!!	3.5
	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	3.5
10	410507	AA355288	Hs.76064	transitional epithelia response protein	3.5
10	412436	AA665089		gb:nu76d01.s1 NCI_CGAP_Alv1 Homo sapiens	3.5
	416933	BE561850	Hs.80506	amaii nuclear ribonucleoprotein polypept	3.5
	437681 408247	AI207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	3.5
		AA053451	Hs.225632	leucine zipper protein 3	3.5
15	440074 422448	AA863045	Hs.10669	ESTs. Wealty similar to T00050 hypotheti	3.5
13	420676	AW372922	Hs.116774	integrin, alpha 1	3.5
	417663	AJ434780	Hs.4248	vav 2 oncogene	3.5
	451089	R07483	Hs.180451	ESTs	3.5
	451448	AA903705 AI826288	Hs.4190	Homo sapiens cDNA: FLJ23269 fis, clone C	3.5
20	414727	BE466904	Hs.171637	hypothetical protein MGC2628	3.5
	421778		Hs.190162	gb:hz28f03.x1 NCI_CGAP_GC8 Homo septens	3.5
	427413	AA428000 BE547647	Hs.283072	actin related protein 2/3 complex, subun	3.5
	414039	M83221	Hs.177781	hypothetical protein MGC5618	3.5
_	456304	AI820973	Hs.858	V-rel avian reticuloendothefiosis viral	3.5
25	449162	AI632740	Hs.10476	gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	3.5
	437774	AW978199	Hs.291648	ESTs	3.5
	426827	AW067805	Hs.172665	ESTs, Weakly similar to 138022 hypotheti	3.5
	452203	X57522	115.172005	methylenetetrahydrofolate dehydrogenase	3.4
	450325	AI935962	Hs.26289	transporter 1. ATP-binding cassette, sub	3.4
30	457211	AW972565	Hs.32399	ESTS	3.4
	419726	U50330	Hs.1274	ESTs, Weakly similar to S51797 vasodilat	3.4
	417409	BE272506	Hs.82109	bone morphogenetic protein 1 syndecan 1	3.4
	412811	H06382		ESTs	3.4
2.0	430758	T91568	Hs.270616	ESTs, Moderately similar to A34087 hypot	3.4
35	425769	U72513	Hs.159488	Human RPL13-2 pseudogene mRNA, complete	3.4
	452682	AA456193	Hs.9071	progesterone membrane binding protein	3.4
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	3.4
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	3.4
40	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	3.4
40	446134	AW161234	Hs.13993	TBP-like 1	3.4
	418669	U85992	Hs.87197	Human clone (MAGE:35527 unknown protein	3.4
	425006	R38685	Hs.222746	ESTs	3.4 3.4
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.4
45	453379	AA035261	Hs.61753	ESTs	3.4
73	448224	R48700	Hs.20733	Homo sapiens cDNA: FLJ22356 fis, clone H	3.4
	455899	BE155112		gb:PM1-HT0350-151299-003-a03 HT0350 Homo	3.4
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.4
	417395 405046	BE564245	Hs.82084	integrin beta 3 binding protein (beta3-e	3.4
50	423178	41023440		C3000978:gi 9280045 db BAB01579.11 (AB0	3.4
-	455142	A1033140	Hs.124983	Homo sapiens mRNA; cONA DKFZp564C142 (fr	3.4
	418819	AW861840		gb:CM0-CT0337-250200-243-g01 CT0337 Homo	3.4
	428289	AA228776 M26301	Hs.191721	ESTs	3.4
	412799	AI267606	Hs.2253	complement component 2	3.4
55	403108	~201000		gb:aq91h03.x1 Stanley Frontal SB pool 1	3.4
•	421637	AF035290	Hs.106300	ENSP00000241415*:Hypothetical 67.7 kDa p	3.4
	419373	NM_003244	Hs.90077	Homo saplens clone 23556 mRNA sequence	3.4
	424408	AJ754813	Hs.146428	TG-interacting factor (TALE family homeo	3.4
	451061	AW291487	Hs.213659	collagen, type V, appla 1	3.4
60	433578	BE336886	Hs.3416	ESTs, Weakly similar to KIAA1357 protein adipose differentiation-related protein	3.4
	439867	AA847510	Hs.161292	ESTs	3.4
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	3.4
	420982	AW576160	Hs.100729	KIAA0692 protein	3.4
65	440826	AW383618	Hs.346256	ESTs. Moderately similar to ALU2_HUMAN A	3.4
65	427687	AW003867	Hs.1570	histamine recentor H1	3.4
	400533			ENSP00000209376":PRED65 protein (Fragmen	3.4
	436314	AI983409	Hs.189226	ESTs	3.3
	418110	R43523	Hs.217754	hypothetical protein FLJ22202	3.3 3.3
70	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	
70	402229	BE262804		mitochondrial ribosomal protein S2	3.3 3.3
	410687	U24389	Hs.65436	lysyl oxidase-like 1	1 2
	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	³ 3.3
	443338	R99575	Hs.302908	ESTs	3.3
75	433062	AK001757	Hs.281348	hypothetical protein FLJ 10895	3.3
, ,	405303	VOLCCO	44 45	Target Exon	3.3
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephatos	3.3
	406673 431721	M34996	Hs.198253	major histocompatibility complex, class	3.3
	426746	AB032996	Hs.268044	KIAA1170 protein	3.3
80	425262	J03826	Hs.2057	uridine monophosphate synthetase (orotat	3.3
	424947	D87119	Hs.155418	GS3955 protein	3.3
	437634	R77952 AW293046	He SEELES	ESTs, Weakly similar to atternatively sp	3.3
	437014	AA808757	Hs.255158	£515	3.3
		- 	Hs.222531	ESTs, Weakly similar to S59501 interfero	3.3

		İ										
	436456		418932									
	408601		453496									rocollagen C-endopepiidase enh
	420886 437162		423169 418049								Hs.196011 E Hs.107125 p	STs lasmatemma vesicle associated
5	445704	5	441243							AW809324	9	b:MR4-ST0121-141099-010-GU
	440700 414747		444427					5	442609 416188		Hs.8518 s Hs.78070 v	elenoprotein N r-myc avian myelocytomatosis vi
	431553		445418						441544		Hs.127137 6	ESTs .
10	405605 431467	10	437762						437860	AA333063		Homo sapiens cDNA: FLJ23165 hypothetical protein
	457561	10	450336 433842					10	419652 443623	AL157485 AA345519	Hs.9641	complement component 1, q sub
	412507 413448		444124						415198	AW009480		natural killer cell transcript 4 ESTs
	444168		423858 454792						441701 426384	AW339828 AI47207B	Hs.303662	hypothetical protein FLJ13189 (F
15	400090 433642	15	412775					16	420886	AA805453		ESTs. Weakly similar to T29012 ESTs
	422938		429609 41395					15	428896 458253	AW291932 AW296952		ESTs
	426318		43332	,		•			456895	AA354771	Hs.43047 Hs.5996	Homo sapiens cDNA FLJ13585 ESTs
20	428896 449277	20	449092 422390	•					434818 424278	AA650097 AK000723	Hs.144517	hypothetical protein FLJ20716
	426509		424899	:				20	434131	A1858275	Hs.143659	ESTs cysteine-rich protein 1 (intestina
	412216 428845		454253 410126						447111 443021	AJ017574 AA368546	Hs.17409 Hs.8904	to superfamily protein
25	431512	25	456508						416677	T83470	Hs.334840	ESTs. Moderately similar to 178
23	41B113 450661	23	405303 420871					25	429973 422545	AJ423317 X02761	Hs.164680 Hs.287820	ESTs fibronectin 1
	448448		44243					23	444008	BE395085	Hs.10086	type I transmembrane protein I FH1/FH2 domain-containing pr
	422631 419687		425769						420116 401841	NM_013241	Hs.95231	NM_015113:Homo sapiens Kl/
30	450963	30	407378					••	414418	AW409985	Hs.76084	hypothetical protein MGC2721
	435060 440274		439764					30	431019 453707	NM_005249 AW003879	Hs.2714 Hs.126522	forkhead box G1B Homo sapiens, clone MGC:16
	437438		422156						432188	AI362952	Hs.2928	solute carrier family 7 (calionic ESTs, Moderately similar to 13
35	435401	35	451489 457350						407378 430701	AA299264 A1760833	Hs.57776 Hs.293971	ESTS MODERATELY SAIMED NO IS
	445314	-	407721					35	429569	AA454993	Hs.138343	ESTs. Weakly similar to 17888
	425870 425294		452371 45966(•		458918 439764	H56499 T26535	Hs.252692 Hs.22744	ESTs, Weakly similar to 13802 hypothetical protein MGC1311
40	416404	40	43708						452221	C21322	Hs.288057	hypothetical protein FLJ2224:
40	413995 422798	40	41985 44008					40	403969 427359	AW020782	Hs.79881	ENSP00000034663:Zinc fing Homo sapiens cDNA: FLJ23(
	426384		44971					40	414396	BE548266	Hs.76057	gatactose-4-epimerase, UDP
	430147 42526		45040 42316	;					444153 414403	AK001610 AW969551	Hs.76064	hypothetical protein FLJ 1074 ribosomal protein L27a
45	40691	45	44996	i					444168	AW379879		ab:RC1-HT0256-081199-011
	42526 40155		45403 41986			•		45	410595 444881	AW629223 AI623288	Hs.64794 Hs.192805	zinc finger protein 183 (RINC ESTs
	43934		423421						440381	AA917808	Hs.190495	5 ESTs
50	41486 45397	50	42035; 42464						416207 43913		5 Hs.79077 Hs.12470	Homo sapiens, clone MGC:: 7 ESTs
	40428	•	45354					50	45757	AB030816	Hs.36761	HRAS-like suppressor
	43288 45149		44787 41968						40673 42017		Hs.18242 Hs.95655	
55	44257	5.5	45102						42806	AA420616	Hs.24948	3 ESTs
55	42836 44375	55	42270 43280					55	44414 40915		6 Hs.16099 Hs.50842	
	41786		44659					33	44942	6 T92251	Hs.19888	32 ESTs
	44389 43886		45772 40379			į			45876 45081		Hs.11133 Hs.24549	
60	45390	60	44541	-					4253	1 AW96212	18	gb:EST374201 MAGE rese
	44771 42658		43870 43457					60	4452° 4413			
	42112		42277,						4506		17	gb:EST382188 MAGE resi
65	41076 43146	65	43343 42796			•			4376 4445		3 Hs.2721 Hs.1166	
	45222		41443					65	4070	47 X65965		gb:H.saplens SOD-2 gene
	41232 42860		42055 45620	İ					4138	34 BE29689		
70	42650	70	41881	******					4397 4355	20 AA29799	O Hs.9315	MNOEL-iso protein
70	40555 42148	70	43894 43908	1				70	4145 4409		1 Hs.1351	
	44858		45173	,				/(4121		2 Hs.106	149 ESTs
	45210 42950		41525 44278						417	36 R70429		
75	4507	75	43267		i				4179	71 BE0490	94	ESTS
	4293 4374		42660 43509		4	ĺ		75	430	144 AW2984		
	4321		43903	1:					425 407			18 dual-specificity tyrosine-(
80	4046 4526	80	45035 40085		;				439	093 AA5341	63 Hs.547	6 Homo sepiens, clone IM
	4214	00	4176					80	0 435	523 NM_00 664 A10320		3819 ESTs
	4190 4535		42579	İ	•				453	085 AW954	243	KIAA0251 protein
	7		41531	1	1					314 AA3690 627 AI7028	501 Hs.23: 95 Hs.42:	
	1		1		÷ ;							

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	415114	D60468	Hs.94181	EST _{\$}	6.0	6.0
	448958	AB020651	Hs.22653	KIAA0844 protein	5.9	5.9
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	5.9	6.0
5	447138 414545	A1439112 AA149287	Hs.93828 Hs.76605	ESTs, Weakly similar to 2109260A B cell ESTs	5.8 5.8	5.8 3.6
-	418202	N48521	Hs.26549	KIAA1708 protein	5.8	5.8
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	5.7	9.6
	444124	R43097	Hs.6818	ESTs	. 5.7	9.3
10	408065 448533	AW954272 AL119710	Hs.21365	gb:EST386342 MAGE resequences, MAGC Homo nucleosome assembly protein 1-like 3	5.6 5.6	5.6
	425523	AB007948	Hs.158244	KIAA0479 protein	5.6	9.6 35.0
	459697	AA406062	Hs.98002	ESTs	5.6	5.4
	408428	NM_014787	Hs.44896	OnaJ (Hsp40) homolog, sublamily B, membe	5.6	5.6
15	420111 450149	AA255652 AW969781	Hs.132863	gb:zs21h11.r1 NOI_CGAP_GC81 Homo sapiens	5.5	3.2
13	424918	R13982	Hs.169309	Zic family member 2 (odd-paired Drosophi myefin-associated oligodendrocyte basic	5.4 5.3	5.4 5.3
	438202	AW169287	Hs.22588	ESTs	5.3	5.3
	448605	AL109678	Hs.21597	Homo sepiens mRNA full length insert cDN	5.3	5.3
20	425580 418868	L11144	Hs.1907	galanin	5.3	3.5
20	430091	T65754 AB032958	Hs.233023	gb:yc11c07.s1 Stratagene tung (937210) H KIAA1132 protein	5.3 5.3	3.8 4.9
	448786	BE048842	Hs.179075	Homo sapiens cDNA FLJ11881 fis, clone HE	5.2	5.2
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	5.2	3.0
25	415666	H72693	15- 64000	gb:yu03c11.r1 Soares fetal fiver spleen	5.2	5.2
LJ	410240 428784	AL157424 Y12851	Hs.61289 Hs.193470	synaptojanin 2 purtnergic receptor P2X, ligand-gated io	5.2 5.2	4.6 7.7
	446692	Z44514	13.133470	Homo sapiens mRNA for KIAA1763 protein,	5.2	33.0
	428508	BE252383	Hs.184668	SBBI31 protein	5.2	4.1
30	446353	AI290919	Hs.153661	ESTs	5.1	5.1
30	423135 437331	N67655 AL353933	Hs.26411 Hs.21710	ESTs hypothetical protein DKFZp761G0313	5.1 5.1	8.2
	413988	M81883	Hs.324784	glutamate decarboxytase 1 (brain, 67kD)	5.1	5.1 5.1
	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	5.1	5.1
35	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	5.0	11.2
33	408068 415734	AW148652 NM_014747	Hs.167398 Hs.78748	ESTs KIAA0237 gene product	5.0	5.0
	439607	BE540565	Hs.159460	ESTs	5.0 5.0	27.4 5.6
	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	4,9	29.3
40	414631	AW970130	Hs.65406	ESTs	4.9	4.9
40	437117 418527	AL049256 AA450386	Hs.122593	ESTs Homo sapiens cDNA: FLI21950 fis. clone H	4.9	3.8
	425073	W39609	Hs.7149 Hs.22003	solute carrier family 6 (neurotransmitte	4.9 4.9	4.9 4.9
	455384	H72176	Hs.4273	hypothetical protein FLJ13159	4.9	4.9
45	443150	AI034467	Hs.34650	ESTs	4.9	7.6
45	422411	AW749443	Hs.22511	ESTs	4.9	12.0
	414931 430456	AK000342 AA314998	Hs.77646 Hs.241503	Homo sepiens mRNA; cDNA DKFZp761M0223 (1 hypothetical protein	4.9 4.8	3.4 4.7
	428186	AW504300	Hs.295605		4.8	3.9
50	433516	AA595802	Hs.33410	ESTs, Wealdy similar to T17279 hypotheti	4.8	4.8
50	427287	NM_014903			4.8	4.8
	416101 447252	R24854 R90916	Hs.268806 Hs.12449	ESTs Homo sapiens transmembrane protein HTMP1	4.B 4.8	3.3 3.2
	458268	AA428403	Hs.106131		4.7	3.9
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	4.7	8.2
55	445102	AW204610	Hs.22270	ESTA	4,7	19.2
	419643 414949	F06066 C15314	Hs.91791 Hs.323349	chromosome 11 open reading frame 25 ESTs	4,7 4,7	4.7
	453534	NM_014796	Hs.33187	KIAA0748 gene product	4.7	3.8 4.7
C 0	445729	H21056	Hs.13223	Homo sapiens mRNA full length insert cDN	4,7	4.0
60	451032	W03692	Hs.323079		4.7	4.9
	434792 447104	AA549253 R19085	Hs.132458 Hs.210706		4.7	3.8
	430537	X62692	Hs.2593	phosphodiesterase 68, cGMP-specific, rod	4.7 4.6	3.0 4.6
	453431	AF094754	Hs.32973	glycine receptor, beta	4.6	4.6
65	453302	NM_000838		glutamate receptor, metabotropic 1	4.6	4.6
	429876	AB028977	Hs.225974		4.6	16.8
	451516 433670	AR600515 AA604405	Hs.12024	ESTs gb:no87h09.s1 NCI_CGAP_AA1 Homo sapiens	4.6 4.6	6.3 3.9
~^	437380	AL359577	Hs.112198		4.5	3.8
70	410366	AI267589	Hs.302689	hypothetical protein	4.5	10.4
	419191	U17195	Hs.89666	A kinase (PRKA) anchor protein 6	4.5	4.5
	429290 424932	AF203032 R14070	Hs.198760 Hs.315369		4.5 4.5	3.3 10.2
	432736	AA788898	Hs.179902	transporter-like protein	4.4	4.0
75	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	4.4	3.2
	428963	AW382682	Hs.258208		4.3	3.3
	435040 451301	A1932350 A1769514	Hs.152825 Hs.209890		4.3	4.7
	452381	H23329	Hs.290880		4.3 4.3	4.3 4.3
80	410305	AF030409	Hs.62185	solute carrier family 9 (sodium/hydrogen	4.3	7.8
	433109		Hs.162430	EST	4.3	3.9
	431342				4.3	8.0
	447163	AW292770	Hs.5542	Dna.I (Hsp40) homolog, subfamily C, membe	4.3	3.4

	422414	AW875237	Hs.13701	ESTs	4.2	5.3
	439274	AF086092	Hs.48372	ESTs	4.2	18.3
	423589	AA328082	Hs.209569	ESTs	4.2	4.2
5	429955	AI374651	Hs.22542	ESTs	4.2	3.2
3	427317 426847	AB028955 S78723	Hs.175780 Hs.298623	KIAA1032 protein	4.2	5.3
	408206	AFQ41853	Hs.43670	5-hydroxytryptamine (serotonin) receptor kinesin family member 3A	4.1 4.1	7.9 4.1
	433803	AI823593	Hs_27688	ESTs S	4.1	4.1
• •	413024	AF036268	Hs.75149	SH3-domain GRB2-like 2	4.1	4.0
10	448117	H49129	Hs.172982	ESTs .	4.1	4.1
	450600 429550	BE079478	Hs.24880	ESTs	4.1	3.9
	448581	AW293055 AL109781	Hs.119357 Hs.21754	ESTs Homo saplens mRNA full length insert cDN	4.1 4.0	6.4 7.2
	458694	F12832	Hs.3610	ESTs	4.0	4.0
15	452197	AW023595	Hs.232048	ESTs	4.0	4.0
	423728	AW891294	Hs.132138	solute carrier family 4, sodium bicarbon	4.0	7.9
	429656 448583	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	4.0	13.1
	419863	NM_015239 AW952691	Hs.21542 Hs.93485	KIAA1035 protein Homo sapiens mRNA; cDNA DKFZp761D191 (fr	4.0 3.9	4.0 21.4
20	442412	R77677	Hs.346644	ESTs	3.9	3.9
	424001	W67883	Hs.137476	paternally expressed 10	3.9	5.4
	440293	Al004193	Hs.22123	ESTS	3.9	3.9
	422890 426054	Z43784	1- 400400	ankyrin 3, node of Ranvier (ankyrin G)	3.9	3.6
25	412949	U12431 AJ471639	Hs.166109 Hs.71913	ELAV (embryonic lethal, abnormal vision, ESTs	3.9 3.8	3.9 3.7
	427457	AW779105	Hs.164682	ESTs	3.8	11.1
	416530	U62801	Hs.79361	katikrein 6 (neurosin, zyme)	3.8	4.4
	442676	AI733585	Hs.130897	ESTs	3.8	3.8
30	434998 424945	AW975157	Hs.26037	ESTs	3.7	3.7
30	415257	AJ221919 F03016	Hs.27513	hypothetical protein FLI10582 ESTs	3.7	30.5
	407886	AW969688	Hs.100826	ESTs	3.7 3.7	8.6 20.2
	400844			NM_003105*:Homo sapiens sortilin-related	3.7	3.1
25	456765	AJ497900	Hs.33067	ESTs	3.7	3.7
35	430287	AW182459	Hs.125759	ESTs, Wealdy similar to LEU5_HUMAN LEUKE	36	7.6
	452667 436773	T87219 AW078629	Hs.13219	ESTs PC4 and SFRS1 interacting protein 1	3.6 3.6	3.6
	424120	T80579	Hs.290270	ESTs	3.6	3.6 14.7
	446574	AJ310135	Hs.335933	ESTs	3.6	3.5
40	432453	AI885537	Hs.27172	ESTs, Moderately similar to PC4259 ferri	3.6	3.9
	408119	W26213	Hs.101672	ESTs, Weakly similar to T00331 hypotheti	3.6	3.6
	449093 439239	AB035356 AI031540	Hs.22998 Hs.235331	neurexin 1 ESTs	. 3.6	3.6
	451625	R56793	Hs.106576	alanine-glyoxylate aminotransterase 2-ti	3.6 3.6	49.5 4.1
45	435059	Z45270	Hs.235873	hypothetical protein FLJ22672	3.6	4.8
	423346	AI267677	Hs.127416	synaptojanin 1	3.6	20.1
	442738	AW002370	Hs.131055	ESTs, Weakly similar to NPM_HUMAN NUCLEO	3.5	3.5
	442106 449117	AW205881 AW449310	Hs.326728 Hs.210262	ESTs ESTs, Weakly similar to HSS2_HUMAN HEPAR	3.5	3.2
50	405819	A11412019	14.210202	NM_002578:Homo sapiens p21 (CDKN1A)-acti	3.5 3.5	3.5 13.5
	452311	AW304029	Hs.252744	ESTS	3.5	3.5
	448902	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp76111912 (f	3.5	21.8
	410224 400098	M55513	Hs.150208	potassium voltage-gated channel, shaker-	3.4	3.4
55	428001	H97428	Hs.219907	Eos Control ESTs, Moderately similar to Transforming	3.4 3.4	3.4 5.9
	437268	AI754847	Hs.227571		3.4	14.0
	443682	Al383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.4	3.3
	417417	F05745	Hs.89512	ATPase, Ca transporting, plasma membrane	3.3	17.1
60	419629 419852	AB020695 AW503756	Hs.91662 Hs.286184	KIAA0888 protein hypothetical protein dJ551D2.5	3.3 3.3	13.4
	417063	N50515	Hs.45061	ESTs	3.3	4.1 3.3
	435071	D60683	Hs.35495	ESTs	3.3	3.3
	446377	AW014022	Hs.170953		3.3	3.3
65	412453 450561	R20205 R49674	Hs.75236	ESTS	3.3	3.3
V.	423829	R44107	Hs.25909 Hs.240905	ESTs ESTs	3.3 3.3	3,3
	415527	F11624	113.2-0303	gb:HSC2ZD101 normalized infant brain cDN	3.3	4.4 3.3
	427386	AW835261	Hs.6727	ESTs	3.3	3.3
70	425121	AI797511	Hs.154679		3.2	3.9
70	452856	AF034799	Hs.30881	protein tyrosine phosphatase, receptor t	3.2	10.7
	442879 417284	AF032922 N62889	Hs.8813 Hs.107242	syntaxin binding protein 3 Homo sapiens cDNA FLJ12985 fis, clone NT	3.2 3.2	3.2 3.2
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	3.2	6.7
	429477	AI275514	Hs.6658	ESTs	3.2	3.2
75	453169		Hs.32156	KIAA1394 protein	3.2	5.7
	408039	AA131424	Hs.336636		3.2	3.2
	426269 409746		Hs.168950 Hs.56294		3.2 3.2	22.1
^^	416874		Hs.42568	ESTs	3.2 3.2	10.6 6.0
80	453919	AW959912	Hs.7076	KIAA1705 protein	3.2	3.2
	444861		Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.2	3.2
	433315 419103		Hs.239706 Hs.96423		3.2	3.1
	412103	444573	113.30423	нуровнечим ргория г сл 23033	3.2	8.4

	40.4440	740054	11: 444 20 0			
	424140 421790	Z48051 AW896201	Hs.141308 Hs.22654	myelin oligodendrocyte glycoprotein	3.2	56.0
	432809	AA565509	Hs.131703	sodium channel, voltage-gated, type I, a ESTs	3.2 3.1	4.1 9.9
	445225	AJ216555	Hs.202398	ESTs	3.1	5.5
5	424087	N59333	Hs.143434	contactin 1	3.1	3.1
	437924	A1935344	Hs.164118	ESTs, Wealthy similar to SL51_HUMAN SODIU	3.1	3.2
	419683 420173	AA248897 AA256151	Hs.48784 Hs.22999	ESTS	3.1	5.9
	411666	AF106564	Hs.71346	ESTs neurofilament 3 (150kD medium)	3.1 3.1	4.1 6.6
10	416220	N49776	Hs.170994	hypothetical protein MGC10946	31	4.5
	425138	H08849	Hs.167464	glutamate receptor, ionotropic, N-methyl	3.1	4.2
	422234	AF119818	Hs.113287	discs, large (Orosophila) homolog-associ	3.1	3.1
	445194 438054	AJ215667 AA776626	Hs.175044 Hs.169309	ESTS	3.1	3.1
15	432149	AW614326	Hs.133483	ESTs ESTs, Weakly similar to T34549 probable	3.1 3.1	10.2 12.2
	445725	AK000956	Hs.13209	hypothetical protein FLJ 10094	3.0	3.0
	414245	BE148072	Hs.75850	WAS protein family, member 1	3.0	11.7
	447673	AI823987	Hs.182285	ESTs	3.0	3.0
20	428392 418410	H10233 AA811441	Hs.2265 Hs.107393	secretory granule, neuroendocrine protei	3.0	42.3
	429024	AJ652297	Hs.119302	chromosome 3 open reading frame 4 complement-c1g tumor necrosis factor-rel	3.0 3.0	3.9 3.7
	426919	AL041228	- 2.7 10002	ELAV (embryonic lethal, abnormal vision,	3.0	9.0
	424724	T06532	Hs.287709	Homo sapiens cDNA: FLJ22674 fis, done H	3.0	3.0
25	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	3.0	10.0
23	408947 426325	AL080093 D28114	Hs.49117 Hs.169309	Homo sapiens mRNA; cONA DKFZp564N1662 (1	3.0	13.5
	429006	AA443143	Hs.50929	myelin-associated ofigodendrocyte basic hypothetical protein FLJ13842	29 29	81.1 6.6
	410711	A8002316	Hs.65746	KIAAD318 protein	29	6.1
20	415486	H12214	Hs.13284	ESTs, Wealdy similar to 2109260A B cell	2.9	15.7
30	424474	AA308883	Hs.148680	catcyon; D1 dopamine receptor-interactin	2.9	3.6
	448299 419518	AA497044 U79289	Hs.20887 Hs.90798	hypothetical protein FLJ10392	2.9	11.5
	426529	AF090100	Hs.170241	Human clone 23695 mRNA sequence Homo sapiens clone IMAGE 23915	2.9 2.9	3.6 5.1
26	430347	NM_002039	Hs.239706	GRB2-associated binding protein 1	2.9	3.2
35	429401	AW296102	Hs.99272	ESTs, Weakly similar to \$32567 A4 protei	2.9	6.1
	450154	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	2.9	5.9
	434277 424790	X77748 AL119344	Hs.3788 Hs.13326	glutamate receptor, metabotropic 3	2.8	28.5
	416836	D54745	Hs.80247	ESTs. Weakly similar to 2004399A chromos cholecystokinin	2.8 2.8	23.1 6.8
40	449277	AA001064	Hs.43570	ESTs	2.8	8.5
	451952	AL120173	Hs_301663	ESTs	2.7	19.2
	408554 413408	AA836381 R51793	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	2.7	3.7
	410343	AA084273	Hs.1440 Hs.76561	OEAD/H (Asp-Glu-Ala-Asp/His) box polypep ESTs, Weakly similar to S47072 finger pr	2.7 2.7	3.0 3.2
45	420489	AA815089	Hs.193513	ESTs	2.7	4.1
	447359	NM_012093	Hs.18268	adenylate kinase 5	2.7	17.2
	423731	T08814		gb:EST06706 Infant Brain, Bento Soares H	2.7	4.0
	409953 424481	AA332277 R19453	Hs.57691 Hs.1787	cadherin 18, type 2	2.7	5.5
50	449714	AB033015	Hs.23941	proteolipid protein 1 (Pelizaeus-Merzbac KIAA1189 protein	. 2.7 2.7	11.5 7.5
	424922	BE386547	Hs.217112	hypothetical protein MGC10825	2.7	3.7
	432447	X92681	Hs.2998	contactin 2 (axonal)	2.7	4.1
	420071 438068	AB028985	Hs.94806	ATP-binding cassette, sub-family A (ABC1	2.7	5.1
55	418512	AI927209 AW498974	Hs.306210	Homo sapiens cONA: FLJ23133 fis, clone L diacytglycerol kinase, zeta (104k0)	2.6 2.6	5.1
	447761	AF061573	Hs.19492	protocadherin 8	2.6	7.9 6.3
	448743	AB032962	Hs.21896	KIAA1136 protein	2.6	23.2
	408547	AA574291	Hs.57837	ESTs	2.6	4.0
60	426380 420898	Al291267 AB002379	Hs.149990 Hs.100113	ESTs KIAA0381 protein	2.6	6.9
•	440357	AA379353	Hs.20950	phospholysine phosphohistidine inorganic	2.6 2.6	3.7 3.7
	424572	M19650		7.3-cyclic nucleotide 3 phosphodieste	2.6	5.9
	418338	NM_002522		neuronal pentraxin I	2.5	6.1
65	427658 410359	H61387 R38624	Hs.30868	nogo receptor	2.5	3.0
05	449717	AB040935	Hs.106313 Hs.23954	ESTs cerebral cell adhesion molecule	2.5	6.3
	424458	M29273	Hs.1780	myelin associated glycoprotein	2.5 2.5	10.1
	450133	AW969769	Hs.105201	ESTs	2.5	40.5
70	428976	AL037824	Hs.194695	ras homolog gene family, member I	2.5	17.4
70	454293 408447	H49739 AK002089	Hs. 134013		2.5	9.5
	414683	\$78298	Hs.45080 Hs.76888	Homo sapiens cDNA FLJ11227 fis, clone PL hypothetical protein MGC12702	2.5 2.5	3.9
	422927	AW247388	Hs.301423		25	7.1 3.0
75	449568	AL157479	Hs.23740	KIAA1598 protein	2.5	3.6
75	454053	AW023006	Hs.27172	ESTs, Moderately similar to PC4259 ferri	2.5	3.6
	428495 431096	NM_013279 AA324358			2.5	3.2
	452371	R40990	Hs.249227 Hs.21658	Homo saplens DNA, cosmid clones TN62 and ESTs	2.4 2.4	3.6 3.3
60	424997	AL138167	Hs.96920	ESTs	2.4	5.2 6.2
80	450310	N62341	Hs.94116	ESTs	24	3.6
	452898	AAB14497	Hs.78792	ESTs	2.4	3.9
	436734 421931	AJ937612 NM_000814	Hs.273758 Hs.1440	hypothetical protein FLJ23112 gamma-aminobutyric acid (GABA) A recepto	2.4	4.7
	-21501			Anima animarchier and (OVDV) v (ROSD()	2.4	3.1

	439428	AA835825	Hs.190490	ESTs	2.4	3.0
	445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	2.4	8.1
	436420	AA443966	Hs.31595	ESTs	24	3.7
_	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	24	3.0
5	451407	AA131376	Hs.343809	fibroblast growth factor 12B	2.4	7.2
-	419757	AA773820	Hs.63970	ESTs	24	3.3
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	24	3.6
	439199	R40373	Hs.26299	ESTs .	2.3	9.5
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	2.3	5.6
10	454048	H05626	Hs.6921	ESTs	23	9.9
• •	412675	AA460716	Hs.9788	hypothetical protein MGC10924 similar to	23	3.3
	434811	AW971205	Hs.114280	ESTs	23	6.7
	431677	AK000496	Hs.306989	hypothetical protein FLJ20489		
	451388	AB029006	Hs.26334		23	3.1
15	447028	AJ973128	Hs.167257	spastic paraplegia 4 (autosomal dominant	23	3.1
	451050	AW937420	Hs.69662	brain link protein-1	2.3	5.6
	437397	AA349847		ESTs	2.3	4.4
	408838	AI669535	Hs.4221 Hs.40369	hypothetical protein DKFZp761H039	23	4.8
	408777			ESTs	2.3	3.0
20	453924	U71204 R49295	Hs.47626 Hs.24886	Ric (Drosophila)-like, expressed in neur	23	3.8
20				ESTS	2.3	13.4
	422709	AA315331	Hs.153485	ESTs	2.3	4.4
	438911	AF085841	Hs.301920	ESTs .	2.3	3.3
	439108	AW163034	Hs.6467	synaptogyrin 3	2.2	6.9
25	420297	A1628272	Hs.88323	ESTs, Wealthy similar to ALU1_HUMAN ALU S	2.2	4.1
25	404819	45040000	44 445445	NM_002688*:Homo sapiens peanut (Drosophi	2.2	5.8
	422544	AB018259	Hs.118140	KIAA0716 gene product	2.2	11.8
	433597	AA708205	Hs.100343	ESTs	22	11.0
	440152	AB002376	Hs.7006	KIAAD378 protein	2.2	14.2
20	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	2,2	82.9
30	409892	AW956113	Hs.7149	gb:EST368183 MAGE resequences, MAGD Homo	2.2	4.2
	425287	R88249	Hs.155524	peanut (Drosophila)-like 2	2.2	6.0
	433657	AJ244368	Hs.8124	PH domain containing protein in retina 1	2.2	5.0
	438703	AI803373	Hs.31599	ESTs	2.2	6.2
25	428845	AL157579	Hs.153610	KIAA0751 gene product	2.2	6.7
35	417865	AW086059	Hs.6529	ESTs, Weakly similar to 178885 serine/th	2.2	3.5
	425897	AA935315	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	2.2	3.2
	419271	N34901	Hs.238532	ESTs	2.2	7.5
	448548	R13209	Hs.21413	solute carrier family 12, (potassium-ch)	22	7.3
40	439415	F05538	Hs.4273	ESTs	2.2	31.3
40	415170	R44386	Hs.164578	ESTs	2.2	10.9
	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-li	2.1	6.2
	443728	AJ083876	Hs.148383	ESTs	2.1	4.1
	452108	AW135982	Hs.203013	hypothetical protein FLJ12748	2.1	5.7
	429037	X81895	Hs.194765	H.sapiens GENX-5624 mRNA, 3' UTR	21	7.1
45	418900	BE207357	Hs.3454	KIAA1821 protein	2.1	4.3
	421268	AJ126821	Hs.30514	ESTs	21	4.2
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	2.1	15.6
	425741	AF052152	Hs.159412	Homo sapiens clone 24528 mRNA sequence	2.1	6.5
	450214	8E439763	Hs.227571	regulator of G-protein signalling 4	2.1	3.3
50	452738	AL133800	Hs.7086	hypothetical protein MGC12435	21	3.5
	447877	AJ435184	Hs.164252	ESTs	2.1	5.1
	422421	AA325138	Hs.235873	hypothetical protein FLJ22672	2.1	8.3
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	2.1	4.2
	410631	AA086469	Hs.47171	ESTs	2.1	5.8
55	407808	AA663559	Hs.279789	histone deacetylase 3	2.1	5.7
	424379	Z42034	Hs.93597	cyclin-dependent kinase 5, regulatory su	2.1	3.2
	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	21	3.0
	433932	AW954599	Hs.169330	neuronal protein	21	6.9
	425130	AA448208	Hs.99163	ESTs	21	3.1
60	402027		113.55166	Target Exon	2.0	3.5
	435191	R15912	Hs.4817	Homo sapiens clone 24461 mRNA sequence		
	420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA he	20	7.5
	404541	70 100170	113.307.30		20	10.7
	420050	AL118615	Hs.94653	NM_030795:Homo seplens stathmin-like 4 (neurochondrin	20	6.0
65	417868	AI078534	Hs.122592		2.0	6.5
00	416602		Ha 70300	ESTs	20	5.6
	436315	NM_006159 BE390513		nel (chicken)-like 2	2.0	3.2
	439340	AB032436	Hs.27935	hypothetical protein MGC4837	2.0	4.2
	429900		Hs.6535	brain-specific Na-dependent inorganic ph	2.0	6.3
70		AA460421 T78028	Hs.30875	ESTs	20	4.2
, 0	437762		Hs.154679		2.0	4.6
	425172	AA447729	Hs.12714	ESTs	2.0	3.1
	419587	\$62907	Hs.91343	gamma-aminobutyric acid (GABA) A recepto	2.0	3.1
	451734	NM_006176		neurogranin (protein kinase C substrate.	2.0	4.9
75	423603	AB007880	Hs.129883		2.0	4.3
,,	438277	AL022326	Hs.6139	synaptogyrin 1	2.0	3.4
	423767	H18283	Hs.132753		2.0	3.2
	434933	R91095	Hs.4276	KIAA1701 protein	2.0	6.1
	426575	M74826	Hs.170808	glutamate decarboxylase 2 (pancreatic is	2.0	4.6

80

TABLE 188: Pkey: CAT number: Accession: Unique Eos probeset identifier number Gene cluster number Genbank accession numbers

	Pkey	CAT Number	Accession				
	408065	103646_1		03154 AA059300 AA046911			
5	415527	1539393_1		2 H08936 R56332 H09256 R52303 R13075 3 H72694 F20990 R08580			
,	415666 418512	1543492_1 176394_1		3 H72094 P20990 R08580 1332 R58460 AA350990 T33788 T30936 AA350905 TI	18592 T09274 AA22429	7 DS4678 T08951 R	15346 AW953188 AA350074
	410012	110034_1	AW890649				
	418866	179788_1	T65754 AA229				
10	420111	190755_1		280911 AW967920 AA262684	140 1000 DECORATE 300	****	
10	422890	222707_1		2 AW572911 AA449369 H17037 R19603 A1632565 A1 53735 A1263703 AA319159 AW964436 A1903440 AW1			
			T87230 AI3	33/33 N203/03 NG 13/33 KTT 30H30 KISWAND KTT	Paris I VIDOS AND MISTO	-0/1 AN330110 C1	3010 DD1142 H17430 H17102543
	423731	231456_1		8 AL120536 AA330218 AW961552 N47159			
16	424572	24097_1	M19650 R188	10 R18721 AW896148 AW889520 AA192362 AA1768	14 F12085 BE255264 BE	251393 T65248 AA	380585 AA380465 BE408684
15				498869 AA776107 BE274289 D45269 M61958 AA378	818 AW663180 AW672	358 H08511 M7816	8 BE393721 AA348660 R36303
	424945	245223_1		.019090 AA001 967 AA348780 AW964077 AW166028 BE540193 N94	800 AA452358 N99604 A	N341345 AW29880	0 AA724961 AA931158 AI741227
	424340	T-ANTEN_I		2626 D81263 D53937 D52496 AA974487 AW043854			
20			Al193687 Al34				
20	426919	273507_1		2004 D61361 AI203314 AI990307 AW900295 AI01830 062234 AW748388	8 AW087473 AW183530	AA393346 H50055	AA935601
	433670 433921	372721_1 377350_1		14549 R36464 R36465			
	433940	37787_1		33 AI651350 AA984734 AI368716 N40915 AI989705 F	709042 T03905 R88588	AF112220	
25	435773	426857_1		857375 N64357 AA731069			
25	446692	689623_1	Z44514 Al352	097 A1803984 AW235923 AW196558 A1954637 A1336	983		
	TABLE 18	C.					
	Pkey:		que number corre	sponding to an Eos probeset			
20	Ref:			he 7 digit numbers in this column are Genbank Identific		m, et al." refers to th	e publication entitled 'The DNA
30	Strand:			chromosome 22" Dunham, et al. (1999) <u>Nature</u> 402:48! I from which exons were predicted.	3-495.		
	Nt_positio			positions of predicted exons.			
25	Pkey	Ref	Strand	Nt_position			
35	400844 402027	9188505 7622350	Plus Plus	24746-24872,25035-25204 51645-51888.52917-53006			
	404541	8318559	Plus	103456-103664	•		
	404819	4678240	Plus	16223-16319,16427-16513,16736-16859,16941-1707	5,17170-17287,17389-1	7529,18261-18357,	18443-18578
40	405560	183148	Plus	5495-5655,6077-6241,6495-6692			
40	405819 406311	4007557 9211559	Plus Minus	2830-2967 137114-139033			
	400011	3211333	HILL CO	13/114133003			
				D GENES SIGNIFICANTLY DOWN-REGULATED IN			
15				genes significantly down-regulated in glioblastoma com			
45	the Allym	etrix/Eos Hu03	GeneChip array	such that the ratio of "average" normal CNS to "average normal CNS tissues. The "average" glioblastoma leve	e glioblastoma was gre	eatile emonest verif) 2. The "average" normal CNS level wa
				S to "average" non-CNS normal adult tissues was calcu			
				The "average" normal non-CNS adult tissue level was			
50				of non-specific hybridization, the 10° percentile value ϵ	mongst non-matignant ti	ssues was subtracte	ed from both the numerator and the
30	denomina Pkey:		ratios were evalu	ated. et identifier number			
	ExAcon:			n number, Genbank accession number			
	Unigenel		rigene number				
55	Unigene		nigene gene title				
22	R1: R2:		atio of CNS to Gli	DOLASIONTA IN-CNS NORMAL ADULT TISSUES			
	TGE.	14	2000 043 8 110	WOOD HOTOMACABOCT TISSOCS			
	Pkey	ExAcca	UnigenetD	Unigene Title	R1	R2	
60	425489	M58594	Hs.1905	prolactin	24.8	10.5	
00	410330 430538	AW023630 AB032435		ESTs differentiation-associated Na-dependent	23.4 22.6	23.4 22.6	
	417275	X63578	Hs.295449	parvalbumin	22.4	6.0	
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	21.8	21.8	
65	408040	A1266496 A1277259	Hs.22905	ESTs, Weakly similar to RHG6_HUMAN RHO-G	19.4	19.4	
05	435145 407039	X00368	Hs.116631	ESTs gb:Human prolactin gene 5' region.	18.5 18.1	3.8 18.1	
	409263	AA069573	Hs.50319	ESTs	16.8	16.8	
	432298	AL118812		Homo sapiens mRNA; cDNA DKFZp761G1111 (f	15,1	15.1	
70	424645	NM_01468		KIAA0535 gene product	15.1	15.1	
70	416018 405560	AW138239 AW88770		proprotein convertase subtilisin/kexin t hypothetical protein FLJ20628	14.0 13.9	14.0 8.0	
	452022	AW07233		ESTs	13.8	13.8	
	413324	V00571	Hs.75294	corticotropin releasing hormone	13.2	13.2	
75	411498	NM_01421		ecotropic viral Integration site 2A	12.9	19.4	
13	423449 433940	AJ497900 H05129	Hs.33067	ESTs cyclic AMP-regulated phosphoprotein, 21	12.4 12.0	14.5 12.0	
	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate potype	11.5	11.5	
	449078	AK001256	Hs.22975	KIAA1576 protein	11.0	16.1	
80	410635		Hs.334372		11.0	6.6	
٥U	453165		Hs.32042 7 Hs.4290	aspartoacylase (aminoacylase 2, Canavan ESTs	10.7 10.4	10.7 10.4	
	417167 420033		/ Hs.4230 Hs.292590		10.4	10.4	
	413293				10.0	10.0	
				201			

	418207	C14685	Hs.34772	ESTs	9.8	9.8
	417175	R44558	Hs.94002	ESTs	9.6	8.9
	444330	AI597655	Hs.49265	ESTs	9.1	9.1
5	427322	AK002017	Hs.176227	hypothetical protein FLJ 11155	8.9	8.9
,	429096 428652	A8011106 AA584272	Hs.196012 Hs.336224	KIAA0534 protein transmembrane protein with EGF-like and	8.6 8.6	8.6
	419347	C15944	Hs.90005	superiorcervical ganglia, neural specifi	8.6	8.6 22.2
	410309	BE043077	Hs.278153	ESTs	8.5	8.5
10	416851	AW963951	Hs.85618	ESTs	8.5	8.5
10	427051	AB032971	Hs.173392	KIAA1145 protein	8.4	8.4
	400438 440209	AF185611 H05049	Hs.115352 Hs.247837	Target neurexin 3	8.3 8.2	5.1 18.7
	422756	AA441787	Hs.119689	glycoprotein hormones, sipha polypeptide	8.1	5.8
16	435648	H24347	Hs.27524	ESTs	8.1	8.1
15	429470	AI878901	Hs.203862	guarrine nucleotide binding protein (G pr	8.0	8.0
	416133 408814	NM_001683 N62499	Hs.89512 Hs.176227	ATPase, Ca transporting, plasma membrane hypothetical protein FLJ11155	8.0 7.9	8.0 8.6
	430004	U27768	Hs.227571	regulator of G-protein signating 4	7.9	15.7
20	436427	AI344378	Hs.143399	ESTs	7.8	7.8
20	434367	AB020700	Hs.3830	KIAA0893 protein	7.8	5.6
	429875 441005	AB028977 Z41305	Hs.225974 Hs.303172	KIAA1054 protein	7.8 7.7	16.8
	442023	AJ187878	Hs.144549	Homo sepiens mRNA; cDNA DKFZp547G133 (ir ESTs	7.7	7.7 5.6
~-	429033	NM_007374	Hs.194756	sine oculis homeobox (Drosophila) homolo	7.6	5.5
25	450642	R39773	Hs.7130	copine IV	7.6	5.6
	437073	A1885608	Hs.94122	ESTS	7.5	7.5
	441264 424153	AA927170 AA451737	Hs.23290 Hs.141496	ESTs MAGE-fike 2	7.3 7.3	7.3 5.1
	450474	AW872844	Hs.117494	ESTs	7.2	7.2
30	450715	A1266484	Hs.31570	ESTs, Wealthy similar to KIAA1324 protein	7.2	7.2
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	7.1	4.8
	423003 433921	AL120077 AA618174	Hs.122957	kelch (Orosophila)-like 2 (Mayven)	7.0 7.0	7.0
	425352	NM_000939	Hs.1897	gb:nq14f01.s1 NCI_CGAP_Thy1 Homo saplens proopiomelanocortin (adrenocorticotropin	6.9	7.0 6.1
35	457012	R41480	Hs.302754	ESTs	6.9	6.9
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	6.9	6.9
	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	6.9	6.9
	409031 453590	AA376836 AF150278	Hs.288856 Hs.33578	ESTs KIAA0820 protein	6.8 6.6	6.8 22.3
40	450181	H05254	Hs.201198	EST8	6.6	7.2
	425580	L11144	Hs.1907	galanin	6.5	3.5
	445279	R41900	Hs.22245	ESTs .	6.4	6.4
	428414	AL049980	Hs.184216	DKFZP564C152 protein	6.4	6.4
45	434104 443244	AF116691 AI457235	Hs. 116459 Hs. 166479	hypothetical protein PRO2198 ESTs	6.4 6.3	4.D 3.0
	447750	AI422234	Hs.143434	contactin 1	6.2	9.8
	415114	D60468	Hs.94181	ESTs	6.0	6.0
	450600	BE079478	Hs.24880	ESTs	5.9	3.9
50	444458 448958	BE041526 AB020651	Hs.31746 Hs.22653	hypothetical protein DKFZp547F072 KIAA0844 protein	5.9 5.9	7,7 5.9
50	447138	AJ439112	Hs.93828	ESTs, Weakly similar to 2109260A B cell	5.8	5.8
	414545	AA149287	Hs.76605	ESTs	5.8	3.6
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHU86 salivary	5.6	9.6
55	450590 408428	AI701507	Hs.273740	ESTs	5.6	3.8
"	442026	NM_014787 AI243749	Hs.44896 Hs.8074	DnaJ (Hsp40) homotog, subfamily B, membe brain-specific angiogenesis inhibitor 3	5.6 5.5	5.6 6.5
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	5.4	5.4
	414699	AJ815523	Hs.76930	syruclein, alpha (non A4 component of am	5.3	4.5
60	438202 448605	AW169287	Hs.22588	ESTS	5.3	5.3
00	418868	AL109678 T65754	Hs.21597	Homo sapiens mRNA full length insert cDN gb:yc11c07.s1 Stratagene lung (937210) H	5.3 5.3	5.3 3.8
	448786	BE048842	Hs.179075		5.2	5.2
	406311			NM_021979":Homo sapiens heat shock 70kD	5.2	11.5
65	443682	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	5.2	3.3
UJ	415666 415101	H72693 R24854	Hs.268806	gb:yu03c11.r1 Soares fetal liver spleen ESTs	5.2 5.2	5.2 3.3
	428508	BE252383	Hs.184668		5.2	4.1
	419318	AW969742	Hs.291005		5.2	3.1
70	439238	N47305	Hs.302161		5.1	5.3
70	446353 412049	AI290919 NS3437	Hs.153661 . Hs.18268	ESTs adenylate kinase 5	5.1	5.1 10.7
	437331	AL353933	Hs.21710	hypothetical protein DKFZp761G0313	5.1 5.1	5.1
	413988	M81883	Hs.324784		5.1	5.1
75	408068	AW148652	Hs.167398		5.0	5.0
13	414631	AW970130	Hs.65408	ESTs	4.9	4.9
	418527 425073	AA450386 W39609	Hs.7149 Hs.22003	Horno sapiens cONA: FLJ21950 fis, clone H solute carrier family 6 (neurotransmitte	4.9 4.9	4.9 4.9
	427224	AL135554	Hs.101937		4.9	3.9
90	433516	AA595802	Hs.33410	ESTs. Weakly similar to T17279 hypotheti	4.8	4.8
80	427287	NM_014903			4.8	4.B
	447252 424932	R90916 R14070	Hs.12449 Hs.315369		4.8	3.2 10.2
	419643		Hs.91791	chromosome 11 open reading frame 25	4.7 4.7	4.7
					•••	

					4	
	414949 453534	C15314	Hs.323349 Hs.33187	ESTs	4.7	3.8
	430537	NM_014796 X62692	Hs.2593	KIAA0748 gene product phosphodiesterase 68, cGMP-specific, rod	4,7 4,6	4.7 4.6
_	453431	AF094754	Hs.32973	glycine receptor, beta	4.6	4.6
5	453302	NM_000838	Hs.32945	glutamate receptor, metabotropic 1	4.6	4.6
	447104	R19085	Hs.210706	Homo sapiens cDNA FLJ13182 fis, clone NT	4.6	3.0
	418202 419191	N48521 U17195	Hs.26549	KIAA1708 protein	4.6	5.8
	459080	AW192083	Hs.89666 Hs.290855	A kinase (PRKA) anchor protein 6 ESTs	4.5 4.5	4.5 13.5
10	451783	R42554	Hs.210862	T-box, brain, 1	4.4	11.2
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	4.4	3.2
	451050	AW937420	Hs.69662	ESTs	4.4	4.4
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	4.4	7.9
15	447745 451301	AW015920 AI769514	Hs.161359 Hs.209890	ESTs EST	4.3 4.3	9.9
	452381	H23329	Hs.290880	ESTs, Wealdy similar to ALU1_HUMAN ALU S	4.3	4.3 4.3
	433109	N58907	Hs.162430	EST	4,3	3.9
	412155	R38167	Hs.12449	Homo saplens transmembrane protein HTMP1	4.3	27.9
20	426365	AA376667	Hs.10283	RNA binding motif protein 88	4.3	4.1
20	423589 432453	AA328082 AI885537	Hs.209569 Hs.27172	ESTs Mandacratatu similar to DC4350 facri	4.2 4.2	4.2
	420489	AA815089	Hs.193513	ESTs, Moderately similar to PC4259 ferri ESTs	4.1	3.9 4.1
	427457	AW779105	Hs.164682	ESTs	4.1	11.1
25	408206	AF041853	Hs.43870	kinesin family member 3A	4.1	4.1
25	433803	AI823593	Hs.27688	ESTs	4.1	4.1
	407868 448117	NM_000950 H49129	Hs.40637 Hs.172982	profine-rich Gla (G-carboxyglutamic acid ESTs	4.1 4.1	3.3
	442106	AW205881	Hs.326728	ESTs	4.1	4.1 3.2
	450757	BE081050	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	4.0	3.2
30	442042	AI990506	Hs.8077	Homo sapiens mRNA; cDNA DKFZp547E184 (fr	4.0	6.2
	458694	F12832	Hs.3610	ESTs	4.0	4.0
	452197 448583	AW023595 NM_015239	Hs.232048	ESTs	4.0	4.0
	418940	H17739	Hs.21542 Hs.288513	KIAA1035 protein Human DNA sequence from clone RP5-899C14	4.0 3.9	4.0 7.0
35	442412	R77677	Hs.346644	ESTs	3.9	3.9
	440293	AI004193	Hs.22123	ESTs	3.9	3.9
	433670	AA604405		gb:no87h09.s1 NCI_CGAP_AA1 Homo sapiens	3.9	3.9
	459697 429290	AA406062 AF203032	Hs.98002 Hs.198760	ESTS	3.9 3.9	5.4
40	426054	U12431	Hs.166109	neurofilament, heavy polypeptide (200kD) ELAV (embryonic lethal, abnormal vision,	3.9	3.3 3.9
-	424001	W67883	Hs.137476	paternally expressed 10	3.8	5.4
	442676	AI733585	Hs.130897	ESTs ·	3.8	3.8
	410240	AL157424	Hs.61289	synaptojanin 2	3.8	4.6
45	409339 434998	AB020686 AW975157	Hs.54037 Hs.26037	ectonucleotide pyrophosphatase/phosphodi	3.7	3.6
73	439450	R51613	Hs.125304	ESTS	3.7 3.7	3.7 8.3
	455364	H72176	Hs.4273	hypothetical protein FLJ13159	3.7	4.9
	400844			NM_003105":Homo saplens sortilin-related	3,7	3.1
50	458765	AI497900	Hs.33067	ESTs	3.7	3.7
20	452667 436773	T87219 AW078629	Hs.13219	ESTs PC4 and SERS1 interaction partoin 1	3.6	3.6
	453220	A8033089	Hs.32452	PC4 and SFRS1 interacting protein 1 Homo sapiens mRNA for KIAA1253 protein,	3.6 3.6	3.6 19.9
	432149	AW614326	Hs.133483	ESTs, Weakly similar to T34549 probable	3.6	12.2
66	408119	W26213	Hs.101672	ESTs, Weakly similar to T00331 hypotheti	3.6	3.6
55	449093	AB035356	Hs.22998	neurexin 1	3.6	3.6
	426968 410011	U07616 AB020641	Hs.173034 Hs.57856	emphiphysin (Stiff-Mann syndrome with br	3.6	15.3
	442738	AW002370	Hs.131055	PFTAIRE protein kinase 1 ESTs, Weakly similar to NPM_HUMAN NUCLEO	3.6 3.5	10.0 3.5
	451032	W03692	Hs.323079		3.5	4.9
60	449117	AW449310	Hs.210262	ESTs, Weakly similar to HSS2_HUMAN HEPAR	3.5	3.5
	416490	AF090116	Hs.79348	regulator of G-protein signalling 7	3.5	12.5
	412268 452311	N59006 AW304029	Hs.26133 Hs.252744	ESTS ESTS	3.5 3.5	30.9
	425649	U30930	Hs.158540		3.5	3.5 38.6
65	410224	M55513	Hs.150208		3.4	3.4
	451516	AI800515	Hs.12024	ESTs	3.4	6.3
	400098	012002	11- 150300	Eos Control	3.4	3.4
	424918 452238	R13982 F01811	Hs.169309 Hs.345757		3.4 3.3	5.3
70	417063	N50515	Hs.45061	ESTs	. 3.3	3.8 3.3
	443992	AW022228	Hs.322922	ESTS	3.3	13.1
	412453	R20205	Hs.75236	ESTs	3.3	3.3
	450561	R49674	Hs.25909	ESTs	3.3	3.3
75	415527 427386	F11624 AW836261	Hs.6727	gb:HSC2ZD101 normalized infant brain cDN ESTs	3.3 3.3	3.3
	423346	AJ267677	Hs.127416		3.3 3.2	3.3 20.1
	431342	AW971018		ESTS	3.2	8.0
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	3.2	9.6
80	442879 417284	AF032922 N62889	Hs.8813	syntaxin binding protein 3	3.2	3.2
	429477	AJ275514	Hs.107242 Hs.6658	Phomo sepiens cDNA FLJ12965 fts, clone NT ESTs	3.2 3.2	3.2 3.2
	410343	AA084273	Hs.76561	ESTs, Wealdy similar to \$47072 finger pr	3.2	3.2
	427317	AB028955	Hs.175780	KIAA1032 protein	3.2	5.3

	408039	AA131424	Hs.336636	ESTs	3.2	3.2
	428976 420297	AL037824 AI628272	Hs.194695 Hs.88323	ras homolog gene family, member 1 ESTs, Weakly similar to ALU1_HUMAN ALU S	3.2 3.2	17.4 4.1
	453919	AW959912	Hs.7076	KIAA1705 protein	3.2	3.2
5	428963	AW382682	Hs.258208	Homo sapiens, clone MGC:15606, mRNA, com	3.2	3.3
	423829	R44107	Hs.240905	ESTs	3.1	4.4
	424087	N69333	Hs.143434	contactin 1	3.1	3.1
	419852 444783	AW503756	Hs.286184	hypothetical protein dJ551D2.5	3.1	4.1
10	422234	AK001468 AF119818	Hs.62180 Hs.113287	anillin (Drosophila Scraps homolog), act discs, large (Drosophila) homolog-associ	3.1 3.1	43.2 3.1
••	446692	Z44514	113.110201	Homo sepiens mRNA for KIAA1763 protein,	3.1	33.0
	437117	AL049256	Hs.122593	ESTa	3.1	3.8
	405819			NM_002578:Homo sapiens p21 (CDKN1A)-acti	3.1	13.5
15	452752	AW044058	Hs.33578	KIAA0820 protein	3.1	13.4
15	416220	N49776 AL359577	Hs.170994	hypothetical protein MGC10946	3.1	4.5
	437380 428001	H97428	Hs.112198 Hs.219907	Homo sapiens mRNA; cDNA DKFZp547M073 (fr ESTs, Moderately similar to Transforming	3.0 3.0	3.8 5.9
	445725	AK000956	Hs.13209	hypothetical protein FLJ10094	3.0	3.0
	447673	AI823987	Hs.182285	ESTs	3.0	3.0
20	427283	AL119796	Hs.174185	ectonucieotide pyrophosphatase/phosphodi	3.0	3.0
	424724	T06532	Hs.287709	Homo sepiens cONA: FLJ22674 fs, clone H	3.0	3.0
	408547 433315	AA574291	Hs.57837	ESTs	3.0	4.0
	439274	R96754 AF086092	Hs.239706 Hs.48372	GRB2-associated binding protein 1 ESTs	3.0 3.0	3.1 18.3
25	410765	Al694972	Hs.66180	nucleosome assembly protein 1-like 2	30	8.0
	458268	AA428403	Hs.106131	ESTs	3.0	3.9
	424641	AB001106	Hs.151413	glia maturation factor, beta	3.0	5.6
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	3.0	14.9
30	442593 426380	R39804 Al291287	Hs.31961 Hs.149990	ESTS	2.9	6.7
50	428536	Al143139	Hs.2288	ESTs visinin-like 1	. 2.9 2.9	6.9 22.1
	417417	F05745	Hs.89512	ATPase, Ca transporting, plasma membrane	29	17.1
	411379	AI816344	Hs.12554	ESTs, Wealty similar to NPL4_HUMAN NUCLE	2.9	11.2
26	422414	AW875237	Hs.13701	ESTs	2.9	5.3
35	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	2.9	3.9
	419518 426919	U79289 AL041228	Hs.90798	Human clone 23695 mRNA sequence	2.9	3.6
	446544	AJ631932	Hs.7047	ELAV (embryonic lethal, abnormal vision, ESTs, Wealdy similar to Unknown [H.sapie	2.9 2.8	9.0 12.4
	422411	AW749443	Hs.22511	ESTs	2.8	12.0
40	416874	H98752	Hs.42568	ESTs	2.8	6.0
	448902	Z45998	Hs.22543	Homo sepiens mRNA; cONA DKFZp76111912 (f	2.8	21.8
	430456	AA314998	Hs.241503	hypothetical protein	2.8	4.7
	429859 429656	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	2.8	5.1
45	437948	X05608 AA772920	Hs.211584 Hs.303527	neurofilament, light polypeptide (68kD) ESTs	2.8 2.8	13.1 24.8
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	2.8	8.2
	414931	AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZp761M0223 (f	28	3.4
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	2.8	4.4
50	446574	AI310135	Hs.335933	ESTs	2.8	3.5
50	422890 410711	Z43784 AB002316	Hs.65746	ankyrin 3, node of Ranvier (ankyrin G)	2.8 2.7	3.6
	422980	N46569	Hs.76722	KIAA0318 protein CCAAT/enhancer binding protein (C/EBP),	2.7	6.1 45.2
	408554	AA836381	Hs.315111		2.7	3.7
	434460	AA478486	Hs.3852	KIAA0368 protein	2.7	4.8
55	431988	AC002302	Hs.77202	protein kinase C, beta 1	2.7	10.5
	447163 437924	AW292770 AI935344	Hs.5542 Hs.164118	DnaJ (Hsp40) homolog, subfamily C, membe	2.7	3.4
	424945	AI221919	rts. 104 (10	ESTs, Weeldy similar to SL51_HUMAN SODIU hypothetical protein FLJ10582	2.6 2.6	3.2 30.5
	425984	AW836277	Hs.165636		2.6	29.3
60	447761	AF061573	Hs. 19492	protocadherin 8	2.6	6.3
	425138	H08849	Hs.167464	glutamate receptor, ionotropic, N-methyl	2.6	4.2
	436568	H12049	Hs.91584	ESTs	2.6	6.8
	408065 430287	AW954272 AW182459	U. 10F7F0	gb:EST366342 MAGE resequences, MAGC Homo	2.6	5.6
65	408777	U71204	Hs.125759 Hs.47626	ESTs, Weakly similar to LEU5_HUMAN LEUKE Ric (Drosophila)-like, expressed in neur	2.6 2.6	7.6 3.8
	420173	AA256151	Hs.22999	ESTs	2.6	4.1
	429550	AW293055	Hs.119357		2.6	6.4
	438068	AI927209	Hs.306210		26	5.1
70	424264	D80400	Hs.239388		2.6	7.3
70	432809	AA565509	Hs.131703		2.6	9.9
	407886 445225	AW969688 AI216555	Hs.100826 Hs.202398		2.5 2.5	20.2
	415257	F03016	Hs.27513	ESTS	2.5	5.5 B.6
	423135	N67655	Hs.26411	ESTs	2.5	8.2
75	438283	AI458931	Hs.37282	ESTs	2.5	7.5
	454053	AW023006	Hs.27172	ESTs, Moderately similar to PC4259 ferri	2.4	3.6
	443150		Hs.34650	ESTs	2.4	7.6
	429958 428392		Hs.22542	ESTs constant ordered control control	2.4	3.2
80	437268		Hs.2265 Hs.227571	secretory granufe, neuroendocrine protei regulator of G-protein signatting 4	2.4 2.4	42.3 14.0
	426529		Hs.170241		2.4	5.1
	430347	NM_002039			2.4	3.2
	422949	AA319435		gb:EST21657 Adrenal gland tumor Homo sap	2.4	7.4

	451952	AL120173	Hs.301663	ESTs	2.4	19.2
	434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	2.4	28.5
	422927	AW247388	Hs.301423	calcium binding protein 1 (calibrain)	2.4	3.0
5	425121	AI797511	Hs.154679	synaptotagmin I	2.4	3.9
3	435059	Z45270 AW014022	Hs.235873	hypothetical protein FLJ22672	2.4 2.4	4.8
	446377 452371	R40990	Hs.170953 Hs.21658	ESTs ESTs	24	3.3 3.3
	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	2.4	8.4
	427658	H61387	Hs.30868	nogo receptor	2.4	3.0
10	448100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	23	3.6
	439607	BE540565	Hs.159460	ESTs	2.3	5.6
	412949	AI471639	Hs.71913	ESTs	2.3	3.7
	419757 410037	AA773820 AB020725	Hs.63970 Hs.58009	ESTs KIAA0918 protein	23 23	3.3 12.2
15	451385	A8029006	Hs.26334	spastic paraplegia 4 (autosomal dominant	2.3	3.1
••	409953	AA332277	Hs.57691	cadherin 18, type 2	2.3	5.5
	419629	AB020695	Hs.91662	KIAA0888 protein	2.3	13.4
	434792	AA649253	Hs.132458	ESTs	2.3	3.8
20	429006	AA443143	Hs.50929	hypothetical protein FLI13842	2.3	6.6
20	445194 422491	AI215667 AA338548	Hs.175044 Hs.117546	ESTs neuronatin	23 23	3.1 3.6
	415734	NM_014747	Hs.78748	KIAA0237 gene product	2.3	27.4
	434933	R91095	Hs.4276	KIAA1701 protein	2.2	6.1
0.0	424922	BE386547	Hs.217112	hypothetical protein MGC10825	2.2	3.7
25	426325	D28114	Hs.169309	myelin-associated oligodendrocyte basic	2.2	81.1
	424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	22 22	56.0
	418410 409746	AAB11441 NM_004794	Hs.107393 Hs.56294	chromosome 3 open reading frame 4 RAB33A, member RAS oncogene family	2.2	3.9 10.6
	439239	AI031540	Hs.235331	ESTs	2.2	49.5
30	450310	N62341	Hs.94116	ESTs	2.2	3.6
	453924	R49295	Hs.24886	ESTs	2.2	13.4
	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	2.2	6.6
	404819			NM_002688*:Homo sapiens peanul (Drosophi	2.2	5.8
35	449568 419271	AL157479 N34901	Hs.23740 Hs.238532	KIAA1598 protein ESTs	2.2 2.2	3.6 7.5
22	424474	AA308883	Hs.148680	calcyon; D1 dopamine receptor-interaction	2.2	3.6
	438208	AL041224	Hs.65379	ES7s	2.2	5.8
	424458	M29273	Hs.1780	myelin associated glycoprotein	2.2	10.1
40	421790	AW896201	Hs.22654	sodium channel, voltage-gated, type I. a	2.2	4.1
40	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	21	4.2
	419863 449277	AW952691 AA001064	Hs.93485 Hs.43670	Homo sapiens mRNA; cDNA DKFZp761D191 (fr ESTs	2.1 2.1	21.4 8.5
	420156	AW449258	Hs.6187	ESTs	2,1	12.5
	452738	AL133800	Hs.7086	hypothetical protein MGC12435	2.1	3.5
45	410366	AI267589	Hs.302689	hypothetical protein	21	10.4
	452106	AJ141031	Hs.21342	ESTs	2.1	3.4
	413409	AI63B418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box potypep	21	9.4
	423641 410909	AL137256 AW898161	Hs.130489 Hs.53112	ATPase, aminophospholipid transporter-li ESTs, Moderately similar to ALU8_HUMAN A	2.1 2.1	6.2 12.5
50	410631	AA086469	Hs.47171	ESTS	2.1	5.8
	412675	AA460716	Hs.9788	hypothetical protein MGC10924 similar to	21	3.3
	448299	AA497044	Hs.20887	hypothetical protein FLJ 10392	2.1	11.5
	444124	R43097	Hs.6818	ESTs	21	9.3
55	408950	AA707814	Hs.14945	long falty scyl-CoA synthetase 2 gene	2.1	8.5
55	432738 429024	AA788898 AI652297	Hs.179902 Hs.119302		21 21	4.0 3.7
	420071	AB028985	Hs.94806	ATP-binding cassette, sub-family A (ABC1	21	5.1
	408822	AW500715	Hs.57079	Homo sapiens cONA FLJ13267 fls, clone OV	2.1	3.0
60	424790	AL119344	Hs.13326	ESTs, Weakly similar to 2004399A chromos	21	23.1
60	426814	AF036943	Hs.172619		2.1	14.2
	425130 449714	AA448208 AB033015	Hs.99163 Hs.23941	ESTs	2.1 2.0	3.1 7.5
	439108	AW163034	Hs.6467	KIAA1189 protein synaptogyrin 3	20	6.9
	415669	NM_005025		serine (or cysteine) proteinase inhibito	20	10.2
65	435040	AI932350	Hs.152825	ESTs	2.0 ⋅	4.7
	440152	AB002376	Hs.7006	KIAA0378 protein	2.0	14.2
	445102		Hs.22270	ESTs	2.0	19.2
	436734 437414	AI937612 AW894071	Hs.273758 Hs.48448	hypothetical protein FLJ23112 hypothetical protein DKFZp547C176	2.0 2.0	4.7 6.4
70	418512		115.40	diacylglycerol kinase, zeta (104kD)	2.0	7.9
	453169		Hs.32156	KIAA1394 protein	2.0	5.7
	420050		Hs.94653	neurochondrin	2.0	6.5
	429900		Hs.30875	ESTs	2.0	4.2
75	432447		Hs.2998	contactin 2 (axonal)	2.0	4.1
13	431677 452856		Hs.306989 Hs.30881	hypothetical protein FLJ20489 protein tyrosine phosphatase, receptor t	2.0 2.0	3.1 10.7
	448681		Hs.21754	Homo sapiens mRNA full length insert cDN	2.0	7.2
	453754				2.0	3.4
90	422544	AB018259	Hs.118140	KIAA0716 gene product	2.0	11.8
80	416836		Hs.80247	cholecystokinin	2.0	6.8
	454048 425741		Hs.6921 Hs.159412	ESTs 2 Homo sapiens clone 24628 mRNA sequence	2.0 2.0	9.9 6.5
	723/41	74 JUL 132	113.133414	admin com conto usana soducina	20	0.3

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	TABLE 198 Pkey:		e Eos probeset i	destifier number			
	CAT numbe		cluster number				
_	Accession:		ank accession n	imbers			
5							
	Pkey	CAT Number 103646_1		02154 44050200 44045041			
	408065 415527	1539393_1		03154 AA059300 AA046911 2 H08938 R56332 H09256 R52303 R13075			
	415666	1543492_1		3 H72694 F20990 R08580			
10	418512	176394_1	AW498974 TO	9332 R58460 AA350990 T33786 T30936 AA350905 T08	592 T09274 AA2242	97 D54678 TO	8951 R15346 AW953188 AA350074
	440056	470700 4	AW890649	063 A ABBOTTO			
	418856 422890	179788_1 222707_1		1857 AA229658 12 AW572911 AA449369 H17037 R19603 A1632565 AWI	104030 RES02530 2	25032 AAR053	24 AA449241 AISS1825 AI2S48S3 AW196918
	422030	222707_1		53735 AI263703 AA319159 AW964436 AI903440 AW59			
15			T87230 AI3				
	422949	223184_1		5456 AAJ 18377 AW961532 T48452 AA894424			
	424945	245223_1		967 AA348780 AW984077 AW166028 BE540193 N9480 12626 D81263 D53937 D52496 AA974487 AW043854 N			
			AI193667 AI3		30463 233331 76432	1901 74301320	FOR AMERICA TESSEE ANTESSE
20	426919	273507_1		2004 D61361 AI203314 AI990307 AW900295 AI018308	AW087473 AW1835	30 AA393346 I	H50055 AA935601
	433670	372721_1		062234 AW748386			
	433921 433940	377350_1		14549 R36464 R36465 33 A1651350 AA984734 A1368716 N40915 A1989705 F0:	MAN TANDAE EIGGEG	0 AE142220	
	436773	37787_1 426857_1		33 Alba 1330 AAS64734 Albab 10 1403 13 Albas 103 PV: 857375 N64357 AA731069	3042 TU33US R0030	0 AF 11222U	
25	445692	689623_1		097 AI803984 AW235923 AW196558 AI954637 AI33698	33		
		_					
	TABLE 19 Pkey:		nua numbas com	sponding to an Eos probeset			
	Ref;			he 7 digit numbers in this column are Genbank Identifier	(GI) numbers, *Dun!	ham, et al." refe	ers to the publication entitled "The DNA
30		seq	uence of human	chromosome 22" Dunham, et al. (1999) Nature 402:489-4			
	Strand:			from which exons were predicted.			
	Nt_positio	n: tha	cates nucleoode	positions of predicted exons.			
	Pkey	Ref	Strand	Nt_position			
35	400844	9188605	Plus	24746-24872,25035-25204			
	404819	4678240	Ptus	16223-16319,16427-16513,16736-16859,16941-17075,	17170-17287,17389	17529,18261	18357,18443-18578
	405560 405819	183148 4007557	Plus Plus	5495-5655,6077-6241,6495-6692 2830-2967			
	406311	9211559	Minus	137114-139033			
40							
	7401 5 2			ED GENES SIGNIFICANTLY DOWN-REGULATED IN LO	************	DI 4070444 C	OMONOCO TO MODIVAL ADMIT CHE
				genes significantly down-regulated in lower grade gliobia			
	59680 pro	besets on the	Affymetrix/Eos H	ut03 GeneChip array such that the ratio of "average" norm	nal CNS to "average"	LGG was gre	ater than or equal to 2. The "average" normal
45				mongst various normal CNS tissues. The "average" LGC			
	CNS spec	cific genes, the	ratio of "average	* CNS to "average" non-CNS normal adult tissues was cr ues. The "average" normal non-CNS adult tissue level w	elculated to be greate	er than or equa	I to 3. The "average" CNS level was set to the
				of non-specific hybridization, the 10° percentile value am			
			the ratios were e		• • • • • • • • • • • • • • • • • • • •	•	
50	Pkey:			et Identifier number			
	ExAccn: Unigenel		emplar Accessio igene number	n number, Genbank accession number			
	Unigene		igene gene title				
	R1:			ared to LOWER GRADE GLIOBLASTOMA			
55	R2:	R	atio of CNS comp	ared to NON-CNS NORMAL ADULT TISSUE			
	Pkey	ExAcon	UnigeneiD	Unigene Title	R1	R2	
	425580	L11144	Hs.1907	gatanin	33.1	3.5	
60	425489	M58594	Hs.1905	protactin	24.7		
UU	430538 417275	AB032435 X63578	Hs.242821 Hs.295449	differentiation-associated Na-dependent parvalbumin	22.6 22.4		
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	21.8		
	408040	AJ266496	Hs.22905	ESTs, Wealty similar to RHG6_HUMAN RHO-G	19.4	19.4	
65	435145	A1277259	Hs.116631	ESTs .	18.5		
05	407039	X00368	H- 104505	gb:Human protactin gene 5' region.	18.1		
	428976 409263	AL037824 AA069573	Hs.194695 Hs.50319	ras homolog gene family, member I ESTs	17.4 16.8		
	424645	NM_01468		KIAA0535 gene product	15.1		
70	416018	AW13823		proprotein convertase subtilisin/kexin t	14.0		
70	405560	AW88770 AW07233		hypothetical protein FLJ20628	13.9 13.8		
	452022 433940	H05129	/ ns.253675	ESTs cyclic AMP-regulated phosphoprotein, 21	12.0		
	413324	V00571	Hs.75294	corticotropin releasing hormone	12.0		
76	410657	AF063228		dynein, cytoplasmic, intermediate polype	11,5		
75	410330	AW02363			11.1		
	453165 420297	S74727 AI628272	Hs.32042 Hs.88323	aspartoacylase (aminoacylase 2, Canavan ESTs, Weakly similar to ALU1_HUMAN ALU S	10.7 10.5		
	417157	AW20643		ESTs	10.4		ii.
00	420033	D59502	Hs.292590	ESTs	10.4	10.4	k ()
80	413293	AL047483			10.0		
	426380 410635		Hs.149990 Hs.334372		9.8 9.5		
	422756				9.1		
				206			

	444330	APENTEEE	Hs.49265	ESTs		
	427322	A\$97655 AK002017	Hs.176227	hypothetical protein FLJ11155	9.1 8.9	9.1 8.9
	421633	AF121860	Hs.106260	sorting nexin 10	8.6	6.7
_	429096	AB011106	Hs.196012	KIAA0534 protein	8.6	8.6
5	428652	AA584272	Hs.336224	transmembrane protein with EGF-like and	8.6	8.6
	410309	BE043077	Hs.278153	ESTS	8.5	8.5
	424932 417175	R14070 R44558	Hs.315369 Hs.94002	Homo sapiens cONA: FLJ23075 fis, clone L ESTs	8.5 8.4	10.2 8.9
	427061	AB032971	Hs. 173392	KIAA1145 protein	8.4	8.4
10	400438	AF185611	Hs. 115352	Target	6.3	5.1
	418207	C14685	Hs.34772	ESTs	8.2	9.8
	440209	H05049	Hs.247837	neuraxin 3	8.1	18.7
	429876 429470	AB028977 AI878901	Hs.225974 Hs.203862	KIAA1054 protein quantine nucleotide binding protein (G pr	8.1	16.8
15	430004	U27768	Hs.227571	regulator of G-protein signalling 4	8.0 7.9	8.0 15.7
	436427	AI344378	Hs.143399	ESTs	7.8	7.8
	408814	N62499	Hs.176227	hypothetical protein FLJ11155	7.8	8.6
	434367	AB020700	Hs.3830	KIAA0893 protein	7.7	5.6
20	441005 416851	Z41305	Hs.303172	Homo sapiens mRNA; cONA DKFZp547G133 (fr	7.7	7.7
20	429033	AW963951 NM_007374	Hs:85618 Hs:194756	ESTs sine ocufis homeobox (Drosophila) homolo	7.7 7.6	8.5 5.5
	437073	AI885608	Hs.94122	ESTs	7.5	7.5
	441264	AA927170	Hs.23290	ESTs	7.3	7.3
25	450715	A1266484	Hs.31570	ESTs, Wealdy similar to KIAA1324 protein	7.2	7.2
25	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	7.1	4.8
	410011 423003	AB020641 AL120077	Hs.57856 Hs.122967	PFTAIRE protein kinase 1	7.1 7.0	10.0 7.0
	433921	AA618174	113.122307	ketch (Drosophila)-like 2 (Mayven) gb:nq14f01.s1 NCI_CGAP_Thy1 Homo sepiens	7.0	7.0
	457012	R41480	Hs.302754	ESTs	6.9	6.9
30	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	6.9	6.9
	425352	NM_000939	Hs.1897	propiomelanocortin (adrenocorticotropin	6.9	6.1
	433558 409031	AA833757 AA376836	Hs.201769 Hs.288856	ESTs, Wealdy similar to T24435 hypotheti ESTs	6.9 6.8	6.9
	419347	C15944	Hs.90005	superforcervical ganglia, neural specifi	6.5	6.B 22.2
35	445279	R41900	Hs.22245	ESTs	6.4	6.4
	437414	AW894071	Hs.48448	hypothetical protein DKFZpS47C176	6.4	6.4
	428414	AL049980	Hs.184216	DKFZP564C152 protein	6.4	6.4
	434104 443244	AF116691 AJ457235	Hs.116459 Hs.166479	hypothetical protein PRO2198 ESTs	6.4 6.3	4.0
40	447761	AF061573	Hs.19492	protocadherin 8	6.3	3.0 6.3
	450600	BE079478	Hs.24880	ESTs	6.2	3.9
	427457	AW779105	Hs.164682	ESTs	6.2	11.1
	416133	NM_001683	Hs.89512	ATPase, Ca transporting, plasma membrane	6.t	8.0
45	432453 432298	AJ885537 AL118812	Hs.27172	ESTs, Moderately similar to PC4259 ferri	6.0	39
73	415114	D60468	Hs.274293 Hs.94181	Homo sapiens mRNA; cDNA DKFZp761G1111 (f ESTs	6.0 6.0	15.1 6.0
	416101	R24854	Hs.268806	ESTs	5.9	3.3
	448958	AB020651	Hs.22653	KIAA0844 protein	5.9	5.9
50	447138	A1439112	Hs.93828	ESTs, Weakly similar to 2109260A B cell	5.8	5.8
20	414545 424153	AA149287 AA451737	Hs.76605 Hs.141496	ESTs	5.8	3.6
	424541	AB001106	Hs.151413	MAGE-like 2 glia maturation factor, beta	5,7 5,6	5,1 5.6
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	5.6	9.6
	432149	AW614326	Hs.133483	ESTs, Weakly similar to T34549 probable	5.6	12.2
55	408428	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	5.6	5.6
	443912 442023	R37257 AJ187878	Hs.184780 Hs.144549	ESTs ESTs	5.5	6.1
	450642	R39773	Hs.7130	copine IV	5.5 5.4	5.6 5.6
	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDN	5.4	9.8
60	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	5.4	5.4
	438202	AW169287	Hs.22588	ESTs	5.3	5.3
	448605 418866	AL109678 T65754	Hs.21597	Homo sapiens mRNA full length insert cDN	5.3	5.3
	448786	BE048842	Hs.179075	gb:yc11c07.s1 Stratagene lung (937210) H Homo sapiens cDNA FLJ11881 fis, clone HE	5.3 5.2	3.8 5.2
65	443682	AJ383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	5.2	3.3
	415666	H72693		gb:yu03c11.r1 Soares fetal liver spleen	5.2	5.2
	428508	BE252383	Hs.184668	SBBI31 protein	5.2	4.1
	446353 442106	Al290919 AW205881	Hs.153661 Hs.326728	ESTs ESTs	5.1	5.1
70	437331	AL353933	Hs.21710	hypothetical protein DKFZp761G0313	5.1 5.1	3.2 5.1
	419318	AW969742	Hs.291005		5.0	ãi
	408068	AW148652	Hs.167398	ESTs	5.0	5.0
	434149	Z43829	Hs.244624		5.0	5.0
75	439238	N47305 AW970130	Hs.302161 Hs.65408		4.9	5.3
,,	414531 447104	R19085	Hs.55406 Hs.210706	ESTs Homo sapiers cDNA FLJ13182 ffs, clone NT	4.9 4.9	4.9 3.0
	418527	AA450386	Hs.7149	Homo sapiers cDNA: FLJ21950 fis, clone H	4.9	4.9
	425073	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	4.9	4.9
80	433516		Hs.33410	ESTs, Weakly similar to T17279 hypotheti	4.8	4.8
80	427287 447252		Hs.174188 Hs.12449		4.8	4.8
	419843		Hs.91791	Homo sepiens transmembrane protein HTMP1 chromosome 11 open reading frame 25	4.8 4.7	3.2 4.7
	414949		Hs.323349		4.7	3.8

	429900			ESTS	4.7	4.2
	422949 430537	AA319435 X62692		gb:EST21657 Adrenal gland tumor Homo sap phosphodiesterase 68, cGMP-specific, rod	4,7 4.6	7.4 4.6
	430537	U17195		A kinase (PRKA) anchor protein 6	4.5	4.5
5	421952	AA300900		ESTs, Moderately similar to AF161511 1 H	4.4	3.2
	406311			NM_021979*:Homo sapiens heat shock 70kD	4.4	11.5
	451050	AW937420	Hs.69662	ESTs	4.4	4.4
	423728 411498	AW891294	Hs.132136 Hs.70499	solute carrier family 4, sodium bicarbon	4.4 4.3	7.9 19.4
10	451301	NM_014210 AI769514	Hs.209890	ecotropic viral integration site 2A EST	4.3	4.3
. •	452381	H23329	Hs_290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.3	4.3
	433109	N58907	Hs.162430	EST	4.3	3.9
	423589	AA328082	Hs.209569	ESTs	4.2	4.2
15	427224	AL135554	Hs.101937 Hs.193513	sine oculis homeobox (Drosophita) homolo	4.2 4.1	3.9 4.1
13	420489 408206	AA815089 AF041853	Hs.43570	ESTs kinesin family member 3A	4.1	4.1
	418202	N48521	Hs.26549	KIAA1708 protein	4.1	5.8
	448117	H49129	Hs.172982	ESTS	4.1	4.1
20	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP1	4.0	27.9
20	458694	F12832	Hs.3610	ESTs	4.0 4.0	4.0 4.0
	452197 408547	AW023595 AA574291	Hs.232048 Hs.57837	ESTs ESTs	4.0	4.0
	433447	U29195	Hs.3281	neuronal pentrazin ()	4.0	3.7
~ ~	448583	NM_015239	Hs.21542	KIAA1035 protein	4.0	4.0
25	442412	R77677	Hs.346644	ESTs	3.9	3.9
	440293	AI004193	Hs.22123	ESTs	3.9 3.9	3.9
	426365 400844	AA376667	Hs.10283	RNA binding motif protein 8B NM_003105*:Homo sapiens sortilin-related	3.9	4.1 3.1
	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	3.9	3.9
30	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	3.8	3.3
	408777	U71204	Hs.47626	Ric (Drosophila)-like, expressed in neur	3.8	3.8
	442676	AJ733585	Hs.130897	ESTs	3.8	3.8
	414699 436476	AI815523 AA326108	Hs.76930 Hs.33829	symuclein, alpha (non A4 component of am bHLH protein DEC2	3.8 3.8	4.5 3.3
35	434998	AW975157	Hs.26037	ESTs	3.7	3.7
	412049	N53437	Hs.18268	adenylete kinase 5	3,7	10.7
	416220	N49776	Hs.170994	hypothetical protein MGC10946	3.7	4.5
	459697	AA406062	Hs.98002	ESTs	3.7	5.4
40	435648 442042	H24347 A1990506	Hs.27524 Hs.8077	ESTs Homo sapiens mRNA; cDNA DKFZp547E184 (tr	3.7 3.7	8.1 6.2
70	456765	AM97900	Hs.33067	ESTs	3.7	3.7
	434933	R91095	Hs.4276	KIAA1701 protein	3.6	6.1
	419518	U79289	Hs.90798	Human clone 23695 mRNA sequence	3.6	3.6
45	452667	T87219	Hs.13219	ESTs	3.6	3.6
43	436773 408119	AW078629 W26213	Hs.101672	PC4 and SFRS1 interacting protein 1 ESTs, Weakly similar to T00331 hypotheti	3.6 3.6	3.6 3.5
	453534	NM_014796		KIAA0748 gene product	3.6	4.7
	449093	AB035356	Hs.22998	neurexin 1	3.6	3.6
50	442738	AW002370	Hs.131055	ESTs, Weakly similar to NPM_HUMAN NUCLEO	3.5	3.5
50	447746	AW015920	Hs.161359	ESTS	3.5 3.5	9.9 3.5
	449117 447750	AW449310 AI422234	Hs.210262 Hs.143434	ESTs, Weakly similar to HSS2_HUMAN HEPAR contactin 1	3.5	9.8
	453590	AF150278	Hs.33578	KIAA0820 protein	3.5	22.3
	409339	AB020686	Hs.54037	ectonucleotide pyrophosphatase/phosphodi	3.5	3.6
55	410240	AL157424	Hs.61289	synaptojanin 2	3.5	4.6
	410224 400098	M55513	Hs.150208	potassium voltage-gated channel, shaker-	3.4 3.4	3.4 3.4
	450181	H05254	Hs.201198	Eos Control ESTs	3.4	7.2
	459080	AW192083	Hs.290855		3.4	13.5
60	417063	N50515	Hs.45061	ESTs	3.3	3.3
	424918	R13982	Hs.169309		3.3	5.3
	453431 412453	AF094754 R20205	Hs.32973 Hs.75236	glycine receptor, beta ESTs	3.3 3.3	4.6 3.3
	450561	R49674	Hs.25909	ESTa	3.3	3.3
65	415527	F11624		gb:HSC2ZD101 normalized infant brain cDN	3.3	3.3
	426968	U07616	Hs.173034	amphiphysin (Stifl-Mann syndrome with br	3.3	15.3
	427386	AW836261		ESTs	3.3	3.3
	424001 439450	W67883 R51613	Hs.137476 Hs.125304		3.2 3.2	5.4 8.3
70	442879		Hs.8813	syntexin binding protein 3	3.2	3.2
	417284		Hs.10724		3.2	3.2
	410343	AA084273	Hs.76561	ESTs, Wealthy similar to \$47072 finger pr	3.2	3.2
	410909			ESTs, Moderately similar to ALU8_HUMAN A	3.2	12.5
75	453919		Hs.7076	KIAA1705 protein 4 contactin 1	3.2 3.1	3.2 3.1
, 5	424087 428963				3.1	3.3
	419852			4 hypothetical protein dJ55102.5	3.1	4.1
	422234	AF119818	Hs.11328	7 discs, large (Drosophila) homolog-associ	3.1	3.1
80	423829		Hs.24090		3.1	4.4
οU	443297 453302		Hs.13302		3.1 3.1	3.1 4.6
	405819		18 Hs.32945	NM_002578:Homo sapiens p21 (CDKN1A)-acti	3.1	13.5
	445725		Hs.13209		3.0	3.0

	447673	AJ823987	Hs.182285	ESTs	3.0	3.0
	433670 450757	AA604405 BE081050	Hs.31570	gb:no87h09.s1 NCI_CGAP_AA1 Horno sapiens ESTs, Weakly similar to KIAA1324 protein	3.0 3.0	3.9 3.2
	424724	T06532	Hs.287709	Homo sapiens cDNA: FLJ22674 fis, clone H	3.0	3.0
5	433315	R95754	Hs.239706	GRB2-associated binding protein 1	3.0	3.1
	451032	W03692	Hs.323079	Homo sapiens mRNA; cDNA DKFZp564P116 (fr	3.0	4.9
	423346	Al267677	Hs.127416	synaptojanin 1	3.0	20.1
	439274	AF086092	Hs.48372	ESTS	3.0	18.3
10	425649 441869	U30930 NM_003947	Hs.158540 Hs.8004	UDP glycosyltransferase 8 (UDP-galactose	2.9	38.6
10	407868	NM_000950	Hs.40637	huntingtin-associated protein interactin profine-rich Gla (G-carboxyglutamic acid	2.9 2.9	14.9 3.3
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	2.9	8.0
	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	2.8	5.9
1.5	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	2.8	9.6
15	425130	AA448208	Hs.99163	ESTs	2.8	3.1
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	2.8	3.7
	452238 446544	F01811 A)631932	Hs.345757 Hs.7047	ESTs ESTs, Wealdy similar to Unknown [H.saple	2.8 2.8	3.8
	433803	AI823593	Hs.27688	ESTs	2.8	12.4 4.1
20	407728	AW071502	Hs.175931	ESTs	2.7	10,2
	414931	AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZp761M0223 (f	2.7	3.4
	410711	AB002316	Hs.65746	KIAA0318 protein	2.7	6.1
	452738	AL133800	Hs.7086	hypothetical protein MGC12435	2.7	3.5
25	451516 454053	AI800515 AW023006	Hs.12024 Hs.27172	ESTs	2.7	6.3
23	450474	AW872844	Hs.117494	ESTs, Moderately similar to PC4259 ferri ESTs	2.7 2.7	3.6 7.2
	422414	AW875237	Hs.13701	ESTs	2.7	5.3
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	2.7	. 3.9
20	431342	AW971018	Hs.21659	ESTs	2.7	8.0
30	423449	AI497900	Hs.33067	ESTs	26	14.5
	427283 426919	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	2.6	30
	437117	AL041228 AL049256	Hs.122593	ELAV (embryonic lethal, abnormal vision, ESTs	2.6 2.6	9.0
	422491	AA338548	Hs.117546	neuronatin	26	3.8 3.6
35	438068	AI927209	Hs.306210	Homo sapiens cDNA: FLJ23133 fis, clone L	2.6	5.1
	432809	AA565509	Hs.131703	ESTs	2.5	9.9
	433551	AJ985544	Hs.12450	protocadherin 9	2.5	18.1
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	2.5	43.2
40	417417 413554	F05745 AA319146	Hs.89512 Hs.75426	ATPase, Ca transporting, plasma membrane	2.5	17,1
70	448902	Z45998	Hs.22543	secretogranin II (chromogranin C) Homo sapiens mRNA; cDNA DKFZp761I1912 (f	2.5 2.5	5.7 21.8
	442910	Al365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	2.5	14.5
	423135	N67655	Hs.26411	ESTs	2.5	8.2
15	452311	AW304029	Hs.252744	ESTs	2.5	3.5
45	418940	H17739	Hs.288513	Human DNA sequence from clone RP5-899C14	2.5	7.0
	432882 422411	NM_013257 AW749443	Hs.279696	serum/glucocorticoid regulated kinase-li	2.5	4.2
	451386	AB029006	Hs.22511 Hs.26334	ESTs spastic paraplegia 4 (autosomal dominant	25 24	12.0 3.1
	404819		113.2000	NM_002688*:Homo sapiens peanut (Drosophi	2.4	5.8
50	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	2.4	13.1
	431988	AC002302	Hs.77202	protein kinase C, beta 1	2.4	10.5
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	2.4	11.2
	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (C/EBP),	24	45.2
55	429859 430287	. NM_007050 AW182459	Hs.225952 Hs.125759	protein tyrosine phosphatase, receptor t ESTs, Wealdy similar to LEUS_HUMAN LEUKE	2.4 2.4	5.1 7.6
7,5	422890	243784	115.123133	ankyrin 3, node of Ranvier (ankyrin G)	24	3.6
	427658	H61387	Hs.30868	nogo receptor	2.4	3.0
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	2.3	3.6
60	412266	N59006	Hs.26133	ESTs .	2.3	30.9
60	435059	Z45270 AA256151	Hs.235873	hypothetical protein FLJ22672	2.3	4.8
	420173 452371	R40990	Hs.22999 Hs.21658	ESTS ESTS	2.3	4.1
	430456	AA314998	Hs.241503	hypothetical protein	2.3 2.3	3.3 4.7
	409953	AA332277	Hs.57691	cadherin 18, type 2	2.3	5.5
65	429006	AA443143	Hs.50929	hypothetical protein FLJ13842	2.3	6.6
	445194	AJ215667	Hs.175044	ESTs	2.3	3.1
	428392	H10233	Hs.2265	sacretory granute, neuroendocrine protei	2.3	42.3
	434460	AA478486	Hs.3852	KIAA0368 protein	2.3	4.8
70	416490 437924	AF090116 AI935344	Hs.79348 Hs.164118	regulator of G-protein signalting 7 ESTs, Wealdy similar to SL51_HUMAN SODIU	2.3	12.5
, 0	418738	AW388633	Hs.6682	soluta carrier family 7, (catlonic amino	2.3 2.2	3.2 16.9
	424945	Al221919	.13.0002	hypothetical protein FLJ10582	2.2	30.5
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	2.2	4.4
76	422927	AW247388	Hs.301423	calcium binding protein 1 (cafbrain)	2.2	3.0
75	438831	BE263273	Hs.6439	synapsin (I	2.2	3.4
	449078	AK001256	Hs.22975	KIAA1576 protein	2.2	16.1
	410631 419271	AA086469 N34901	Hs.47171	ESTs ESTs	2.2	5.8
	452752	AW044058	Hs.238532 Hs.33578	KIAA0820 protein	2.2 2.2	7.5 13.4
80	446574	AJ310135	Hs.335933		2.2	3.5
	452106	AI141031	Hs.21342	ESTs	2.2	3.4
	415910	U20350	Hs.78913	chemokina (C-X3-C) receptor 1	2.2	28.9
	44445B	8E041526	Hs.31746	hypothetical protein DKFZp547F072	2.2	7.7

					••	***	
	446692	244514	414 400446	Homo sapiens mRNA for KIAA1763 protein,	22 22	33.0 8.5	
	412788 419103	AA120960 Z40229	Hs.198416 Hs.96423	ESTs hypothetical protein FLJ23033	22	8.4	
	424474	AA308883	Hs.148680	cateyon; D1 dopamine receptor-interactin	2.2	3.6	
5	451783	R42554	Hs.210852	T-box, brain, 1	2.1	11.2	•
	434792	AA649253	Hs.132458	ESTs	21	3.8	
	424922	BE386547	Hs.217112	hypothetical protein MGC10825 hypothetical protein FLJ13159	21 21	3.7 4.9	
	455364 413988	H72176 M81883	Hs.4273 Hs.324784	glutamate decarboxylase 1 (brain, 67kD)	21	5.1	
10	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	21	3.6	•
	443150	AI034467	Hs.34650	ESTs	21	7.6	
	453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	2.1	19.9 6.5	
	420050	AL118615	Hs.94653 Hs.166161	neurochondrin dynamin 1	2.1 2.1	5.1	
15	408449 423841	NM_004408 AL137256	Hs.130489	ATPase, aminophospholipid transporter-li	2.1	6.2	
	430347	NM_002039	Hs.239706	GRB2-associated binding protein 1	2.1	3.2	
	449568	AL157479	Hs.23740	KIAA1598 protein	21	3.6 3.3	
	412675	AA460716	Hs.9788 Hs.119357	hypothetical protein MGC10924 similar to ESTs	21 21	5.4	
20	429550 446782	AW293055 AI653048	Hs.114006	ESTS	2.1	9.0	
20	453924	R49295	Hs.24886	ESTs	2.1	13.4	
	437948	AA772920	Hs.303527	ESTs	21	24.8	
	451952	AL120173	Hs.301663	ESTs	2.0 2.0	19.2 3.4	
25	453754 448765	AW972580 R15337	Hs.172753 Hs.21958	ESTs Homo sapiens mRNA; cDNA DKFZp547D086 (fr	20	3.9	
23	447163	AW292770	Hs.5542	DnaJ (Hsp40) homolog, subfamily C, membe	20	3.4	•
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	20	11.5	
	411668	AF106564	Hs.71346	neurofilament 3 (150kD medium)	20 20	6.6 10.1 ·	
30	424458 434277	M29273 X77748	Hs.1760 Hs.3786	myelin essociated glycoprotein glutamate receptor, metabotropic 3	2.0	28.5	•
50	440152	AB002376	Hs.7006	KIAA037B protein	2.0	14.2	
	429956	AI374651	Hs.22542	ESTs	2.0	3.2	
	450590	AJ701507	Hs.273740		2.0 2.0	3.8 3.7	
` 35	429024 430643	A1652297 AW970065	Hs.119302 Hs.287425		2.0	4.1	
,,,	415734	NM_014747		KIAA0237 gene product	20	27.4	
	419757	AA773820	Hs.63970	ESTs	2.0	3.3	
	421264	AL039123	Hs.103042		2.0 2.0	23.8 5.6	
40	439607 435624	BE540565 AF218942	Hs.159460 Hs.24889	ESTs formin 2	2.0	12.2	
70	425121	AJ797511	Hs.154679		2.0	3.9	
	431677	AK000496	Hs.306989		2.0	3.1	
	442593	R39804	Hs.31961	ESTs	. 20 . 20	6.7 10.4	
45	410366 426575	AI267589 M74826	Hs.302689 Hs.170808		2.0	4.6	
73	452856	AF034799	Hs.30881	protein tyrosine phosphatase, receptor t	20	10.7	
	437380	AL359577	Hs.112198	Homo sapiens mRNA; cDNA DKFZp547M073 (fr	2.0	3.8	
	424893	AW295112			2.0 2.0	3.8 4.7	
50	436734 422544	AI937612 AB018259	Hs.273758 Hs.118140		20	11.8	
50	440105	AA694010		Homo sapiens clone 23809 mRNA sequence	2.0	8.2	
	425741	AF052152			2.0	6.5	
	450310	N62341	Hs.94116	ESTs	2.0	3.6	
55	TABLE	208:					
	Pkoy:		nique Eos prob	eset identifier number			
	CAT nu		ene cluster nun				
	Access	ion: C	enbank access	on numbers			
60	Pkey	CAT Num	ber Accession				
	415527			43212 H08936 R56332 H09256 R52303 R13075			
	415666			208673 H72694 F20990 R08580 A229857 AA229658			
	418866 422890		7/1784 6	213382 AW572911 AA449369 H17037 R19603 AI632	565 AW004030 BE502530 Z	25032 AA80532	24 AA449241 AJ651825 AJ264883 AW196918
65	10000		AA94826	7 AI953735 AI263703 AA319159 AW964438 AI90344	0 AW594171 AJ857447 AW	204071 AW9561	110 C15616 D81142 H17038 AW162343
	****		T87230 A				
	422949 424949			5 N56456 AA319377 AW961532 T48452 AA894424 9 Z19967 AA348780 AW964077 AW166028 BE54019	3 N94800 AA452368 N9960	4 AI341345 AW	/298800 AA724961 AA931158 AI741227
	42434;	243223	AIROGGG	AI982626 D81263 D53937 D52496 AA974487 AWO	3854 N50483 Z39997 AI49	2961 AI361526	F04002 AA452141 T23551 AI472655
70			Al193667	7 AI341			
	42691			8 D82004 D61361 AJ203314 AJ990307 AW900295 AJ	D18308 AW087473 AW1835	30 AA393346 H	150055 AA935601
	43367			% BE062234 AW748386 4 A1114549 R36464 R36465			
	43392 43394		H05129	N63433 Al651350 AA984734 Al368716 N40915 Al989	705 F09042 T03905 R8858	8 AF112220	
75	43677		1 AW0788	29 AI857375 N64357 AA731069			
	44669			AL352097 AL803984 AW235923 AW196558 AL954637	AJ336983		
	TABLE	5 20C-					
	Pkey:		Unique number	corresponding to an Eos probeset			
80	Ref:		Sequence soun	ce. The 7 digit numbers in this column are Genbank k	lentifier (GI) numbers. "Dun	ham, et al." refe	ers to the publication entitled "The DNA
	Para-	4.	sequence of hu	man chromosome 22" Dunham, et al. (1999) Nature 4	UZ:489-495.		
	Strand Nt_po	a. sition:	indicates meta-	strand from which exons were predicted. otide positions of predicted exons.			
	,				• •		

WO 03/025138

	Pkey	Ref	Strand	Nt_position	
	400844	9188605	Plus	24746-24872,25035-25204	
5	404819	4678240	Plus	16223-16319,16427-16513,16736-16859,16941-1707	75.17170-17287,17389-17529,18261-18357,18443-18578
,	405560 405819	183148 4007557	Plus Plus	5495-5655,6077-6241,6495-6692 2830-2967	
	406311	9211559	Minus	137114-139033	
10	TABLE 21	A: ABOUT 410	GENES SIGNI	FICANTLY DOWN-REGULATED IN GLIOBLASTOMA	MULTIFORMA COMPARED TO NORMAL ADULT CNS
	Table 21A	lists about 410 q	enes significa	ntly down-regulated in allablastoms multiforms (GBM)	compared to normal artiff CNS issues. Those were relected from 60000 conhecuts
	ייכו פתופו	percentile amon	osi vanous nor	mai CNS fissues. The "average" GBM lovel was set to	prage" GBM was greater than or equal to 2. The "average" normal CNS level was set to the 95th percentile amongst various tumor samples. In order to remove gene-specific
16	Dackgroun	a sevets of non-s	pecific hybridia	ation, the 10th percentile value amongst various non-m	ratignant discuss was subtracted from both the numerator and the denominator before
15	the ratio w Pkey:	as evaluated.		d identifier number	
	ExAcen:			number, Genbank accession number	
	UnigenetD	t. Unige	ine number		
20	Unigens T R1:		w CNS P CI I	OBLASTOMA MULTIFORMA	
		14250	W 043 W 00	OCCUSIONA NUCLIFORMA	
	Pkey	ExAcon	UnigeneiD	Unigene Title	R1
	417275 428505	X63578 AL035461	Hs.295449 Hs.2281	parvafburnin chromogranin 8 (secretogranin 1)	18.6 13.8
25	415672	N53097	Hs.193579	ESTs	13.5
	459080	AW192083	Hs.290855	ESTS	12.9
	432298 400302	AL118812 N48056	Hs.274293 Hs.1915	Homo sepiens mRNA; cDNA DKFZp761G1111 (f folate hydrolase (prostate-specific memb	11.7 10.9
20	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.1
30	424645	NM_014682		KIAA0535 gene product	8.2
	415274 413324	AF001548 V00571	Hs.78344 Hs.75294	myosin, heavy polypeptide 11, smooth mus corticotropin releasing hormone	7.5 7.5
	417167	AW206437	Hs.4290	ESTs	7.3
35	422728 410330	AW937826 AW023630	Hs. 103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	6.8
55	450590	A1701507	Hs.159425 Hs.273740	ESTS ESTS	6.5 . 6.5
	453165	S74727	Hs.32042	aspartoacytase (aminoacytase 2, Canavan	6.5
	454076 419956	AW204712 AL137939	Hs.61957 Hs.40096	EST8	6.3
40	416851	AW963951	Hs.85618	ESTs ESTs	6.3 6.2
	428874	W32133	Hs.194366	transthyretin (prealburnin, amyloidosis t	6.0
	409743 449078	N48721	Hs.183506	hypothetical protein FLJ14213	5.9
	448072	AK001256 AI459306	Hs.22975 Hs.24908	KIAA1576 protein ESTs	5.6 5.6
45	412622	AW664708	Hs.171959	ESTs	5.6
	428414 427322	AL049980	Hs.184216	DKFZP564C152 protein	5.5
	411498	AKD02017 NM_014210	Hs.176227 Hs.70499	hypothetical protein FLJ11155 ecotropic viral integration site 2A	5.5 5.4
50	453344	BE349075	He 44571	CCT.	5.4
50	441790 443037	AW294909 AW500305	Hs.132208 Hs.8906	ESTs	5.3
	445529	H14421	Hs.180513	syntaxin 7 ATP-binding cassette, sub-family A (ABC)	5.3 5.2
	447750	AI422234	Hs.143434	contactin 1	5.2
55	444409 409031	AJ792140 AA376836	Hs.49265 Hs.288856	ESTs ESTs	5.2
-	453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	5.1 5.0
	452022	AW072330	Hs.293875	ESTs .	4.9
	408428 444922	NM_014787 AI921750	Hs.44896 Hs.144871	OnaJ (Hsp40) homolog, subfamily B, membe Homo sapiens cDNA FLJ13752 fls, clone PL	4.8
60	443622	AI911527	Hs.11805	ESTs	4.8 4.8
	442023	A1187878	Hs.144549	ESTs .	4.7
	445618 429611	H79667 AI889077	Hs.237642 Hs.211388	Homo sepiens cDNA FLJ12052 fis, clone HE Homo sepiens BAC clone CTB-60N22 from 7q	4.6 4.5
	414290	AI568801	Hs.71721	ESTs	4.4
65	450715 428508	A1266484	Hs.31570	ESTs, Wealty similar to KIAA1324 protein	4.4
	425649	BE252383 U30930	Hs.184668 Hs.158540	SBBI31 protein UDP glycosyltransferase 8 (UDP-galactose	4.4 4.3
	459247	N48243	Hs.110373	ESTs, Highly similar to T42626 secreted	4.3
70	434064	AL049045	Hs.180758	hypothetical protein PRO0082	4.3
,,	414602 416133	AW630088 NM_001683	Hs.76550 Hs.89512	Homo sapiens mRNA; cDNA DKFZp56481264 (f ATPase. Ca transporting, plasma membrana	4.3 4.3
	426471	M22440	Hs.170009	transforming growth factor, alpha	4.2
	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein	4.2
75	448958 410657	AB020651 AF063228	Hs.22653 Hs.65248	KIAA0844 protein dynein, cytoplasmic, intermediate polype	4.2 4.1
-	447138	AI439112	Hs.93828	ESTs, Weakly similar to 2109260A B cell	4.1 4.1
	440736	D56919	Hs.265848	myomegalin	4,1
	407245 441976	X90568 AA428403	Hs.172004 Hs.106131	ttiin ESTs	4.1 4.3
80	450642	R39773	Hs.7130	copine IV	4.1
	432799 428465	NM_016161	Hs.278960		4.0
	407868	AW970976 NM_000950	Hs.293653 Hs.40637	ESTs profine-rich Gla (G-carboxyglutamic acid	4.0 4.0
				201	7.8

						4.0
	433558	AA833757	Hs.201769- Hs.203862	ESTS.	Wealdy similar to T24435 hypotheti ne nucleotide binding protein (G pr	4.0
	429470 415665	AJ878901 H72693	15.20002	ab:vu	03c11,r1 Soares fetal liver spieen	3.9 3.9
	407988	N47760	Hs.285107	hypot	hetical protein FLJ1339/	3.9
5	427051	AB032971	Hs.173392 Hs.237225		1145 protein thetical protein HT023	3.9
	430261 440624	AA305127 AF017987	Hs.7306	secre	ded frizzled-related protein 1	3.8
	431668	AW969610	Hs.151179	EST		3.8 3.8
	446692	Z44514		Hom	o sapiens mRNA for KIAA1763 protein, s. Moderately similar to 138022 hypot	3.8
10	408739	W01556 NM_006379	Hs.238797 Hs.171921	EST:	a domain, Immunoglobulin domain (Ig).	3.8
	426716 450103	R08665	Hs.17244	hypo	thetical protein FLJ13605	3.7 3.7
	426775	AA384564	Hs.3628	EST		3.7
1.5	403469	10000	Hs.201198		et Exon	3.7
15	450181 438202	H05254 AW169287	Hs.22588	EST		3.7 3.7
	445279	R41900	Hs.22245	EST		3.7
	422546	AB007969	Hs.301478		A0500 protein	3.6
20	435712 417620	AA694607 R02530	Hs.176956 Hs.19119	EG.	te .	3.6
20	421952	AA300900	Hs.98849	FS'	To. Moderately similar to AF161511 1 H	3.6 3.6
	453655	AW960427	Hs.34287		sforming growth factor, beta recepto A binding motif protein 88	3.6
	426365	AA376667 J05401	Hs.10283 Hs.80691	COS	atine kinase, mitochondrial 2 (sarcom	3.6
25	416982 438085	AA336519	Hs.83623	nu nu	clear receptor subfamily 1, group I, m	3.6 3.6
	424704	AI263293	Hs.15209		ochrome P450, subfamily IU (arachido	3.6
	414631	AW970130			iTs iTs	3.6
	453698 438704	AA037615 AI435060	Hs.3282		STs .	3.5 3.5
30	437073	A1885608	Hs.9412		STS	3.5
	434460	AA478486		7 pl	AA0368 protein dehyde dehydrogenase 1 family, member	3.5
	414541 423665	BE293116 BE167153		0 E	STs	3.5 3.5
	446390		3 Hs.1499	2 h	rpothetical protein FLJ11151	3.5 3.5
35	441264) Hs.2329 Hs.1335	ř	STs STs	3.5
	433629 411811			9 6	b:PM4-SN0016-100500-004-h09 SN0016 Homo	3.5 3.4
	410140		5 Hs_2478	337 n	eurexin 3	3.4
40	415114		Hs.9411		STs b:RC1-BT0313-110500-017-c04 BT0313 Homo	3.4
40	455649 43367				b:no87h09.s1 NCI_CGAP_AA1 Homo sapiens	3.4 3.4
	41717		Hs.940	02 E	STs	3.4
	42717	6 AW3815		34	ESTs Home sapiens prostein mRNA, complete cds	3.4
45	44851		65 Hs.278 Hs.302	754 1	ERTa	3.3
43	45701 40535		, 2,002		CX000321:0il6671579tref[NP_031518.1] 8/1	3.3 3.3
	44587	2 AI68157			Homo sapiens cDNA FLI11997 fis, clone HE	3.3
	43380				ESTs ESTs	3.3
50	44901 41454			202	CCT-	3.3 3.3
50	4090	10 AI64867	75 Hs.10		Homo sapiens, Similar to RIKEN cDNA 1700 v-erb-b2 avian erythroblastic leukemia v	3.3
	4261				ESTs	3.3
	4224 4288				ECTe .	3.3 3.2
55	4069	22 S70284	Hs.11	9597	gb:stearoyi-CoA desaturase [human, adipo	3.2
	4295			6459	ESTs hypothetical protein PRO2198	3.2
	4341 4272				ESTA	3.2 3.2
-	4444	158 BE041			hypothetical protein DKFZp547F072 ESTs, Weakly similar to S65824 reverse t	3.2
60) 4333 4121			35729	ESTs. Weakly similar to unnamed protein	3.2
	440				hynothetical protein FLJ10477	3.2 3.1
	442	117 AW66		28899	ESTs; hypothetical protein for IMAGE:447 KIAA1054 protein	3.1
6:	429			25974 1570	FSTs. Weakly similar to KIAA1324 protein	3.1
U.		757 BE081 327 BE401		85254	ESTs. Weakly similar to 124435 hypother	3.1 3.1
	459	399 BE40	7712 Hs.1	53998	creatine kinase, mitochondrial 1 (ubiqui	3.1
		582 BE54 752 AW04		48016 33578	ESTs KIAA0820 protein	3.0
7		752 AW04 165 AA02		5162	KCNO1 overlanging transcript 1	3.0 3.0
•	409	3403 AA66	8224 Hs.	5634	Homo sapiens cDNA: FLJ22547 fis, clone H	3.0
				13701	ESTs gb:yc10d08.s1 Stratagene lung (937210) H	3.0
		7173 T643 8583 NM_(21542	MAA1035 protein	3.0 3.0
7		9043 A182	4977 Hs.	145319	ESTs	3.0
	45	2990 AA81		246970 324841		3.0
				.227011	G-substrate	3.0 2.9
	43	4348 BE3	93191 Hs	.181795	putative b,b-carotene-9,10-dioxygenase	2.9
8	30 42	27115 AWS		.11223 .24282		2.9
				.24202 .17924		2.9
		05403			Target Exon	2.9
						302

		**********	Hs.232048	ESTs		2.9
	452197 437357	AW023595 AL359559	Hs.331666	Homo	sapiens mRNA; cDNA DKFZp762O2215 (f	29 29
	436427	AJ344378	Hs.143399	ESTs		2.9
_	417787	R14948	Hs.23883	ESTs		29
5	439272 454247	AA832474 AJ243950	Hs.25851 Hs.46735	ESTs	ess locus associated putative guarti	2.9
	415839	R40611	Hs.94694	ESTS		2.9 2.9
	408814	N62499	Hs.176227	hypot	netical protein FLJ11155	2.9
	408468	AI909712	Hs,93837	phos	haticylinositol transfer protein, m 24-HT0373-130200-011-a03 HT0373 Homo	29
10	431304	BE157283	Hs.61289		tojanin 2	2.9
	410240 444783	AL157424 AK001468	Hs.62180	enilli	(Drosophita Scraps homolog), act	2.8 2.8
	408438	AB011180	Hs.100950	KIAA	0608 protein	2.8
	458793	N80159	Hs.121849	micro	tubule-associated proteins 1A/18 fill (S. cerevisiae)-like	2.8
15	429788	U87791	Hs.221040 Hs.239388	Hum	an DNA sequence from clone RP1-304B14	2.8
	424264 433109	D80400 N58907	Hs.162430	EST		2.8 2.8
	427974	BE093023	Hs.188767	EST		2.8
	432268	AK000385	Hs.274222		thetical protein FLJ20378	2.8
20	414764	AW013887	Hs.31522	EST ob:F	M4-PT0019-141299-009-F08 PT0019 Homo	2.8
	411918 404563	AW876354			et Exon	2.8 2.8
	445468	AJ765890	Hs.16341	MA	VD binding protein	2.8
	444755	AA431791	Hs.113823	Gp.	((caselnolytic protease X, E. cofi) no sapiens clone 24468 mRNA sequence	2.7
25	445898	AF070623	Hs.13423 Hs.17418	nor ect	nucleotide pyrophosphatase/phosphodi	2.7
	427283 400138	AL119795	113.11410	Eos	Control	2.7 2.7
	458676	AI692464	Hs.20226			2.7
	459697	AA406062	Hs.98002			2.7
30	444420	AI148157	Hs.14876 Hs.24011	2 1/1	AMORE evotein	2.7
	430371 449117	D87466 AW449310		2 60	To Woody similar to HSS2 HUMAN HEPAR	2.7
	424994			nh.	ECTRASOS MAGE resequences, MAGO RUMO	2.7 2.7
	400339		Hs.24820		A histone family, member F, pseudogene	2.7
35	417494		Hs.22213		its Its	2.7
	427166		Hs.9915	~	/000+3R+-ci17512767loid[[12477 hypothe	2.7
	404746 411361		3	e l	CM3.1 T0066-030100-109-406 L10000 momo	2.7 2.7
	428356		Hs.1019	16 5	amonti disease 3 (autosoma) dominanti	2.7
40	406625		Hs.1195		earcyl-CoA desaturase (delta-9-desatur STs	2.7
	41610		Hs.2688	Ť	met Even	2.7
	40460 43392		1	a	o:nq14f01.s1 NCI_CGAP_Thy1 Homo sapiens	2.7 2.7
	41427		Hs.4698	38 E	STs	2.7
45	41804	7 R37633	Hs.484		STs	2.7
	42108			י פטו	IAA1350 protein b:RCD-MT0013-280300-021-c10 MT0013 Homo	2.7
	41224				CTAIRE protein kinase 3	2.6 2.6
	42415		7 Hs.141	496	MAGE-like 2	2.6
50			Hs.563		ESTs	2.6
	4544				ESTs valiturein 3, (prostate specific antigen	2.6
	4267- 4567		Hs.133	220	ECE recentor activating protein 1	2.6 2.6
	4057				ENSP00000005198":Mixed lineage kinase ML	26
55	4254	94 N55540			ESTs, Westly similar to similar to ankyr	2.6
	4308				HSPC125 protein ESTs	2.6
	4357 4101		Hs.13		ESTs	2.6 2.6
	432		072 Hs.11	5960	KIAA0939 protein	26
60					kruppel-related zinc finger protein hcKr ESTs, Wealdy similar to T43458 hypotheti	2.6
	414				ESTS. VIGALLY SATELLE D. TABLES 1.7	2.6
	429	269	14 15.0	,	Eas Control	2.5 2.5
	443	992 AW022		22922	ESTs	2.5
6:	5 451	926 AW134			Homo sapiens, Similar to clone FLB3816,	2.5
		145 AI2772		16631	ESTs ESTs, Weakly similar to ALU5_HUMAN ALU S	2.5
		309 AW043		3918	hypothetical protein PP5395	2.5
		5530 U5280		9361	kallikrein 6 (neurosin, zyme)	2.5 2.5
7		1678 AI907	114 Hs.7	1465	squalene epoxidase	2.5
		8119 W262		01672	ESTs, Weakly similar to T00331 hypotheti tatly acid binding protein 1, liver	2.5
		6624 T6429 8268 AA42		106131	ESTs	2.5
		8268 AA42 1338 AI264		3610	FSTe	25 25
7		6924 AI631	510 Hs.	196956	ESTs. Highly similar to match to EST AA3	2.5
•	45	5040 AW8		****	gb:QV0-CT0225-100400-187-d08 CT0225 Homo	2.5
		0033 D595		292590 179075	ESTs Homo sepiens cDNA FLU11881 fis, clone HE	2.5
				232165	polycythemia rubra vera 1; cell surface	2.5 2.5
8		08206 AFO4	1853 Hs	43670	kinesin family member 3A	2.5 2.5
	4	40205 T869		.105448	ESTs, Weatly similar to B34087 hypotheti Homo sapiens cDNA: FLJ21784 fis, clone H	2.5
				.13303 .90787	ESTs	2.4
	•	20912 AW		.,.,.,	203	1

	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic teukemia v	2.4
	421025	AW958975	Hs.29397	Homo sapiens cDNA FL113226 hs, done UV	24 24
	439973	AJ733308	Hs.124563	EST8 Homo sapiens cDNA: FLJ21930 fs, clone H	24
5	446847	T51454 Al218038	Hs.82845 Hs.48504	ESTs, Moderately similar to ALUS_HUMAN A	24
,	414672 451522	BE\$65817	Hs.26498	hypothetical protein FLJ21657	24
	433068	NM_006456	Hs.288215	sialytransferase	24 24
	446620	AA128808	Hs.179902	transporter-like protein	24
10	423803	NM_005709 AW385129	Hs.132945 Hs.41717	POZ-73 protein phosphodiesterase 1A, calmodulin-depende	24
10	407978 42 5 907	AA365752	Hs.155965	ESTs	24
	433819	AW511097	Hs.112765	ESTs	24 24
	446066	A1343931	Hs.149383	ESTs	2.4
16	430573	AA744550	Hs.136345	ESTs ESTs	2.4
15	444992 434975	R37658 AA657884	Hs.21375 Hs.314413	ESTs	24
	458227	Z40670	Hs.181340	ESTs	24 24
	443244	AI457235	Hs.156479	ESTS ALL STATE A SERIO Y Enhan	24
20	432408	N39127		ESTs, Weakly similar to A45010 X-linked US snRNP-specific protein, 116 kD	2.3
20	401600 419066	BE247275 298492	Hs.6975	PRO1073 protein	2.3
	424823	NM_006226	Hs.153322	nhospholipase C. eosãon	2.3
	402124			NM_031891:Homo sapiens cadherin 20, type	2.3 2.3
0.5	416678	NB0448	Hs.269106	ESTS	23
25	444897	AW137088 BE018485	Hs.144857 Hs.30977	ESTs ESTs, Wealdy similar to B34087 hypotheti	2.3
	425111 400538	BE010403	110.00371	NM 000681":Homo sapiens adrenergic, alph	2.3
	427544	AI767152	Hs.181400	ESTs, Wealdy similar to 178885 serine/th	23 23
	459511	A1142379		gb:qg64c01.r1 Soares_testis_NHT Homo sap	23
30	415111	R39039	Hs.279041 Hs.117323	EST ESTs	2.3
	433331 440293	A1738815 A1004193	Hs.22123	ESTS	2.3
	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	2.3 2.3
	416964	D87467	Hs.80620	guaraine nucleotide exchange factor for R	2.3
35	419386	AA236867		ESTs, Wealthy similar to 138022 hypotheti mannosidase, alpha, class 1A, member 1	23
	402493 401783	AJ743260		NM_003771":Homo sapiens keratin, hair, a	2.3
	420548	AA278248	Hs.920	ESTs	2.3 2.3
	419763	AI039691	Hs.12748		2.3
40	421750	· AK000768	Hs.10787	2 hypothetical protein FLJ20761 Target Exon	2.3
	406023 454024		Hs.29390		23
	401586			Target Exon	2.3 2.3
	404091			Target Exon	2.3
45	456773		Hs.12976		2.3
	414108 454288				2.3
	441879		Hs.1071	9 novel protein similar to archaeal, yeast	2.3
	42472	T06532	Hs.2877	9 Homo sapiens cDNA: FLJ22674 fis, clone H	23 23
50	41569		Hs.4737		2.2
	41628 40465		Hs.1672	ENSP00000239999":HYPOTHETICAL 34.7 kDa P	2.2
	42995		Hs.2254	2 ESTs ·	2.2 2.2
	42967	0 L01087	Hs.2115		2.2
55	42965		Hs.2115 Hs.7937		2.2
	45892 43646		Hs.6656		2.2
	40899			2 ESTs	2.2 2.2
	41330	3 AW8361		7 hypothetical protein FLJ13910	2.2
60				nuclear receptor subfamily 1, group I, m nuclear transcription factor Y, beta	2.2
	41840 4229				2.2
	4463			953 ESTs	2.2 2.2
	4292	90 AF20303		760 neurofilament, heavy polypeptide (200kD)	2.2
65			15 Hs.239		2.2
	4084 4100				2.2
	4109			gb:MR4-ST0125-021199-017-e07 ST0125 Homo	2.2
	4471	63 AW2927	770 Hs.554		2.2 2.2
70			194 Hs.107		22
	4037		87 Hs.241	Target Exon 172 ESTs	2.2
	4533 4113				2.2
	413		Hs.84	interleukin 13	2.2
7:	5 409	028 AB0145	513 Hs.49	998 Z-band alternatively spliced PDZ-motif	2.2 2.2
	413		364 Hs.75	516 setadin-1 Target Exxon	22
		463 068 AW148	652 Hs.16		2.2
	_ 407	819 R4218		2720 ESTs	22
8	0 414	203 BE262	170 Hs.78	629 ATPase, Na? transporting, beta 1 polypep	2.2 2.2
		045 AJ297			2.2
		1835 AW975		0784 ESTS	2.2
	400	M41 V4450		····	

	414276	8E297862		gb:601174780F1 NIH_MGC_17 Homo sapiens c	2.2
	427493	H09037		Target CAT	2.2
	458441	AW842283	Hs.288232	cyclin I	21
5	410705 444647	BE004107 H14718	Hs.11506	gb:CM0-8N0102-150300-288-112 BN0102 Homo Human clone 23589 mRNA sequence	2.1 2.1
_	405502	***************************************	113.11550	C7000609":gij628012[pirl]A53933 myosin 1	2.1
	400818			Target Exon	2.1
	435059	Z45270	Hs.235873	hypothetical protein FLJ22672	21
10	426559 445200	AB001914 AA084460	Hs.170414 Hs.12409	paired basic amino acid cleaving system somatostatin	21 21
. •	453396	AW162768	Hs.22620	ESTs	2.1
	443819	AB033076	Hs.9873	Exety homolog of rat kinase D-interacti	2.1
	401929			C17001690:g36005701[ref]NP_009099.1] AT	2.1
15	451032 433862	W03692 D66960	Hs.323079 Hs.3610	Homo saplens mRNA; cDNA DKFZp564P116 (fr KIAA0205 gene product	21 21
••	458694	F12832	Hs.3610	ESTs	21
	417063	N50515	Hs.45061	ESTS	21
	416935	AA190712		gb:zp87f09.r1 Stratagene HeLa cell s3 93	21
20	414446 434581	AA147534 AA642402	Hs.142019 Hs.59142	ESTs, Wealthy similar to 1207289A reverse ESTs	21 21
	413835	AJ272727	Hs.249163	fatty acid hydroxylase	2.1
	426137	AL040683	Hs.167031	DKF2P566D133 protein	2.1
	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	21
25	454339 407786	AW381980 AA687538	Hs.38972	gb:QV4-HT0316-091199-028-d05 HT0316 Homo tetraspan 1	2.1 2.1
	421296	NM_002666	Hs. 103253	peniipin	21
	444200	AA327113	Hs. 149057	ESTS	2.1
	409339	AB020686	Hs.54037	ectonucleotide pyrophosphatase/phosphodi	2.1
30	418410 414759	AA811441 AW295157	Hs.107393 Hs.47587	chromosome 3 open reading frame 4 ESTs	2.1 2.1
-	449511	AI436187	Hs.296261	guardine nucleotide binding protein (G pr	2.1
	451606	AA018791	Hs.7945	AIE-75 binding protein protein	2.1
	437924	A1935344	Hs.164118	ESTs, Wealdy similar to SL51_HUMAN SODIU	2.1
35	449119 431568	AI631195 AW972316	Hs.232193 Hs.283703	ESTs ESTs	2.1 2.1
33	447932	AA837474	Hs.20021	vesicle-associated membrane protein 1 (s	2.1
	433516	AA595802	Hs.33410	ESTs, Wealdy similar to T17279 hypotheti	2.1
	44 1987	AW452234	Hs.128293	ESTs	2.1
40	414055 445066	AW818687 BE178734	Hs.5366 Hs.197422	hypothetical protein FLJ21522 ESTs	2.1 2.1
	455546	AW994075	113.13.422	gb:RC3-BN0036-090200-011-g06 9N0036 Homo	2.1
	413607	T64741		gb:yc48f11.r1 Stratagene liver (937224)	21
	456401	W28146		gb:43f11 Human retina cDNA randomly prim	2.0
45	407341 425055	AA918886 AW961959	Hs.204918 Hs.96940	ESTs, Weakly similar to ALUS_HUMAN ALU S ESTs	2.0 2.0
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	2.0
	419647	AA348947	Hs.91816	hypothetical protein	2.0
	412266	N59006	Hs.26133	ESTs	2.0
50	449658 424505	A1964033 AA446131	Hs.195730 Hs.124918	ESTs, Wealdy similar to CTXN RAT CORTEXI KIAA1795 protein	2.0 2.0
	438219	Al916151	Hs.257194	ESTs	2.0
	425068	AL048716	Hs.154387	KIAA0103 gene product	2.0
	412949 418866	AJ471639	Hs.71913	ESTS	2.0
55	445071	T65754 A1280246	Hs.149504	gbryc11c07.s1 Stratagene lung (937210) H ESTs	2.0 2.0
	456529	AF014643	Hs.100072		20
	406475			C15000508*:gij2558825 gbjAAC53387.1 (AF	2.0
	429656 431542	X05608 H63010	Hs.211584 Hs.5740	neurofilament, light polypeptide (68kD) ESTs	2.0
60	452625	AA724771	Hs.61425	ESTs	2.0 2.0
	410378	R23324	Hs.41693	DnaJ (Hsp40) homolog, subfamily B, membe	2.0
	409767	AW501470		gb:UI-HF-BP0p-aid-b-03-0-UI.r1 NIH_MGC_5	2.0
	446873 453938	AI554439 AF082569	Hs.30724 Hs.36794	ESTs O-type cyclin-interacting protein 1	2.0 2.0
65	423605	AF047826	Hs.129887		2.0
	420061	AW024937	Hs.29410	ESTs	20
	439559	AW364675	Hs.173921	ESTs, Wealdy similar to 2109260A B cell	2.0
	449901 428304	AI674072 AI743177	Hs.98422	gbtwd15h01x1 Soares_NFL_T_GBC_S1 Horno s ESTs	20
70	432278	AL137506	Hs.274256		2.0 2.0
	458480	AI792298		p30 D8C protein	2.0
	404559			Target Exon	2.0
	445831 427523	NM_006055 BE242779		LanC (bacterial lantibiotic synthetase c	20
75	413055	AV655701	Hs.179526 Hs.75183	upregulated by 1,25-dihydroxyvitamin D-3 cytochrome P450, sublamily IIE (ethanol-	2.0 2.0
-	444904	AW452054	Hs.161139	ESTs	2.0
	443713	AJ082810	Hs.204934	EST _{\$}	2.0
	448743 428186	AB032962	Hs.21896	KIAA1136 protein	20
80	448770	AW504300 AA326683	Hs.295605 Hs.21992	mannosidase, alpha, class 2A, member 2 likely ortholog of mouse variant polyade	2.0 2.0
	453994	BE180964	Hs.165590		20
	420290	AW977318	Hs.194480	ESTs	2.0
	431467	N71831	Hs. 256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	2.0

	447965	AW292577	Hs.94445	ESTs	20 20
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr hypothetical protein FLJ14547	20
	459256 411906	AW967468 AW875765	Hs.99821	gb:QV2-PT0012-020500-186-a08 PT0012 Homo	20
5	441984	AB037763	Hs.8059	synaptotagmin IV	2.0
,	437900	AI763301	Hs.107331	ESTs	2.0
	436092	AI345995	Hs.127383	ESTs	20
	415529	AW009370	Hs.115772	ESTs	2.0
	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	20
10	444749	Al190672	Hs_65926	ESTs	2.0
	445277	AI284218	Hs.159204	ESTs DIVINOUS TO A CONTROL OF THE CO	20
	452550	AA026735	Hs.326048	Homo sapiens mRNA; cDNA DKFZp434M0420	20 20
	445725	AK000956	Hs.13209	hypothetical protein FLJ10094	2.0
16	409265	T78737	Hs.321062	ESTs ESTs	20
15	426736	AA431615 AJ939409	Hs.130722 Hs.157803	ESTS	2.0
	447098 403582	M333403	15.13/000	Target Exon	2.0
	70000				
	TABLE 21	B:			
20	Pkey:			set identifier number	
	CAT num!	_	e cluster numl		
	Accession	ı: Gen	bank accessio	n unmoers	
	Ólean.	CAT Number	Accession		
25	Pkey 409767	1154015_1	AW401470	AW502931 AW499500	
25	410705	1217235_1	BE004107	BE004105 AW901093 AW797879 AW901094 AW	97881 AW797880 BE004108
	410912	1226543_1	AW810224	I AW810337 AW810295 AW810333 AW810335 A\	/810296 AW816053
	411361	1240611_1		AW839234 AW839230 AW878302 AW839109 AV	/843897
	411811	1259427_1		AW864319 AW864504	
30	411906	1265204_1	AW875769	5 H50294 AW875444	2016126 AUI076100 AUI076100
	411918	1265807_1	AW876354	4 AW876179 AW876318 AW876290 AW876234 A 5 AW947637 AW902869 AW947537 AW947531 A	VQ47532 AWQ47530
	412244	1284692_1 1379911_1	TEA741 D	E158393 BE152805	1911 DEL MITOTO
	413607 414276	14321151			
35	415666	1543492_1		08673 H72694 F20990 R08580	
"	416935	163179_1	44400745	A A 400CCC A A 7E7CCA	
	418154	17249_1	BE165866	BE165832 AA319621 AA401166 AI811901 H788	7 X56199 R93797 AW896675 AA401072 AW374411 H52942 AW896685 AA348138
			A1399764	AA010244 W90159 N90874 AA339496 AW96713	W38705 AA029093 AW444847 BE175700 AV651656 AV651847 AA332039 AV649227
40			AV649164	4 AV649491 N87956 AA332262 BE001561 H/549	BEZ 18742 AA333298 AA095633 AA091968 M78602 T05342 W17094 AA126501 I43 AA693541 AI681019 AV658257 AV658133 BE045335 BE089546 AA300830 AA361376
40			AW37466	5 AI452905 AW316900 AI183060 AI202920 AI931	06054 A1871563 AA808652 A1500693 AW342032 AA147066
					MINISTER FOR THE PROPERTY AND AND AND AND AND AND AND AND AND AND
	418856	179788_1		A229857 AA229658 7 AA237066 AA354236 AW957759 H08961	
	419386 424994	184356_1 245786_1	AW95453	25 AI372685 AA349501 AI372687 H10564	
45	427493	279541_2	H09037	W974937 AA657521 H86138 H86513 H09016 AA	104410 AA404454
75	431304	331286_1	BE15728	3 BE157287 AA502438	
	432408	346286_2	N39127 f	F20776 AI082691 AA865520 F36964 F33894	
	433670	372721_1	AA60440	5 8E062234 AW748386	
~^	433921	377350_1	AA61817	4 A1114549 R36464 R36465	16 T53219 T48785 T64166 AA706930 R29613 T55913 T56518 T64679 R29666 M10617
50	436624	4237_5	T64297 /	\$A894931 NM_001443 M10050 AYV643109 A1096	133 T53220 AW082135 AW272775 T29562 T55862 AI343047 AI345671 T68235 T68121
			AI/6859		33 130220 ATTOCK TO THE TENED TO THE TOTAL THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO T
	446692	689623_1	744514	AI352097 AIB03984 AW2359 23 A W196558 AI9S46	37 A1336983
	449901			2 BE268487	
55	454339		AW3819	80 BE152244 BE152235 BE152238 BE152232	
	455040		I AW8522	86 AW851934 AW852096 AW852274	
	455546	1324614_	1 AW9940	75 AW994386	0.4674 DFAC4625
	455649			51 BE155165 BE064764 BE155231 BE064648 BE	646/1 BEU64636
4۸	456401		2 W28146	i W28187 I8 H14121 Al375113 AA960851 AA744592 AV648	39 A1298360 AW293609
60	458480	59843_1	A179225	10 M 14151 W313113 W300031 W1 +1335 W4000	00 74E0000 7777E0000
	TABLE	21C:			
	Pkey:		Inique number	corresponding to an Eos probeset	
	Ref.	Š	equence sour	ce. The 7 digit numbers in this column are Genba	k Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
65		8	equence of hi	ıman chromosome 22° Dunham, et al. (1999) <u>Natu</u>	g 402:489-495.
	Strand		ndicates DNA	strend from which exons were predicted.	
	Nt_par	sition: t	ndicates nucle	cotide positions of predicted exons.	
	-	n.,	C1	Nt_position	
70	Pkey	Ref 6 9797380	Strand Minus	170994-172025	
70	40053 40081		Plus	172644-172765,173085-173200	
	40158		Minus	93974-94099	
	40160		Minus	27363,27518 28727,28891 29526,29731	
	40178	3 7249190	Plus		990,141496-141657,141757-141882,142063-142283
75			Minus	3167-3286,4216-4310	
	40212		Plus	164206-164459	
	40249			205146-205240,205428-205542 102596-102879	
	40346 40346			4831-7707	
80	4035			18308-18458	
	4037			34481-34671	
	4040	91 7684554	Minus	82121-83229	
	4045		Minus	73499-73651,89575-89739	
					306

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	404563	9838310	Plus	100136-100343
	404606	9212936	Minus	22310-23269
	404659	9797068	Minus	65026-67930
	404745	7219894	Minus	32643-32834
5	405354	2642452	Plus	52213-53089
5	405403	6850244	Minus	37491-37670,40951-41031
	405502	9211311	Minus	50360-50584
	405715	4156209	Plus	26293-26706
	406023	.8272661	Ptus	205623-205936
10	406475	9797684	Plus	125417-125563,128052-128180

TABLE 22A: ABOUT 301 GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS
Table 22A 8st a about 301 genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on the
Affymetrize is Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 2. The "average" normal CNS tevel was set
to the 75th per certibe amongst various normal CNS tissues. The "average" glioblastoma level was set to the 95th per certibe amongst various tumor samples. In order to remove geneto the 75th per certibe amongst various normal CNS tissues. The "average" glioblastoma level was set to the 95th per certibe amongst various tumor samples. In order to remove geneto the 75th per certibe amongst various tumor samples. In order to remove geneto the 75th per certibe amongst various tumor samples. In order to remove geneto the 75th per certibe amongst various tumor samples. In order to remove geneto the 75th per certibe amongst various tumor samples. In order to remove geneto the 75th per certibe amongst various tumor samples. In order to remove geneto the 75th per certibe amongst various tumor samples. In order to remove geneto the 75th per certibe amongst various tumor samples. In order to remove geneto the 95th per certibe amongst various tumor samples. In order to remove geneto the 95th per certibe amongst various tumor samples. In order to remove geneto the 95th per certibe amongst various tumor samples. The "average" normal CNS to 95th per certibe amongst various tumor samples. The "average" normal CNS to 95th per certibe amongst various tumor samples. The "average" normal CNS to 95th per certibe amongst various tumor samples. The "average" normal CNS to 95th per certibe amongst various tumor samples. The "average" normal CNS to 95th per certibe amongst various tumor samples. The "average" normal CNS to 95th per certibe amongst various tumor samples. The "average"

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	Dha	E = 4	Unigene!D	Uniosne Title	RI
25	Pkey 418318			transmembrane 4 superfamily member 3	10.1
23	445529		Hs.180513	ATP-binding cassette, sub-family A (ABC1	9.4
	415274		Hs.78344	myosin, heavy polypeptide 11, smooth mus	7.5
	417167			ESTs	7.3
	453165	S74727	Hs.32042	aspartoacytase (aminoacytase 2, Canavan	6.5
30	454076	AW204712		ESTs	6.3
50	417275	X63578	Hs.295449	parvalbumin	6.2
	412636	NM_004415		desmoplatin (OPI, DPII)	6.0
	409743	N48721	Hs.183506	hypothetical protein FLJ14213	5.9
	424645	NM_014682	Hs.151449	KIAA0535 gene product	5.6
35	427322	AK002017	Hs.176227	hypothetical protein FU11155	5.5
22	446390	AA233393	Hs_14992	hypothetical protein FLJ11151	5.2
	444409	AI792140	Hs.49265	ESTs	5.2
	409031	AA376836	Hs.288856	ESTs	5.1
	408428	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	4.8
40	428414	AL049980	Hs.184216	DKFZP564C152 protein	4.8
40	428874	W32133	Hs.194366	transthyretin (prealburnin, armyloidosis t	4.6
	420605	BE391491	Hs.99291	HSPC156 protein	4.6
	445618	H79667	Hs.237642	Homo saplens cDNA FLJ12052 fis, clone HE	4.6
	450715	A1266484	Hs.31570	ESTs, Wealthy similar to KIAA1324 protein	4.4
45	428508	BE252383	Hs.184668	S88131 protein	4.4
7.5	434064	AL049045	Hs.180758	hypothetical protein PRO0082	4.3
	410330	AW023630	Hs.159425	ESTs	4.2
	426471	M22440	Hs.170009	transforming growth factor, alpha	4.2
	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein	4.2
50	448958	AB020651	Hs.22653	KIAAQ844 protein	4.2
••	428465	AW970976	Hs.293653	ESTs	4.0
	429470	AJ878901	Hs.203862	guantne nucleotide binding protein (G pr	4.0
	432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA DKFZp761G1111 (I	3.9
	427061	AB032971	Hs.173392	KIAA1145 protein	3.9 3.9
55	430261	AA305127	Hs.237225	hypothetical protein HT023	3.9
-	435145	A1277259	Hs.116831	ESTS	3.8
	416101	R24854	Hs.268806	ESTs	3.8
	426716	NM_006379	Hs.171921		3.8
	438202	AW169287	Hs.22588	ESTs	3.7
60	433558	AA833757	Hs.201769		3.7 3.7
	419958	AL137939	Hs.40096	ESTs	3.7
	430573	AA744550	Hs.136345		3.7
	422546	AB007969	Hs.301478		3.6
	453344		Hs.44571	ESTs	3.6
65	417620		Hs.191198	ESTS	3.6
	421952		Hs.98849	ESTs. Moderately similar to AF161511 1 H	3.6
	414631		Hs.65406	ESTs	3.5
	437073		Hs.94122	ESTs	3.5
	441264		Hs.23290		3.5
70	433629		Hs.13359		3.4
	415114		Hs.94181	ESTs	3.4
	411770		8 Hs.71992	heat shock protein (hsp110 family)	3.4
	415666			gb:yu03c11.r1 Soares fetal liver spleen	3.4
	416851				3.4
75	443037			syntaxin 7 11 quanine nucleotide binding protein (G pr	3.4
	44951		Hs.29626		3.4
	42717				3.3
	43870		Hs.32825		3.3
00	41717		Hs.94002	ESTs HSPC125 protein	3.3
80	43088		Hs.5232		3.3
	45701		Hs.3027	54 ESTs CX000321:gij6671579[ref]NP_031518.1] ari	3.3
	40535				3.3
	43279	9 NM_0161	61 Hs.2789	On white it to the special discovery contribute and con-	

	429876	AB028977	Hs.225974 H	JAA1054 protein	3.3
			He 181795 c	utative h h-camtene 9.10-dioxygenase	3.3
	441071		Hs.7149	lomo sepiens cDNA: FLJ21950 fis, clone H	3.3
_	445279	R41900	Hs.22245	STs	3.2 3.2
5	414541	BE293116		ideliyde dehydrogenase 1 family, member	3.2
	448072	AI459306		ESTS	3.2
	402429	414/200150	Hs.23644	Farget Exon ESTs, Wealdy similar to \$65824 reverse t	3.2
	433328 400138	AW298159		Eas Control	3.1
10	414327	BE408145	Hs.185254	ESTs. Westdy similar to T24435 hypotheti	3.1
10	459399	BE407712	Hs.153998	creating kinase, mitochondrial 1 (ubiqui	3.1
	433582	BE548749		ESTs	3.1 3.0
	434104	AF116691	Hs.116459	hypothetical protein PRO2198	30
1.0	404606			Target Exon gb:yc10d08.s1 Stratagene lung (937210) H	3.0
15	407173	T64349	Hs.193579	ESTs	3.0
	415672 448583	N53097 NM_015239	Hs.21542	KIAA1035 protein	3.0
	429043	AI824977	Hs.145319	ESTs	3.0
	439165	AA029517	Hs.95162	KCNO1 overlapping transcript 1	29
20	449561	AJ022240	Hs.17924	ESTs, Moderately similar to ALU1_HUMAN A	29 29
	436427	A1344378	Hs.143399	ESTs	29
	405403		14 000040	Target Exon	29
	452197	AW023595 AL359559	Hs.232048 Hs.331666	ESTs Homo sapiens mRNA; cDNA DKFZp762O2215 (f	2.9
25	437357 439272	AA832474	Hs.25851	ESTs	29
23	415839	R40611	Hs.94694	ESTA	2.9
	411906	AW875765		ab:QV2-PT0012-020500-186-a08 PT0012 Homo	2.9
	409403	AA66B224	Hs.6834	Homo sapiens cDNA: FLJ22547 fts, clone H	2.9 2.8
	412258	AA376768	Hs.324841	hypothetical protein FLJ2622	2.8
30	435836	AW292532	Hs.343667	homolog of yeast long chain polyunsatura	2.8
	433109	N58907	Hs.162430	EST Target Exon	2.8
	404563 427974	BE093023	Hs.188767	ESTs	2.8
	413324	V00571	Hs.75294	corticotropin reteasing hormone	2.7
35	409263	AA069573	Hs.50319	ESTs	2.7 2.7
-	454247	AJ243950	Hs.48735	dealness locus associated putative guani	2.7
	449180	A1633836	Hs.195649	ESTs Homo sapiens cDNA: FLJ23597 fis, clone L	2.7
	416004	D11880	Hs.299254	gb:EST366595 MAGE resequences, MAGC Homo	2.7
40	424994 430371	AW954525 D87466	Hs.240112	KIAAD275 prolein	2.7
40	449117	AW449310	Hs.210262		2.7
	451007	H38108	Hs.32759	ESTs	2.7
	414502	AL133721	Hs.224680	ESTs	2.7 2.7
	458793	N80159	Hs.121849		27
45	459053	AI807052	Hs.210361		2.7
	427229	AJ799751 U30930	Hs.5635 Hs.158540	ESTs UDP glycosyltransferase 8 (UDP-galactose	2.7
	425649 444922	AI921750	Hs. 144871	Homo saniens cDNA FLJ13752 fis, clone PL	2.7
	433921	AA618174	14.144	gb:nq14f01.s1 NCI_CGAP_Thy1 Homo sapiens	2.7
50	414272		Hs.46988	ESTS	2.7 2.7
	418047		Hs.4847	ESTs	27
	421089				26
	416498		Hs.79351 Hs.71721	ESTs	2.6
55	414290 433703			nemo-like kinase	2.6
33	408739		Hs.23879	7 ESTs, Moderately similar to 138022 hypot	2.6
	414602			Homo sapiens mRNA; cDNA DKFZp564B1264 (f	26
	42213	7 AJ236885			2.6 2.6
	44202				26
60	42170				26
	42674			gb:RCO-MT0013-280300-021-c10 MT0013 Homo	2.6
	41224 41938			ESTs. Wealdy similar to 138022 hypotheti	2.6
	42366) ESTs	2.6
65	43032			18 uncharacterized hypothalamus protein HCD	2.6
	40846				2.6 2.6
	41065			dynein, cyloplasmic, intermediate polype	2.6
	44887				2.6
70	41451 45908				2.5
/ (45504 45504			gb:QV0-CT0225-100400-187-d08 CT0225 Homo	2.5
	4357				2.5
	4316				2.5
_	4359	D2 AA7018		26 ESTs	2.5 2.5
75	4366	24 164297		fatty acid binding protein 1, liver	25
	4431		Hs.237		25
	4391				2.5
	4263 4200				2.5
80	O 4084			960 KIAA0608 protein	2.5
J.	4402			448 ESTs. Weakly similar to 834087 hypotheti	25
	4487	86 BE0488	42 Hs.179	075 Homo sapiens cDNA FLJ11881 fis, clone HE	2.5 2.5
	4322		983 Hs.232	165 polycythernia rubra vera 1; cell surface	2.5

	427115	AW972853	Hs.112237	ECT.	
	433670	AA604405	113.112231	ESTs gb:no87h09.s1 NCI_CGAP_AA1 Homo sapiens	2.4 2.4
	452022	AW072330	Hs.293875	ESTs	24
-	408814	N62499	Hs.176227	hypothetical protein FLJ11155	2.4
5	403469			Target Exon	2.4
	450374	AA397540	Hs.60293	Homo sapiens clone 122482 unknown mRNA	24
	451926 443622	AW134519 AI911527	Hs.96125 Hs.11805	Homo sapiens, Similar to clone FLB3816, ESTs	2.4
	456791	H05202	Hs.133968	FGF receptor activating protein 1	24 24
10	414672	AI218038	Hs.48504	ESTs. Moderately similar to ALU5_HUMAN A	24
	451522	BE565817	Hs.26498	hypothetical protein FLJ21657	24
	422414	AW875237	Hs.13701	ESTs	24
	425383 438086	D83407 AA336519	Hs.156007 Hs.83623	Down syndrome critical region gene 1-lik	2.4
15	410240	AL157424	Hs.61289	nuclear receptor subfamily 1, group 1, m synaptojanin 2	24 24
	432408	N39127		ESTs, Weakly similar to A46010 X-linked	24
	458227	Z40670	Hs.181340	ESTs	24
	431325	AW026751	Hs.5794	ESTs. Weakly similar to 2109260A B cell	24
20	401600 422963	BE247275 M79141	Hs.13234	U5 snRNP-specific protein, 116 kD	23
	444897	AW137088	Hs.144857	ESTs ESTs	23 23
	418207	C14685	Hs.34772	ESTs	23
	445071	AJ280246	Hs.149504	ESTs	23
25	407868	NM_000950	Hs.40637	proline-rich Gla (G-carboxyglutarnic acid	2.3
23	433331 440293	A1738815 A1004193	Hs.117323 Hs.22123	ESTs	2.3
	428850	AA934975	Hs.185076	ESTs ESTs	2.3 2.3
	401783		113.100010	NM_003771":Homo sepiens keratin, hair, a	2.3
20	419763	AI039691	Hs.127486	ESTs .	2.3
30	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	2.3
	420912 442097	AW853156 AW015799	Hs.90787	ESTs ESTs	2.3
	425907	AA365752	Hs.128474 Hs.155965	ESTs	2.3
~ ~	404091			Target Exon	2.3 2.3
35	414106	8E300325	Hs.77135	RNA binding protein	2.3
	454268	BE222648	Hs.241432	ESTs, Highly similar to c380A1.1b [H.sap	2.3
	441040 424724	AW449782 106532	Hs.178803 Hs.287709	ESTs	2.3
	441879	AJ521936	Hs.107149	Homo sapiens cDNA: FLJ22674 fis, clone H novel protein similar to archaeal, yeast	2.3 2.3
40	407988	N47760	Hs.285107	hypothetical protein FLJ13397	2.3
	452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	2.2
	458676	A1692464	Hs.202263	ESTs	2.2
	418407 453938	AL044818 AF082569	Hs.84928 Hs.36794	nuclear transcription factor Y, beta	2.2
45	407978	AW385129	Hs.41717	D-type cyclin-interacting protein 1 phosphodiesterase 1A, calmodulin-depende	2.2 2.2
	420548	AA278246	Hs.920	ESTs	2.2
	422907	AI879263	Hs.77273	Human glucose transporter pseudogene	2.2
	446351	AW444551	Hs.35380	x 001 protein	2.2
50	442117 429598	AW664964 AA811257	Hs.128899 Hs.269710	ESTs; hypothetical protein for IMAGE:447 ESTs	2.2
•	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	2.2 2.2
	411361	AW839073		gb:CM2-LT0066-030100-109-d06 LT0066 Homo	2.2
	459697	AA406062	Hs.98002	ESTs	2.2
55	409856	AW502082	11- 000000	gb:UI-HF-BROp-eig-g-04-0-UI.r1 NIH_MGC_5	2.2
55	444760 443258	AI796296 AF169301	Hs.208062 Hs.9098	ESTs suffate transporter 1	2.2
	428206	AB020643	Hs.183006	KIAA0836 protein	2.2 2.2
	410119	F07841	Hs.13926	EST ₅	22
60	413427	U31120	Hs.845	interleukin 13	2.2
QQ.	438021 428652	AV553790 AA584272	Hs.324275 Hs.336224	WW domain-containing protein 1	2.2
	429655	U48959	Hs.211582	transmembrane protein with EGF-like and myosln, light polypeptide kinase	2.2
	424153	AA451737	Hs.141496	MAGE-like 2	2.2 2.2
CF	413303	AW836130	Hs.75277	hypothetical protein FLJ13910	2.2
65	427287	NM_014903	Hs.174188	KIAA0938 protein	2.2
	449658 441984	Af964033 AB037763	Hs.195730	ESTs, Weakly similar to CTXN RAT CORTEX	2.2
	449709	BE410592	Hs.8059 Hs.23918	synaptolagmin IV hypothetical protein PPS395	2.2 2.2
70	408068	AW148652	Hs.167398	ESTs	2.2
70	407819	R42185	Hs.102720	ESTs	2.2
	414203	BE262170	Hs.78629	ATPase, Na? transporting, beta 1 polypep	2.2
	454339 448045	AW381980 AJ297436	Hs.20166	gb:QV4-HT0316-091199-028-d05 HT0316 Homo	2.2
	458480	Al792298	113.20100	prostate stem cell antigen p30 DBC protein	2.2 2.2
75	449835	AW979300	Hs.293813	ESTs	2.2
	458547	AW204314	Hs.170784	ESTs	2.2
	411678	AI907114	Hs.71465	squalene epoxidase	2.1
	444783 424632	AK001468 AB014523	Hs.62180 Hs.151406	anillin (Drosophila Scraps homolog), act	2.1
80	449901	A1674072	(13.131400	KIAA0623 gene product gb.wd15h01.x1 Soares_NFL_T_GBC_S1 Homo s	2.1
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	2.1 2.1
	410538	AW753115		gb:PM0-CT0248-131099-001-h12 CT0248 Homo	2.1
	426775	AA384564	Hs.3628	ESTs	2.1
				200	

	499009	000000	Hs.3610	MIA ARRAGO TO A A	•
	433862 458694	D86960 F12832	Hs.3610	KIAA0205 gene product ESTs	2.1 2.1
	417063	N50515	Hs.45061	ESTs	2.1
	416935	AA190712		gb:zp87f09.r1 Stratagene HeLa cell s3 93	2.1
5	436489	AJ272269	Hs.121429	zinc-binding protein Rbcc728	21
	431128	AJ203545	Hs.296169	S-phase response (cyclin-related)	2.1
	442310 432434	AF033199 AL161977	Hs.8198 Hs.2994	zinc finger protein 204	2.1
	400339	X57131	Hs.248209	PCTAIRE protein kinase 3 H2A histone family, member F, pseudogene	2.1 2.1
10	432266	AK000385	Hs.274222	hypothetical protein FLJ20378	21
	414759	AW295157	Hs.47587	ESTS	2.1
	438219	AI916151	Hs.257194	ESTs	2.1
	451336	AJ264643	Hs.3610	ESTs	21
15	430538 413493	AB032435 BE144444	Hs.242821	differentiation-associated Na-dependent gb:MR0-HT0168-141199-002-f09 HT0168 Homo	2.1 2.1
	428501	AL041162	Hs.98587	ESTs	2.1
	431568	AW972316	Hs.283703	ESTS	21
	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	21
20	441976 421311	AA428403 N71848	Hs.106131 Hs.283609	ESTs hypothetical protein PRO2032	21
20	428358	AA993222	Hs.101915	Stargard disease 3 (autosomal dominant)	21 21
	439973	AJ733308	Hs.124663	ESTs	21
	446185	Al279191	Hs.149454	ESTs, Weakly similar to DSR6_HUMAN DOWN	2.1
25	451606	AA018791	Hs.7945	AIE-75 binding protein protein	2.1
23	433516 441987	AA595802 AW452234	Hs.33410 Hs.128293	ESTs, Wealdy similar to T17279 hypotheti ESTs	2.1 2.1
	457140	AI279960	Hs.178140	ESTs	2.1
	414055	AWB18687	Hs.5366	hypothetical protein FLJ21522	2.1
30	445066	BE178734	Hs.197422	ESTs	2.1
30	459265 425337	AJ003616 AA355442	Hs.169054	gb:AJ003616 Selected chromosome 21 cDNA ESTs	2.0
	409339	AB020686	Hs.54037	ectonucleolide pyrophosphalase/phosphodi	2.0 2.0
	453023	AW028733	Hs.31439	serine protease inhibitor, Kunitz type,	2.0
35	425055	AW961959	Hs.96940	ESTs	2.0
33	425068 444700	AL048716 NM_003645	Hs.154387 Hs.11729	KIAA0103 gane product fatty-acid-Coenzyme A ligase, very long-	2.0
	424823	NM_006226		phospholipase C, epsilon	2.0 2.0
	450103	R08665	Hs.17244	hypothetical protein FLJ13605	2.0
40	448519	AW175665	Hs.278695	Homo sapiens prostein mRNA, complete cds	2.0
70	440808 429968	AK001339 AA322503	Hs.7432 Hs.227011	hypothetical protein FLJ 10477 G-substrate	2.0 2.0
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	2.0
	433068	NM_006456		sialyltransferase	2.0
45	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcom	2.0
42	423479 407341	NM_014326 AA918886	Hs.129208 Hs.204918	death-associated protein kinase 2 ESTs. Weakly similar to ALUS_HUMAN ALU S	2.0 2.0
	452625	AA724771	Hs.61425	ESTs	2.0
	410378	R23324	Hs.41693	DnaJ (Hsp40) homolog, subfamily B, membe	2.0
50	409767 415925	AW501470 H09474	U- 200244	gb:UI-HF-BP0p-ajd-b-03-0-UI.r1 NIH_MGC_5	20
50	405670	1103474	Hs.202341	Homo sapians cDNA: FLJ23573 fis, clone L C2000627":gi[12034653]gb]AAG45951.1JAF22	2.0 2.0
	408206	AF041853	Hs.43870	kinesin family member 3A	20
	458560	AJ299739	Hs.99601	hypothetical protein FLJ 12553	2.0
55	432278 404559	AL137506	Hs.274256	hypothetical protein FLJ23563	2.0
-	403728			Target Exon Target Exon	2.0 2.0
	413055	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	2.0
	407786	AA687538	Hs.38972	tetraspan 1	2.0
60	413266 453994	BE300352 BE180964	Hs.165590	gb:600944231F1 NIH_MGC_17 Homo sepiens c	2.0
v	451583	AI653797	Hs.24133	ribosomal protein S13 ESTs	2.0 2.0
	443244	A1457235	Hs.166479		2.0
	453396	AW162768	Hs.22620	ESTS	2.0
65	415694 459511	AW194301 AI142379	Hs.339283	Human DNA sequence from clone RP1-187J11	2.0
45	450757	BE081050	Hs.31570	gb:qg64c01.r1 Soares_testis_NHT Homo sap ESTs, Weakly similar to KIAA1324 protein	2.0 2.0
	451032	W03692	Hs.323079		2.0
	440509	BE410132	Hs.134202		20
70	444647 447932	H14718 AA837474	Hs.11506	Human clone 23589 mRNA sequence	2.0
	444749	AI190672	Hs.20021 Hs.65926	vesicle-associated membrane protein 1 (s ESTs	2.0 2.0
	446277	AI284218	Hs.159204	ESTs	2.0
	452550	AA026735	Hs.326048		2.0
75	453843 445725	D25215 AK000956	Hs.35804 Hs.13209	hect domain and RLD 3	2.0
	409265	T78737	Hs.321062	hypothetical protein FLJ10094 ESTs	2.0 2.0
					2.0
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	409767 409856	1154015_1 1156268_1		V502931 AW499500 V502979 AW502807 AW501876		
5	410538 411361 411906	1207341_1 1240611_1 1265204_1	AW839073 AV AW875765 H5	V753113 R45779 V839234 AWB39230 AW878302 AWB39109 AV 0294 AW875444		
	412244 412636	1284692_1 13165_1	NM_004415 A AW849074 AY	V997139 AW799304 AW799309 BE0770 20 BE	8723 AW376697 AW376 077017 BE185187 AW99	817 AW376699 AW848371 AW376782 AW848789 AW361413 97196 BE156621 BE179915 BE006561 BE143155 AW890985
10			AW607238 AV AW265328 AV BE001925 BE AW995615 BE	V377700 AW377699 BE082526 BE082505 BEI VB47678 AW847688 AW365151 AW365148 AV 182166 BE144243 BE001923 AI951766 A434. E184948 BE159546 AW606653 AA098891 AA1	082507 BE082514 AW170 V365153 AW365156 AW 0518 BE184920 BE184933 31128 AA337270 AA340	6475 BE160433 J05211 BE082576 BE082584 BE004047 8000 AW177933 AI905935 AW747877 AW748114 BE148516 365175 AW365157 AW365154 AW068840 BE005272 AW365145 3 AI284090 BE184941 AW804674 BE184924 C04715 W39488 777 AW384371 AA852212 R58704 AW366566 AW364859
15	ć		T87267 AW85 H93284 AAD2 AA040018 BE BE167165 N8	i3812 AA852213 W74149 BE009090 AA05640 6863 AW177787 AA026654 AW177788 BE092 185331 BE182164 AA368564 AW951576 T299 4767 H27408 H30146 A1190590 C03378 A155	I H91011 AW368529 AW 134 BE092137 BE092130 118 AA131077 W95048 W 403 AI205263 AA128470	487 AA377127 AW890264 AW609750 AW391912 AW849690 (390272 C18487 AW674920 N57176 AA026480 AW576787 8 AW177784 A1022862 BE091653 AW376811 AW848592 V25458 AW205789 H90899 N28754 W32490 R20904 BE167181 2 A1392926 AF139065 AW370813 AW370827 AW788417
20			A1700963 AA4 AA702424 A14 A1270345 AW A1910434 A18	151923 aj340326 aj590975 748793 aj568096 117612 aj306554 aj686869 aj568892 aw1905 021347 aw166807 aw105614 aj346078 aa5: 19984 ai858282 ai078449 au025932 ai860584	A1142882 AA039975 A147 55 A1571075 A1220573 A 12300 W95070 A1494069 A1635878 AA026047 AA	AW370829 AA247685 BE002273 A/760818 A/439101 AW879451 70146 AA946936 BE067737 BE067788 W19287 AA644381 A056527 A4471874 A/304772 AW517828 A/915596 A/627383 A/911702 AA149191 AA026864 A/830049 A/887258 AW780435 A/03232 D12062 AW192085 AA658154 AW514597 AW591892
25	413266	1356260_1	AW015480 A\ W02156 Al90	2066 AW243815 AW150028 AW268383 AW00 M771865 AI270027 AA961816 AA283207 AI07 5927 AA022701 W38382 R20795 T77861 AW8 (299274 BE075351 BE297444	6962 A1498487 A1348053	19 AW473233 A1804485 AW169216 A1572669 AA602182 3 A1783914 H44405 AW799118 AA128330 AA515500 AA918281
30	413493 415666 416935 419386 424994	1373555_1 1543492_1 163179_1 184356_1 245786_1	AA190712 AA AA236867 AA AW954525 A	173 H72694 F20990 R08580 N190665 AA252564 N237066 AA354236 AW957759 H08961 1372685 AA349501 A1372687 H10564		
35	432408 433670 433921 436624	346286_2 372721_1 377350_1 4237_5	AA604405 BE AA618174 AI T64297 AA89 AI768596 AA	76 anb2691 aab6552d f36964 f33894 5062234 aw748386 114549 R36464 R36465 14931 nm_001443 M10050 aw843109 a16985 101894 w90338 a1742193 aw752206 aa0994	16 T53219 T48785 T6416 33 T53220 AW082135 AV	56 AA706930 R29613 T55913 T56518 T64679 R29666 M10617 W272775 T29562 T55862 AI343047 AI345671 T68235 T68121
40	449901 454339 455040 458480 459265	818599_1 1122972_1 1250028_1 59843_1 966590_1	AW852286 A AI792298 H1	268487 E152244 BE152235 BE152238 BE152232 W851934 AW\$52096 AW852274 4121 AI375113 AA960851 AA744592 AV64873 003554 AJ003617	9 Al298360 AW293609	
45	TABLE 2					•
	Pkey: Ret:	Uni Sec	quence source. 1	esponding to an Eos probeset The 7 digit numbers in this column are Genbani chromosome 22° Dunham, et al. (1999) <u>Nature</u>		"Dunham, et al." refers to the publication entitled "The DNA
50	Strand: NL position Pkey	on: Indi	icates nucleotide	d from which exons were predicted. positions of predicted exons.		
55	401600 401783 402429 403469 403728 404091	Ref 4388746 7249190 9796372 9929739 7534291 7684554	Strand Minus Plus Minus Minus Minus Minus	Nt_position 27363-27518,28727-28891,29526-29731 139359-139827,140509-140591,140834-1409 57622-57793,59282-59402,59624-59827 4831-7707 34481-34671 82121-83229	90,141496-141657,14175	57-141882,142063-142283
60	404559 404563 404606 405354 405403	8748893 9838310 9212936 2642452 6850244	Minus Ptus Minus Ptus Minus	73499-73651,89575-89739 100138-100343 22310-23269 52213-53089 37491-37670,40951-41031		
65	405670	4662655	Plus	96543-96870		
70	Table 23 on the Ai to the 75 backgrou	A lists about 44 fymetrix/Eos Hi P percentile am	1 genes significa u03 GeneChip ar ongst various no	Tay such that the ratio of "average" normal CNS rmal CNS tissues. The "average" LGG level wa	t (LGG) compared to nome to "average" LGG was go s set to the 95° percentile	COMPARED TO NORMAL ADULT CNS mall adult CNS tissues. These were selected from 59680 probesets reater than or equal to 2.5. The "everage" normal CNS level was sele a smongst various tumor samples. In order to remove gene-special was subtracted from both the numerator and the denominator before
75	Pkey: ExAcon: Unigenel Unigene R1:	Un Ex D: Un Tibe: Un	emplar Accession igene number igene gene title	et identifier number n number, Genbank accession number WER GRADE GLIOBLASTOMA		
80	Pkey 415388 418318 445529 417433	ExAcon AF018081 U47732 H14421 BE270266	UnigenelD Hs.78409 Hs.84072 Hs.180513 Hs.82128	Unigene Tide collagen, type XVIII, alpha 1 transmembrane 4 superfamily member 3 ATP-binding cassette, sub-family A (ABC1 5T4 oncofetal trophobiast glycoprotein		R1 10.3 10.1 9.9 7.8

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	422746	NM_004484	Hs.119651	glypican 3	7,7
	448362	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	7.7
	430573	AA744550	Hs.136345	ESTs	7.6
5	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	7.5
,	419290 424670	AI128114 W61215	Hs.112885 Hs.116651	spinal cord-derived growth factor-8 epithelial V-like antigen 1	7.4
	417167	AW206437	Hs.4290	ESTs	7.3 7.3
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	7.3
10	424532	AB014523	Hs.151406	KIAA0623 gene product	6.9
10	453165 411770	S74727 NM_014278	Hs.32042 Hs.71992	aspartoacylase (aminoacylase 2, Canavan heat shock protein (hsp110 family)	6.5
	439272	AA832474	Hs.25851	ESTs	6.5 6.5
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	6.4
15	454076	AW204712	Hs.61957	ESTs	6.3
13	446390 430865	AA233393 Al073424	Hs.14992 Hs.5232	hypothetical protein FLJ11151 HSPC125 protein	6.3
	434064	AL049045	Hs.180758	hypothetical protein PRO0082	6.3 6.2
	417458	NM_005655	Hs.82173	TGF8 inducible early growth response	6.1
20	412636	NM_004415		desmoplakin (DPI, DPII)	6.0
20	409743 430998	N48721 AF128847	Hs.183506 Hs.204038	hypothetical protein FLJ14213	5.9
	434725	AK000796	Hs.4104	indolethylamine N-methyltransferase hypothetical protein	5.8 5.6
	417175	R44558	Hs.94002	ESTs	5.6
25	417275	X63578	Hs.295449	parvalbumin	5.5
25	427322 431009	AK002017 BE149762	Hs.176227	hypothetical protein FLJ11155	5.5
	420297	A)628272	Hs.48956 Hs.88323	gap junction protein, beta 6 (connexin 3 ESTs, Wealdy similar to ALU1_HUMAN ALU S	5.4 5.4
	412472	AW975398	Hs.293836	ESTs	5.4
30	443258	AF169301	Hs.9098	sulfate transporter 1	5.3
30	427210 442064	8E396283	Hs.173987 Hs.88594	eukaryotic translation initiation factor	5.3
	438868	AJ422867 AW246243	Hs.334800	ESTs hypothetical protein FLJ20974	5.2
	444409	A1792140	Hs.49265	ESTs	5.2 5.2
25	442310	AF033199	Hs.8198	zinc finger protein 204	5.1
35	409031	AA376836	Hs.288856	ESTs	5.1
	438460 411939	AB020702 AI365585	Hs.6224 Hs.146246	KIAA0895 protein ESTs	5.1
	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	5.0 5.0
40	413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	5.0
40	408968	AI652236	Hs.49376	hypothetical protein FLJ20644	5.0
	443491 448960	AW499665 AF006513	Hs.9456	SWI/SNF related, matrix associated, acti	4.9
	416101	R24854	Hs.22670 Hs.268806	chromodomain helicase DNA binding protei ESTs	4.9 4.9
	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	4.9
45	424845	NM_014682	Hs.151449	KIAA0535 gene product	4.8
	437679	NM_014214	Hs.5753	inositol(myo)-1(or 4)-monophosphatase 2	4.8
	408428 414502	NM_014787 AL133721	Hs.44896 Hs.224680	OnaJ (Hsp40) homolog, subfamily B, membe ESTs	4.8
	442572	AJ001922	Hs.135121	hypothetical protein FLJ22415	4.8 4.8
50	412700	BE222433	Hs.239208	ESTs, Weakly similar to 138022 hypotheti	4.8
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	4.8
	420605 422482	BE391491 Al439905	Hs.99291 Hs.344476	HSPC156 protein	4.7
	416636	N32536	Hs.42645	gb:ti57g08.x1 NCI_CGAP_tym12 Homo saplen solute carrier family 16 (monocarboxylic	4.7 4.7
55	409263	AA069573	Hs.50319	ESTs	4.7
	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype	4.6
	457216 433423	AA452554 BE407127	Hs.283697	ESTs, Wealdy similar to A41796 neural re	4.6
	449901	AIB74072	Hs.8997	heat shock 70kD protein 1A gb:wd15h01.x1 Soares_NFL_T_GBC_S1 Homo s	4.6 4.6
60	445618	H79667	Hs.237642	Homo sapiens cONA FL/12052 fis, clone HE	4.6
	431582	F07136	Hs.261828	G protein-coupled receptor kinase 7	4.5
	424875 449 5 11	NM_005512	Hs.151641	glycoprotein A repetitions predominant	4.5
	401500	AI436187 BE247275	Hs.296261	guanine nucleotide binding protein (G pr US snRNP-specific protein, 116 kD	4.5
65	447135	T58148		gb:yb98g08.s1 Stratagene lung (937210) H	4.5 4.5
	426689	8E245550	Hs.171825	basic helix-loop-helix domain containing	4.4
	429598	AA811257	Hs.269710	ESTs	4.4
	428206 450715	AB020643 AI266484	Hs.183006 Hs.31570	KIAA0836 protein	4,4
70	428508	BE252383	Hs.184668	ESTs, Wealdy similar to KIAA1324 protein SBBI31 protein	4.4 4.4
	435145	AJ277259	Hs.116631	ESTs	4.4
	405670	A FRE '		C2000627*:gi[12034653igb]AAG45951.1JAF22	4.4
	442321 427570	AF207664 8E612888	Hs.8230	a disintegrin-like and metalloprotease (4.3
75	428465	AW970976	Hs.180224 Hs.293653	myosin regulatory light chain ESTs	4.3
	449180	AI633836	Hs.195649	ESTs	4.3 4.3
	402354	AV653231		CCAAT/enhancer binding protein (C/EBP),	4.3
	426471	M22440	Hs.170009	transforming growth factor, alpha	4.2
80	419386 441408	AA236867 AJ733249	Hs.126897	ESTs, Wealdy similar to I38022 hypotheti ESTs	4.2
	419631	AW188117	Hs.303154	popeye protein 3	4.2
	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein	4.2
	448958	AB020651	Hs.22653	KIAA0844 protein	4.2
				212	

	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	4.2
	422278	AF072873	Hs.114218	frizzled (Drosophila) hornolog 6	4.2
	459053	AI807052	Hs.210361	ESTs	4.1
5	450600	BE079478	Hs.24880	ESTs	4.1
3	415839	R40611	Hs.94694	ESTs	4.1
	450374	AA397540	Hs.60293	Homo sapiens clone 122482 unknown mRNA	4,1
	422270 405674	AF114494	Hs.114062	protein lyrosine phosphatase-like (proti	4.1
	453906	AW444952		NM_022775:Homo sapiens hypothetical prot	4.1
10			Hs.257054	ESTs	4.1
10	419318 456382	AW969742	Hs.291005	ESTs	4.0
	435902	NM_001126 AA701867	Hs.90011 Hs.297726	adenylosuccinate synthase	4.0
	449483	AK001971	Hs.23607	ESTS	4.0
	434228	Z42047	Hs.283978	hypothetical protein FLJ11109	4.0
15	403890	545041	10.200310	Homo sapiens PRO2751 mRNA, complete cds	4.0
	429470	AJ878901	Hs.203862	C5002036":gij10241574jembjCAC09416.1j (A - guanine nucleotide binding protein (G pr	4.0
	409856	AW502082	15.20002	gb:UI-HF-BR0p-ajq-g-04-0-UI.r1 NIH_MGC_5	4.0
	443682	AI383061	Hs.47248	ESTs. Highly similar to similar to Cdc14	4.0 4.0
	420230	AL034344	Hs.284186	forkhead box C1	4.0
20	410509	AW840743		gb:QV1-CN0002-080300-102-07 CN0002 Homo	4.0
	428414	AL049980	Hs.184216	DKFZP564C152 protein	3.9
	400138			Eos Control	3.9
	451522	BE565817	Hs.26498	hypothetical protein FLJ21657	39
25	436521	AW203986	Hs.213003	ESTs	3.9
25	401507			C15000810":gi]11131272[spjP79331]ATS2_BO	3.9
	449785	A1225235	Hs.288300	hypothetical protein FLJ23231	3.9
	434815	AF155582	Hs.46744	core 1 UDP-galactose:N-acetylgalactosamin	3.9
	411906	AW875765		gb:QV2-PT0012-020500-186-a08 PT0012 Homo	3.9
30	440509	BE410132	Hs.134202	ESTs, Weakly similar to T17279 hypotheti	3.9
30	427061	AB032971	Hs.173392	KIAA1145 protein	3.9
	430261	AA305127	Hs.237225	hypothetical protein HT023	3.9
	449658	AI964033	Hs.195730	ESTs, Wealdy similar to CTXN RAT CORTEXI	3.8
	429876	AB028977	Hs.225974	KIAA1054 protein	3.8
35	410330	AW023630 BE184455	Hs.159425	ESTs	3.8
55	431369 437659	AB007944	Hs.251754	secretory leukocyte protease inhibitor (3.8
	438171	AW976507	Hs.5737 Hs.293515	KIAA0475 gene product	3.8
	418394	AF132818	Hs.84728	ESTs Kruppel-lika factor 5 (intestinal)	3.8
	405586	AF 132010	FIS.04720	NM_000299:Homo sapiens plakophilin 1 (ec	3.8
40	432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA DKFZp761G1111 (f	3.8
. •	426716	NM 006379	Hs.171921	sema domain, immunoglobulin domain (lg),	3.8
	438202	AW169287	Hs.22588	ESTs	3.8 - 3.8
	404606	************	113.22300	Target Exon	3.8
	425329	AI961644	Hs.145444	Homo sapiens cDNA FLJ11494 fis, clone HE	3.8
45	407604	AW191962	Hs.288061	collagen, type VIII, alpha 2	3.8
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	3.7
	430868	W93178	Hs.5232	HSPC125 protein	3.7
	457008	AA410446	Hs.112011	ESTs, Weakly similar to unknown (H.sapie	3.7
50	458660	AI299739	Hs.99601	hypothetical protein FLJ12553	3.7
50	408732	AL117490	Hs.47225	Ras-associated protein Rap1	3.7
	436281	AW411194	Hs.85195	myeloid leukemia factor 1	3.7
	413493	BE144444		gb:MR0-HT0168-141199-002-109 HT0168 Homo	3.7
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	3.7
55	445797	A1253414		gb:aq14f04.x1 Stanley Frontal NS pool 2	3.7
"	457121	AI743770	Hs.180513	ESTs, Weakly similar to KIAA0822 protein	3.6
	417620	R02530	Hs.191198	ESTs	3.6
	421952 454247	AA300900 AJ243950	Hs.98849	ESTs, Moderately similar to AF161511 1 H	3.6
	431662	AA513406	Hs.46735	deafness tocus associated putative guard ESTs	3.6
60	426908	AW815163	Hs.152307 Hs.172851		3.6
- •	438519	Al186033	Hs.147025	arginase, type II ESTs, Wealdy similar to C57785 zinc fing	3.6
	415606	W70022		gb:zd51e10.r1 Soares_fetal_heart_NbHH19W	3.6
	444859	AW449137	Hs.157487	ESTs	3.6
	414631	AW970130	Hs.65406	ESTs	3.6 3.6
65	428897	AJ245719	Hs.194385	hypothetical protein FLJ20234	3.5
	437073	A1885608	Hs.94122	ESTs .	3.5
	427287	NM_014903	Hs.174188	KIAA0938 protein	3.5
	415927	AL120168	Hs.78919	Kell blood group precursor (McLeod pheno	3.5
70	450235	AA007512	Hs.17538	ESTs	3.5
70	447263	AW965667	Hs.322406	hypothetical protein FLJ14494	3.5
	419440	AB020689	Hs.90419	KIAA0882 protein	3.5
	427254	AL121523	Hs.97774	ESTs	3.5
	434348	8E393191	Hs.181795	putative b,b-carotene-9',10'-dioxygenase	3.5
75	441264	AA927170	Hs.23290	ESTs	3.5
13	433629	R13140	Hs.13359	ESTs	3.5
	446494	AA463276	Hs.288906	WW Domain-Containing Gene	3.5
	441585	A1760755	Hs.202383	ESTs	3.5
	438704	AI435060	Hs.32825	ESTs	3.4
80	445279 415114	R41900 D60468	Hs.22245	ESTs EST-	3.4
	415114 449561	AI022240	Hs.94181 Hs.17924	ESTS	3.4
	452420	BE564871	Hs.29463	ESTs, Moderately similar to ALU1_HUMAN A centrin, EF-hand protein, 3 (CDC3) yeast	3.4
	416517	AA775987	Hs.79357	protessome (prosome, macropain) 26S subu	3.4
			110.13331	Processing (Proportio, mouroball) 509 5000	3.4
				212	

	441134	W29092	Hs.346950	collidat estinais suid bludius sentais 1	• •
	427176	AW381569	Hs.40334	cellutar retinoic acid-blnding protein 1 ESTs	3.4 3.4
	415668	AW957684	Hs.306814	hypothetical protein FLJ21889	3.4
5	450928	AI744417		gb:tr10h12.x1 NCI_CGAP_Ov23 Homo sapiens	3.4
,	457012 405354	R41480	Hs.302754	ESTs	3.3
	408855	T83061	Hs.319946	CX000321:gi[6671579]ref[NP_031518.1] ari Homo sapians mRNA for KIAA1727 protein,	3.3 3.3
	418525	AW450369	Hs.86937	ESTs	33
10	420174	AI824144	Hs.23912	ESTs	3.3
10	437124	AASS4458	Hs.279860	KIAA0666 protein	3.3
	419211 424335	BE270817 AW021508	Hs.37617 Hs.28170	ESTs, Wealthy similar to A53933 myosin I	3.3
	453344	BE349075	Hs.44571	ESTs ESTs	3.3 3.3
	428065	AI634046	Hs.157313	ESTs	3.3
15	417248	AA329449	Hs.247302	twisted gastrulation	3.3
	429415	NM_002593	Hs.202097	procollagen C-endopeptidase enhancer	3.3
	411393 406976	AW797437 M60299	Hs.69771	B-factor, propertin	3.3
	441071	D79550	Hs.7149	gb:Human alpha-1 collagen type II gene, Homo sapiens cDNA: FLJ21950 fis, clone H	3.3 3.3
20	414327	BE408145	Hs.185254	ESTs, Weakly similar to T24435 hypotheti	3.3
	433703	AA210863	Hs.3532	nemo-like kinase	3.3
	418880	N87353	Hs.89421	CBF1 Interacting corepressor	3.3
	445947 437334	AW612084 AL353947	Hs.298494 Hs.283780	ESTS	3.3
25	434795	BE620794	Hs.4147	hypothetical protein DKFZp761N1814 translocating chain-associating membrane	3.3 3.2
	400127			Eas Control	3.2
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	3.2
	402429 428695	AI355647	16- 400000	Target Exon	3.2
30	427699	AU333647 AW965076	Hs.189999 Hs.180378	purinergic receptor (family A group 5) hypothetical protein 669	3.2
	403442	***************************************	14.100070	Target Exon	3.2 3.2
	419272	AA663904	Hs.89862	TNFRSF1A-associated via death domain	3.2
	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	3.2
35	407581 412633	R48402 AF001691	Hs.173508	PSECSL	3.2
55	433328	AW298159	Hs.74304 Hs.23644	periplakin ESTs, Wealdy similar to \$65824 reverse t	3.2
	449294	AI651786	Hs.195045	ESTs	3.2 3.1
•	442799	AI564739	Hs.68505	ESTs	3.1
40	434045	AI065133	Hs.152316	hypothetical protein PRO0971	3.1
40	409403 420033	AA668224 D59502	Hs.6634 Hs.292590	Homo sapiens cDNA; FLJ22547 fis, clone H ESTs	3.1
	422137	AJ236885	Hs.112180	zinc finger protein 148 (pHZ-52)	3.1 3.1
	444760	Al796296	Hs.208062	ESTs	3.1
45	403488			ENSP00000201948:KARYOPHERIN BETA2B HOMOL .	3.1
43	411359 443037	H86088 AW500305	Hs.22635	ESTs	3.1
	407127	R45970	Hs.8906 Hs.235349	syntaxin 7 EST	3.1 3.1
	416851	AW963951	Hs.85618	ESTs	3.1
50	416838	D84109	Hs.80248	RNA-binding protein gene with multiple s	3.1
50	443030	R68048	Hs.9238	hypothetical protein FLJ23516	3.1
	410389 459399	AW954049 BE407712	Hs.8177 Hs.153998	ESTs, Weakly similar to PIHUB6 salivary	3.1
	433582	BE548749	Hs.148016	creatine kinase, mitochondrial 1 (ubiqui ESTs	3.1 3.1
<i></i>	431128	AI203545	Hs.296169	S-phase response (cyclin-related)	3.1
55	420411	AI581085	Hs.2467B	sphingosine-1-phosphatase	3.1
	459584 449883	AI910884 AI004464	Hs.346429 Hs.344156	ESTS	3.1
	445320	AA503887	Hs.167011	gb:ot56e06.s1 Soares_testis_NHT Homo sap Homo sapiens cDNA: FLJ21362 fis, ctone C	3.1 3.1
60	410786	AW803340		gb:IL2-UM0079-090300-050-D02 UM0079 Homo	3.1
60	418207 420521	C14685	Hs.34772	ESTs	3.0
	425890	A1915734 H24530	Hs.87298	ESTs	3.0
	416749		Hs.273294 Hs.79732 ome	hypothetical protein FLJ20069 fibulin 1	3.0 3.0
15	412258	AA376768	Hs.324841	hypothetical protein FLJ22622	3.0
65	407173	T64349		gb:yc10d08.s1 Stratagene tung (937210) H	3.0
	415672 448583	N53097 NM_015239	Hs.193579	ESTs	3.0
	429043	AI824977	Hs.21542 Hs.145319	KIAA1035 protein ESTs	3.0
70	404091		141140015	Target Exon	3.0 3.0
70	406085			Target Exon	3.0
	438825	BE327427	Hs.79953	ESTs	3.0
	457441 403512	BE467737	Hs.146125	ESTs C3000579*:gi 12643308;pp C9Y4K1 AIM1_HUM	3.0
20	416866	AA297356	Hs.80324	serine/hreonine protein phosphatase cat	3.0 3.0
75	439877	H39685	Hs.250700		3.0
	441984	AB037763	Hs.8059	synaptotagmin IV	3.0
	436765 445071	AB028952 Al280246	Hs.5307 Hs.149504	synaptopodin ESTs	3.0
00	404333		113.143304	C7001735":gij7768636kbijBAA95483.1 (AB	3.0 3.0
80	422907	AI879263	Hs.77273	Human glucose transporter pseudogene	3.0
	413266	BE300352	40 80.00-	gb:600944231F1 NIH_MGC_17 Homo sepiens c	3.0
	429393 415337	AA383024 Z44881	Hs.201603 Hs.9012	Homo sapiens mRNA, cDNA DKFZp434D0917 (f	3.0
	0007	~~~~	113.3014	ESTs. Wealthy similar to S26650 DNA-bindi	3.0

	415044	AA419108	Hs.77840	annexin A4	2.9
	403469			Target Exon	2.9
	416928	AA190573	Hs.85902	ESTs, Weakly similar to MCHU calmodulin	2.9
5	430195	AW969308	Hs.188594	ESTs	29
3	458544	A)631036	Hs.196843	ESTs	29
	440667	BE076969	Hs.7337	hypothetical protein FLJ10936	2.9
	424641	AB001106	Hs.151413	glia maturation factor, bela	2.9
	428820	AA436187	Hs.172631	Integrin, alpha M (complement component	29
10	405403	414500000	Lie Anno co	Target Exon	2.9
10	452197 437357	AW023595	Hs.232048	ESTS	2.9
	423479	AL359559	Hs.331666	Homo sepiens mRNA; cDNA DKFZp762O2215 (I	29
	404559	NM_014326	Hs.129208	death-associated protein kinase 2	29
	406270			Target Exon	2.9
15	422190	H17399	Hs.11506	Target Exon	2.9
	431300	AA502346	NS.11300	Human clone 23589 mRNA sequence	2.9
	420286	A1796395	Hs.111377	gb:ne26b03.s1 NCI_CGAP_Co3 Homo sapiens ESTs	29
	422964	AW439476	Hs.256895	ESTs	2.9 2.9
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	29
20	428595	AB037795	Hs.186547	KIAA1374 protein	29
	402198			NM_024323:Homo sepiens hypothetical prot	29
	416246	U47413	Hs.79101	cyclin G1	29
	427593	AK001132	Hs.179752	Homo sapiens cDNA FLJ10270 fis, clone HE	2.9
	446351	AW444551	Hs.35380	x 001 protein	2.9
25	440432	AI239637	Hs.202653	ESTs, Wealty similar to T14267 Xin prote	2.9
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	2.8
	400965			C11002190*:gi[12737279]ref[XP_012163.1]	2.8
	436489	AJ272269	Hs.121429	zinc-binding protein Rbcc728	2.8
20	458793	N80159	Hs.121849	microtubule-associated proteins 1A/1B li	2.8
30	406810	U82275	Hs.94498	teukocyte immunoglobulin-like receptor.	2.8
	445577	N40696	Hs.137054	cytoplasmic polyadenylation element bind	2.8
	428874	W32133	Hs.194366	transthyretin (prealbumin, amyloidosis t	2.8
	418745	AW882645	Hs.88044	sprouty (Orosophila) homolog 1 (antagoni	2.8
35	433095	AK001092	Hs.302480	Homo sapiens cONA FLJ10230 fis, clone HE	2.8
55	425580	L11144	Hs.1907	galanin	2.8
	416233 438219	AA176633	11- 257104	gb:zp13g01.s1 Stratagene fetal retina 93	2.8
	404661	AI916151	Hs.257194	COCCCC-114222770010VD cocccq or b	2.8
	435836	AW292532	Hs.343667	C9000306*:gi 12737280 ref XP_006682.2 k	28
40	423665	BE167153	Hs.24380	homolog of yeast long chain polyunsatura ESTs	2.8 2.8
. •	430320	BE245290	Hs.239218	uncharacterized hypothalamus protein HCD	2.8
	401783	300 1000	1.0.200210	NM_003771*:Homo sepiens keratin, hair, a	2.8
	423837	AW937063	Hs.275150	gb:PM3-DT0037-231299-001-g11 DT0037 Homo	2.8
	447271	AL041747	Hs.170261	ESTs	2.8
45	438913	AJ380429	Hs.172445	ESTs	2.8
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	2.8
	444385	BE278964	Hs.11085	CGI-111 protein	2.8
	432278	AL137508	Hs.274256	hypothetical protein FLJ23563	2.8
50	415666	H72693		gb:yu03c11.r1 Soares fetal liver spleen	2.8
50	452345	AA293279	Hs.29173	hypothetical protein FLJ20S15	2.8
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	2.8
	439556	AI623752	Hs.163603	ESTs	2.8
	405474	41070070		NM_001093*:Homo sapiens acetyl-Coenzyme	2.8
55	426208	AI370379	Hs.132216	ESTS	2.B
	419461 428501	A1452601 AL041162	Hs.288869 Hs.98587	nuclear receptor subfamily 2, group F, m ESTs	28
	413427	U31120	Hs.845	interleukin 13	2.8
	433109	N58907	Hs.162430	EST	2.8
	427974	BE093023	Hs.188767	ESTs	2.8 2.8
60	455040	AW852288		gb:QV0-CT0225-100400-187-d08 CT0225 Homo	2.8
	453994	BE180964	Hs.165590	ribosomal protein S13	2.8
	459171	AW967801	Hs.64783	ESTs, Weakly similar to T42705 hypotheti	2.8
	404845			C22000163*:gi 10242166 gb AAG15318.1 AF2	2.8
	408182	AA047854		gb:zf49g04.r1 Soares retina N2b4HR Homo	2.8
65	427111	AA351026	Hs.173594	serine (or cysteine) proteinase inhibito	2.7
	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member	2.7
	432815	Z30045	Hs.293676	ESTs .	2.7
	404035			Target Exon	2.7
70	418157	W99382	Hs.283709		2.7
, 0	426403	NM_000361	Hs.2030	thrombomodulin	2.7
	439659	AW970780	Hs.59483	Homo sapiens cDNA FLJ14471 ffs, clone MA	2.7
	443932 444930	AW888222	Hs.9973 Hs.301183	tensin	2.7
	419269	BE185536 AA235838	rs.301183		2.7
75	415004	D11880	LL= 20024 A	gb:zs41b04.s1 Soares_NhHMPu_S1 Homo sapi	2.7
	430371	D87466	Hs.299254 Hs.240112		2.7
	449117	AW449310	Hs.210262		2.7
	451007	H38108	Hs.32759	ESTS	2.7 2.7
	421202	AF193339	Hs.102506		2.7
80	406308			NM_025192:Homo sapiens hypothetical prot	2.7
	413208	BE071799		gb:RC0-8T0522-071299-011-b10 8T0522 Homo	27
	421420	AI024235	Hs.123296	ESTs, Weakly similar to PEC1_HUMAN PLATE	2.7
	445693	AW800444	Hs.76507	LPS-induced TNF-alpha factor	2.7
				·	

	452351	AA025647		gb:ze85d01_r1 Soares_letal_heart_NbHH19W	2.7
	410538	AW753115	11. 01000	gb:PM0-CT0248-131099-001-h12 CT0248 Homo	2.7
	448072 420912	AI459306 AW853156	Hs.24908 Hs.90787	ESTs .	2.7
5	453830	A4534296	Hs.20953	ESTs ESTs	27
	457791	AW117431	Hs.191906	ESTs	2.7 2.7
	417735	AA188175	Hs.82506	KIAA1254 protein	27
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	2.7
	417076	AW973454	Hs.238442	ESTs, Moderately similar to ALU7_HUMAN A	2.7
10	436476	- AA326108	Hs.33829	bHLH protein DEC2	2.7
	440945	AW505345	Hs.7540	f-box and leucine-rich repeat protein 3A	2.7
	425826	U97698		mucin 6, gastric	2.7
	422795	AB033109	Hs.120856	KIAA1283 protein	2.7
15	433921	AA618174		gb:nq14f01.s1 NCI_CGAP_Thy1 Homo sapiens	2.7
13	414272 418047	AI651603	Hs.46988	ESTS	2.7
	421089	R37633 AB037771	Hs.4847 Hs.101799	ESTs KIAA1350 protein	2.7
	419763	AI039691	Hs.127486	ESTs	2.7 2.7
	459265	AJ003616	10.12.400	gb:AJ003616 Selected chromosome 21 cDNA	2.7
20	410970	AW812151		gb:RC5-ST0178-081099-011-A06 ST0178 Homo	27
	401925	N98378		sialyltransferase 1 (beta-galactoside al	27
	418504	BE159718	Hs.85335	Homo sapiens mRNA; cDNA DKFZp564D1462 (f	2.6
	433789	AA220977		gb:zr01a08.r1 Stratagene NT2 neuronal pr	26
25	418308	AA215738	Hs.182514	ESTs, Weakly similar to A46010 X-linked	26
23	444618	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATIO	2.6
	406299 422963	M79141	Lin 42224	Target Exon	2.6
	441244	BE612935	Hs.13234 Hs.184052	ESTs SSI201 and the	2.6
	439954	AL046748	Hs.6790	PP1201 protein DnaJ (Hsp40) homolog, subfamily 8, membe	2.6
30	405088	720-101-10	15.0750	Target Exon	2.6 2.6
	404741			Target Exon	2.6
	451927	AL355687	Hs.27261	Homo sapiens mRNA full tength insert cDN	2.6
	439103	AF085959	Hs.38705	EST8	2.6
26	437241	AL137318	Hs.306450	Homo sapiens mRNA: cDNA DKFZp434L171 (fr	2.6
35	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	2.6
	457394	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	2.6
	427229	AJ799751	Hs.5635	ESTs .	2.6
	414630 406744	BE410857 AA554082	Hs.16064	gb:601301177F1 NIH_MGC_21 Homo sapiens c	2.6
40	443984	Al424415	Hs.279860 Hs.143719	turnor protein, translationally-controlle ESTs	26
	421221	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	2.6 2.6
	421709	AA159394	Hs.107056	CEO-6 protein	26
	426747	AA535210	Hs.171995	katikrein 3, (prostate specific antigen	2.6
	439480	AL038511	Hs.125316	ESTs, Wealdy similar to S33990 finger pr	2.6
45	419567	AW339890	Hs.128187	ESTs	2.6
	421922	AW295043	Hs.109590	genethonin 1	2.6
	421859	AA356620	Hs.108947	KIAA0050 gene product	2.6
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.6
50	444843	AA400172	Un 1027	gb:zu69e01.r1 Soares_testis_NHT Homo sap	2.6
50	416729 439238	U46165 N47305	Hs.1027 Hs.302161	Res-related associated with diabetes ESTs	2.6
	4391B3	AW970600	Hs.303261	ESTS	2.6
	408739	W01556	Hs.238797	ESTs, Moderately similar to 138022 hypot	2.6 2.6
	412061	AA833763	Hs.330211	ESTs	26
55	432114	AL036021	Hs.8934	ESTs	2.6
	425337	AA355442	Hs.169054	ESTS	2.6
	424299	AK000377	Hs.82294	homolog of mouse C2PA	2.6
	448871	BE616709	Hs.159265	knuppel-related zinc finger protein hcKr	26
60	414516 456235	Al307802 AA203637	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	2.6
00	456235 410429	AA203637 AA310600	Hs.63657	gb:zx58b12.r1 Soares_fetal_fiver_spleen_	2.6
	449251	AW151660	Hs.31444	peptide:N-glycenese similar to yeast PNG ESTs	2.6
	436545	AW023329	Hs.132743		2.6 2.6
	450546	AA010200	Hs.175551	ESTA	2.6
65	437255	R58970	Hs.9887	ESTs	2.6
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	2.6
	427983	M17706	Hs.2233	colony stimulating factor 3 (granulocyte	2.5
	413341	H78472	Hs.191325		2.5
70	423763	R98203	Hs.132724		2.5
, 0	413282 415590	8E078159	LL 170004	gb:CM0-BT0615-140200-175-e06 BT0615 Homo	2.5
	408215	T74068	Hs.170081		2.5
	453938	AF082569	Hs.36794	Target Exon D-type cyclin-interacting protein 1	2.5
	424310	AA338648	Hs.50334	testes development-related NYO-SP22	2.5 2.5
75	442097	AW015799	Hs.128474		2.5 2.5
	456650	AA620501	Hs.106773		2.5
	413231	D87461	Hs.75244	BCL2-like 2	2.5
	457297	AW968188		gb:EST380383 MAGE resequences, MAGJ Homo	2.5
Q Λ	444942	AW293458	Hs.283807	chromosome 11 open reading frame 16	2.5
80	425764	AW996009	Hs.112572		2.5
	435712	AA694607	Hs. 176956		2.5
	436624 443155	T64297 R54485	Hs.23772	fatty acid binding protein 1, liver	2.5
	- 10100	100	14.23112	ESTs	2.5

	425907	AA365752	Hs.155965	ESTS	2.5	
	414759	AW295157	Hs.47587	ESTs	2.5	
	414699	AI815523	Hs.76930	symuclein, alpha (non A4 component of am	2.5	
5	411426 404492	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	2.5	
,	425153	AW023193	Hs.27046	C8000067*:gij10432400 emb CAC10290.1 (A ESTs	2.5 2.5	
	426372	BE304680	Hs.169531	DEAD/H (Asp-Glu-Ala-Asp/Hs) box polypep	25	
	434803	AW974640	Hs.303413	ESTs	2.5	
	425694	U51333	Hs. 159237	haxokinase 3 (white cell)	25	
10	433069	X76732	Hs.3164	nucleobindin 2	2.5	
	428054	AI948688	Hs.266619	ESTs	2.5	
	424823	NM_006226	Hs.153322	phospholipase C, epsilon	2.5	
	456972 431405	AI054347 AI470895	Hs.2017 Hs.334895	ribosomal protein L38	2.5	
15	427982	NM_016156	Hs.181326	ribosomal protein L10a KIAA1073 protein	2.5 2.5	
••	412831	AA121352	Hs.143314	ESTs	2.5	
	437114	AA836641	Hs.163085	ESTs	2.5	
	426157	AA370977	Hs.345728	STAT induced STAT inhibitor 3	2.5	
20	448786	BE048842	Hs.179075	Homo sapiens cDNA FLJ11881 fis, clone HE	2.5	
20	432251 449239	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	2.5	
	453572	T24653 AA382590	Hs.23360 Hs.46366	Ekely ortholog of yeast ARV1	2.5	
	433072	~~002330	113.40300	KIAA0948 protein	2.5	
	TABLE 23	B:				
25	Pkey:		ie Eas probes	set identifier number		
	CAT numb		cluster numb			
	Accession:	: Gent	ank accessio	n numbers		
	Pkey	CAT Number	Accession			
30	408182	104479_1		AA057506 AA053841		•
	409856	1156268_1		AW502979 AW502807 AW501876		
	410509	1206699_1	AW840743	AW752404 H43469		
	410538	1207341_1		AW753113 R45779		
35	410786	1221063_1		AW803280 AW803275 AW803415 AW803343 AW803422		
55	410970 411426	1228131_1 1245515_1		AW812186 AW812166 AW845993 AW845989		
	411906	1265204_1		H50294 AW875444		
	412636	13165_1		5 AL031058 M77830 BE149760 AW752599 AW848723 AV	V376697 AW376817 AW376699 A	WR4R371 AW3767R2 AWR4R7R9 AW361413
40		-	AW849074	AW997139 AW799304 AW799309 BE077020 BE077017	BE185187 AW997196 BE156621 I	E179915 BE006561 BE143155 AW890985
40			BE002107	AW103521 AA857316 AW383133 BE011378 AW170253 I	IE 185750 AW886475 BE 160433 J	05211 BE082576 BE082584 BE004047
			AW607238	AW377700 AW377699 BE082526 BE082505 BE082507 I	E082514 AW178000 AW177933	U905935 AW747877 AW748114 BE148516
				AW847678 AW847688 AW365151 AW365148 AW36515		
			AW005616	BE182166 BE144243 BE001923 AI951766 AI434518 BE1 BE184948 BE159646 AW606653 AA099891 AA131128 A	84920 BE 184933 AI284090 BE 184 A337770 AA340777 AW39A374 A	941 AW804674 BE184924 C04715 W39488
45				AA025852 AA455100 AA719958 AW352220 AW996245 B		
			187267 AV	/853812 AA852213 W74149 BE009090 AA056401 H9101	I AW368529 AW390272 C18467	W674920 N57176 AA026480 AW576767
			H93284 AA	.026863 AW177787 AA026654 AW177788 BE092134 BE(92137 BE092136 AW177784 AI02	2862 BE091653 AW376811 AW848592
				BE185331 BE182164 AA368564 AW951576 T29918 AA1		
50			BE 167165	N84767 H27408 H30146 AI190590 C03378 AI554403 AI2	05263 AA 128470 A1392926 AF 139	065 AW370813 AW370827 AW798417
50			AVV/98/80	AW798883 AW798569 R33557 AA149190 C03029 AW17 VA451923 Al340326 Al590975 T48793 Al568096 Al14288	7783 AAU88866 AW370829 AA24	7685 BE002273 AI760816 AI439101 AW879451
			AA702424	Al417612 Al306554 Al686869 Al568892 AW190555 Al57	1075 A1220573 AA056527 A147181	4 AIRNA772 AWS17828 AIR15595 AIR27383
			AJ270345 A	W021347 AW166807 AW105614 AJ346078 AA552300 W	95070 Al494069 Al911702 AA149	91 AA026864 AIB30049 AI887258 AW780435
				AI819984 AI858282 AI078449 AI025932 AI860584 AI6358		
55				782066 AW243815 AW150038 AW268383 AW004633 AI		
	•			AW771865 A1270027 AA961818 AA283207 A1076982 AI	198487 A1348053 A1783914 H4440	5 AW799118 AA128330 AA515500 AA918281
	413208	1353610_1		905927 AA022701 W38382 R20795 T77861 AW860878 BE071804 BE071788		
	413266	1356260_1		BE299274 BE075351 BE297444		
60	413282	1358147_1	BE078159	BE078276 BE078163 BE078277 BE078279 BE078158		
	413493	1373555_1	BE 144444			
	415606	1540470_1		35201 F12763 T74725 H63485 Z45782 H61126		
	415666	1543492_1	H72693 R0	08673 H72694 F20990 R08580		
65	416233 419269	158010_1 183444_1	AA175633 AA235838	AW961842 AA309418		
•	419386	184356_1		AA237066 AA354236 AW957759 H08961		
	425826	25682_1	U97698 AV	W815264 AI791966 AI732669 AAS88236 AI521662 AI8047	60 AI955717 AW292169 AI46822	7 AIA20AR3 AAG03459 AIRGR225 AI919551
	431300	331217_1	AA502345	BE159863		74424400744007557400022072515551
70	433789	37421_1		AF091029 AA701227		
70	433921 436624	377350_1		AI114549 R36464 R36465		
		4237_5	164297 AJ	N894931 NM_001443 M10050 AW843109 AI698516 T532	IQ TARTRS TRAIRR AATORQRO RTQ	R13 T55913 T56518 T64679 R29666 M10617
	100024				00 411/000400 411/00000 700400	765666 446 456 47 446 45664 TOOGG TOOGG
	100024		AU/68596	1	20 AW082135 AW272775 T29562	T55862 Al343047 Al345671 T68235 T68121
_ -	444843	62260_1	AW842284		20 AW082135 AW272775 T29562	T55862 AI343047 AI345671 T68235 T68121
75	444843 445797	650943_1	AW842284 AA400172	AA400146 AV651691 AI366014 R34822	20 AW082135 AW272775 T29562	T55862 AI343047 AI345671 T68235 T68121
75	444843 445797 447135	650943_1 70963_1	AW842284 AA400172 AI253414 T58148 AV	1 AA400146 AV651691 AI366014 R34822 W\$16579 AW059603	20 AW082135 AW272775 T29562	T55862 AI343047 AI345671 T68235 T68121
75	444843 445797 447135 449901	650943_1 70963_1 818599_1	AW842284 AA400172 Al253414 T58148 AV Al674072	1 AA400146 AV651691 A1366014 R34822 W516579 AW059603 BE268487	20 AW082135 AW272775 T29562	T55862 A1343047 A1345671 T68235 T68121
75	444843 445797 447135 449901 450928	650943_1 70963_1 818599_1 851593_1	AW842284 AA400172 A1253414 T58148 AV AI674072 AI744417	1 AA400145 AV651691 Al366014 R34822 %516579 AW059603 BE268487 R31614 H77385	20 AW08213S AW272775 T29562	T55862 AI343047 AI345671 T68235 T68121
75 80	444843 445797 447135 449901 450928 452351	650943_1 70963_1 818599_1 851593_1 91233_1	AW842284 AA400172 AI253414 T58148 AV AI674072 AI744417 AA025647	1 AA400145 AV651691 AI366014 R34822 W516579 AW059603 BE268487 R91614 H77385 R45716 AW753786	20 AW08213S AW272775 T29562	T55862 AI343047 AI345671 T68235 T68121
	444843 445797 447135 449901 450928	650943_1 70963_1 818599_1 851593_1	AW842284 AA400172 AI253414 T58148 AV AI674072 AI744417 AA025647 AW852286	1 AA400145 AV651691 Al366014 R34822 %516579 AW059603 BE268487 R31614 H77385	20 AW082135 AW272775 T29562	T55862 AI343047 AI345671 T68235 T68121
	444843 445797 447135 449901 450928 452351 455040	650943_1 70963_1 818599_1 851593_1 91233_1 1250028_1	AW84228- AA400172 AI253414 . T58148 AV AI674072 AI744417 AA025647 AW85228- AA203637 AW96818	1 AA400146 AV651691 AI366014 R34822 N516579 AW059603 BE268487 R91614 H77385 R45716 AW753786 5 AW851934 AW852096 AW852274	20 AW082135 AW272775 T29562	T55862 AI343047 AI345671 T68235 T68121

TABLE 23C: Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402-489-495. 5 Indicates DNA strand from which exons were predicted. Indicates nucleotide positions of predicted exons. Strand: Nt_position: Pkey Strand Nt position 10 7770576 7534110 173043-173564 71055-71259 ANNORS Minus 401507 Plus 4388746 7249190 401600 Minus 27363-27518,28727-28891,29526-29731 139369-139827,140509-140591,140834-140990,141496-141657,141757-141882,142063-142283 138252-138469,140239-140364,140437-140598,141037-141193,141925-142007,142787-143230 401783 Phrs Minus 3892083 15 8576116 402198 Plus 79041-79191 402364 Minus 54983-55240,56507-56785,56982-57365 402429 9796372 Minus 57622-57793,59282-59402,59624-59827 174560-175270 403442 7210003 Plus 9929739 9966615 Minus Minus 4831-7707 12450-12753 403469 20 403488 7656757 7710561 403512 114487-114610 403890 83165-83350 Plus 404036 404091 65247-67529,112537-114863 7684554 Minus 82121-83229 137948-138024,138111-138300 25 404333 404492 9802821 Minus 8123400 Minus 138612-138803 73499-73651,89575-89739 8748893 9212936 9797073 404559 404606 Minus Minus 22310-23269 33374-33675,33769-34008 404661 Plus 30 143025-143467 47174-47326.52928-53146.53312-53602 404741 8574139 Plus 404845 7958980 Minus 405088 8072518 2642452 Minus 405354 52213-53089 Plus 6850244 8439781 405403 37491-37670,40951-41031 35 405474 Plus 172005-172175 405586 5002511 38810-39017 405670 4662655 4589984 Plus 96543-96870 405674 Plus 68302-68429 18665-18843 310-432 406085 9123888 Ptus 40 7342161 7534217 5686278 406215 Plus 13136-13591 35655-36119 406270 Plus 406299 Minus 406308 9211532 358408-358651 45 TABLE 24A: ABOUT 1260 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT TISSUES
Table 24A lists about 1260 genes up-regulated in glioblastoma compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrio/Eos Hu03 GeneChip array such that the ratio of "everage" glioblastoma to "everage" normal adult tissues was greater than or equal to 2.5. The "everage" glioblastoma level was set to the 75° percentile amongst various glioblastoma tumors. The "everage" normal adult tissue lavel was set to the 85° percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10° percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the denominator 50 before the ratio was evaluated. Pkey: ExAcon: Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Unigene number Unigene gene title UnigenetD: 55 Unigene Title: Ratio of 75th percentile tumor to 85th percentile normal body tissue Pkey 431917 UnigeneID Hs.2868 Unigene Title peripheral myelin protein 2 protein kinase C binding protein 2 SRY (sex determining region Y)-box 2 D16181 75.2 74.6 60 427343 455601 Hs.176977 A1368680 Hs.816 428321 412719 AI699994 Hs.2868 peripheral myelin protein 2 AW016610 Hs.129911 449494 415817 AW237014 U88967 BE242870 Homo sapiens cDNA: FLJ23075 fis, clone L Hs.315369 66.3 64.3 Homo sapiens CDNA: FLUXBY as, cone L protein tyrosine phosphatase, receptor-t solute carrier family 1 (gliat high affi delta (Drosophila)-like 3 Homo sapiens mRNA: cDNA DKFZp761C1712 (I NK-2 (Drosophila) homotog B 65 Hs.78867 Hs.75379 413472 60.1 52.3 456759 435147 BE259150 Hs.127792 AL133731 Hs.4774 425842 412733 AI587490 AA984472 Hs.159623 40.1 70 NA-2 (Urosophaa) nominog B KIAA0080 protein synaptosomal-associated protein, 25kD SRY (sax determining region Y)-box 11 Homo sapiens mRNA; cDNA DKFZp761J1324 (I fibroblast growth factor 1 (acidic) catenin (cadherin-associated protein), d Hs.74554 Hs.84389 39.0 418375 NM_003081 38.7 1123752 453392 Hs 32964 37.2 AL157425 M74028 423849 Hs.133315 36.8 32.8 Hs.75297 Hs.80220 413333 75 416829 AB013805 431941 436878 AK000106 BE465204 Hs.272227 Homo sapiens cDNA FLJ20099 fis, clone CO 31 B

30.9

30.4

30.2 28.3

26.9 25.9

Hs.4744B

Hs.169309

Hs. 1619

Hs.12450

Hs.12825

Hs.169395

Hs.12827

426325

425057

446711

439415

430838

429466

80

D28114

FASSIR

N46664

M85835

AAB26434

AF169692

FSTs

ESTs

protocadherin 9

myelin-associated oligodendrocyte basic

hypothetical protein FLJ12015 ESTs

achaete-scute complex (Drosophila) homol

	447004	414-000000			
	447004 424581	AW296968 M62062	Hs.157539 Hs.150917	ESTs catenin (cadherin-associated protein), a	25.3 24.8
	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (tr	24.8
•	441285	NM_002374	Hs.167	microtubule-associated protein 2	24.3
5	453642	Al370936	Hs.34074	dipeptidytpeptidase VI	24.3
	424140 450133	Z48051 AW969769	Hs.141308 Hs.105201	myelin oligodendrocyte głycoprotein ESTs	24.2 24.2
	408562	AI436323	Hs.31141	Homo saplens mRNA for KIAA1568 protein,	23.3
10	448672	AI955511	Hs.225106	ESTs	22.7
10	435708 407034	AI362949 U84540	Hs.75169	ESTs	22.0
	407168	R45175	Hs.117183	gb:Human dystrobrevin isoform DTN-3 (DTN ESTs	21.9 21.7
	431019	NM_005249	Hs.2714	forthead box G1B	21.5
15	409049	A1423132	Hs.146343	ESTs	21.4
13	433896 445041	AW294729 T64183	Hs.274461 Hs.282982	ESTs solute carrier	21.1
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	21.0 20.4
	444378	R41339	Hs.12569	ESTs	20.0
20	411305	BE241596	Hs.69547	myelin basic protein	19.9
20	437414 441016	AW894071 AW138653	Hs.48448 Hs.25845	hypothetical protein DKFZp547C176 ESTs	19.8
	440435	AL042201	Hs.21273	transcription factor NYD-sp10	19.6 18.5
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transi	18.4
25	452461 409395	N78223	Hs.108106	transcription factor	18.1
23	417183	U48745 R52089	Hs.54435 Hs.172717	dystrobrevin, alpha ESTs	18.1 18.0
	409638	AW450420	Hs.21335	ESTs	18.0
	428392	H10233	Hs.2265	secretory granute, neuroendocrine protei	18.0
30	449611 446692	AJ970394 Z44514	Hs.197075 Hs.156829	ESTs	17.0
20	425088	AA663372	Hs.150029	Homo sapiens mRNA for KIAA1763 protein, hypothetical protein FLJ12015	16.9 16.9
	444471	AB020684	Hs.11217	KIAA0877 protein	16.8
	421659	NM_014459	Hs.106511	protocadherin 17	16.7
35	431725 429276	X65724 AF056085	Hs.2839 Hs.198612	Norrie disease (pseudoglioma) G protein-coupled receptor 51	16.6
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	18.6 16.5
	441440	AI807981	Hs.30495	ESTs	15.7
	449433 421264	Al672096 AL039123	Hs.9012	ESTs, Weakly similar to S26650 DNA-bindi	15.7
40	415910	U20350	Hs.103042 Hs.78913	microtubule-associated protein 18 chemokine (C-X3-C) receptor 1	15.5 15.3
	413597	AW302885	Hs.117183	ESTs	15.1
	424945	AI221919	Hs.173438	hypothetical protein FLJ10582	14.9
	447414 426269	D82343 H15302	Hs.18551 Hs.168950	neuroblastoma (nerve tissue) protein	14.9
45	416857	AA188775	Hs.292453	Homo sapiens mRNA; cDNA DXFZp566A1046 (I ESTs	14.8 14.7
	419721	NM_001650	Hs.288650	aqueporin 4	14.6
	411078	AJ222020	Hs.182364	CocoaCrisp	14.4
	453924 409389	R49295 AB007979	Hs.24888 Hs.301281	ESTs Homo saplens mRNA, chromosome 1 specific	14.4 14.3
50	430130	AL137311	Hs.234074	Homo sapiens mRNA: cDNA DKFZp761G02121 (14.1
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALUS_HUMAN A	14.0
	412266 412986	N59006 XB1120	Hs.26133 Hs.75110	ESTs cannabinoid receptor 1 (brain)	14.0
	424790	AL119344	Hs.13326	ESTs, Wealdy similar to 2004399A chromos	14.0 14.0
55	439239	AI031540	Hs.235331	ESTs	14.0
	441497 445495	R51064	Hs.23172	ESTs	14.0
	414245	8E622641 BE148072	Hs.38489 Hs.75850	ESTs, Weakly similar to t38022 hypotheti WAS protein family, member 1	14.0 13.7
~ 0	429900	AA460421	Hs.30875	ESTs	13.6
60	448595	AB014544	Hs.21572	KIAA0644 gene product	13.6
	449605 452526	AW138581 W38537	Hs.198416 Hs.280740	ESTs hypothetical protein MGC3040	13.6
	420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA he	13.6 13.3
65	441350	AB020690	Hs.7782	paraneoplastic entigen MA2	13.3
03	420077 424120	AW512260	Hs.87767	ESTs .	13.2
	456965	T80579 AW131888	Hs.290270 Hs.172792	ESTs ESTs, Weakly similar to hypothetical pro	13.2
	423361	AW170055	Hs.47628	ESTs	13.2 13.1
70	428409	AW117207	Hs.98523	ESTs _	12.9
,,	417160 451621	N76497 A1879148	Hs.1787	proteofipid protein 1 (Pelizaeus-Merzbac	12.6
	411379	AI816344	Hs.26770 Hs.12554	fatty acid binding protein 7, brain ESTs, Weakly similar to NPL4_HUMAN NUCLE	12.5 12.5
	436954	AA740151	Hs.130425	ESTs	12.4
75	430691	C14187	Hs.103538	ESTs	12.4
,,,	433551 422544	AI985544 AB018259	Hs.12450 Hs.118140	protocadherin 9 KIAA0716 gene product	12.4
	427540	R12014	Hs.20976	ESTs	12.2 12.1
	435624	AF218942	Hs.24889	formin 2	12.1
80	415849 428845	R20529 AL157579	Hs.6806 Hs.153610	ESTs	12.1
- •	442671	AI005668	Hs.134779		11.9 11.9
	444396	T65213	Hs.4257	ESTs	11.8
	452752	AW044058	Hs.33578	KIAA0820 protein	11.8

				-	
	425523	AB007948	Hs.158244	KIAA0479 protein	11.8
	416072	AL110370	Hs.79000	growth associated protein 43	11.7
	440184	AB002297 AL037824	Hs.7022	dedicator of cyto-kinesis 3	11.7
5	428976 444783	AK001468	Hs.194695 Hs.62180	ras homolog gene family, member I	11.6
_	448299	AA497044	Hs.20887	anilin (Drosophila Scraps homolog), act	11.6
	414214	D49958	Hs.75819	hypothetical protein FLJ 10392 glycoprotein M6A	11.6
	428982	NM_005097	Hs.194704	leucine-rich, glioma inactivated 1	11.5
	405238			mount of British montaction a	11,5 11,4
10	420362	U79734	Hs.97206	huntingtin interacting protein 1	11.4
	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (C/EBP).	11.4
	424918	R13982	Hs.159309	myefin-essociated oligodendrocyte basic	11,4
	434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	11.4
15	451952	AL120173	Hs.301663	ESTs	11.3
13	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	11.3
	424278	AK000723	Hs.144517	hypothetical protein FLJ20716	11.3
	429418 429918	AI381028	Hs.118769	ESTS	11.3
	443912	AW873986 R37257	Hs.119383 Hs.184780	ESTs ESTs	11.3
20	448743	AB032962	Hs.21896	KIAA1136 protein	11.3
	420092	AAB14043	Hs.88045	ESTs Protein	11.3
	408081	AW451597	Hs.167409	ESTs	11.2 11.2
	411642	NM_014932	Hs.71132	neuroligin 1	10.9
25	415170	R44386	Hs.164578	ESTs	10.9
25	426320	W47595	Hs.169300	transforming growth factor, beta 2	10.8
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 ffs, clone NT	10.8
	425799	T08133	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	10.8
	423853	AB011537	Hs.133466	stit (Drosophita) homotog 1	10.7
30	400293 447773	N51002	Hs.306480	Homo sapiena mRNA; cDNA DKFZp761E2112 (/	10.7
50	448321	AI423930 NM 005883	Hs.36790 Hs.20912	ESTs, Weakly similar to putative p150 (H	10.7
	448533	AL119710	Ms.21365	adenomatous polyposis cofi like	10.5
	440684	AI253123	Hs.127356	nucleosome assembly protein 1-like 3 ESTs, Highly similar to S21424 nestin (H	10.5
	444017	U04840	Hs.214	neuro-oncological ventral antigen 1	10.3
35	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	10.3 10.3
	440471	AA886145	Hs.307944	ESTs	10.2
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	10.1
	439978	BE139460	Hs.124673	Homo sepiens cDNA FU11477 fis, clone HE	10.1
40	448902	Z45998	Hs.22543	Homo saplens mRNA; cDNA DKFZp761I1912 (I	10.1
40	424932	R14070	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	9.9
	431721	AB032996	Hs.268044	KIAA1170 protein	9.9
	419088	AI538323	Hs.52620	Integrin, beta 8	9.8
	420602 436511	AF060877	Hs.99236	regulator of G-protein signalling 20	9.8
45	414696	AA721252 AF002020	Hs.291502	ESTs	9.8
	449539	W80363	Hs.76918 Hs.58445	Niemann-Pick disease, type C1 ESTs	9.7
	412959	D87458	Hs.75090	KIAA0282 protein	9.7
	412811	H06382	Hs.21400	ESTs	9.6 9.6
	449300	AI656959	Hs.222165	ESTs	9.6 9.6
50	426344	H41821	Hs.322469	transcriptional activator of the c-fos p	9.5
	419271	N34901	Hs.238532	ESTs	9.5
	419078	M93119	Hs.89584	insulinoma-associated 1	9.4
	451516	AI800515	Hs. 12024	ESTs	9.4
55	422656	AIB70435	Hs.1569	LIM homeobox protein 2	9.3
"	449318	AW235021	Hs.78531	Homo sapiens, Similar to RIKEN cONA 5730	9.3
	414175	Al308876	Hs.103849	hypothetical protein DKFZp761D112	9.3
	415279 428784	F04237 Y12851	Hs.1447 Hs.193470	gilal fibrillary acidic protein	9.2
	429903	AL134197	Hs.93597	purinergic receptor P2X, ligand-gated to	9.2
60	424541	AB001106	Hs.151413	cyclin-dependent kinase 5, regulatory su glia maturation factor, beta	9.2
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	9.1 9.1
	449448	D60730	Hs.57471	ESTs	9.1
	408508	AI806109	Hs.135736	KIAA1580 protein	9.0
65	452785	AL359942	Hs.296434	erythroid differentiation and denucleati	9.0
03	448986	H42169	Hs.18653	hypothetical protein FLJ14627	8.9
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	8.9
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	8.9
	408926	AF217525	Hs.49002	Down syndrome cell adhesion molecule	8.8
70	449625 400292	NM_014253 AA250737	Hs.23796	odz (odd Oz/ten-m, Drosophila) homolog 1	8.8
. •	417404	NM_007350	Hs.72472 Hs.82101	ESTs	8.7
	420345	AW295230	Hs.25231	pleckstrin homology-like domain, family ESTs	8.7
	429927	NM 001115	Hs.2522	adenylata cyclase 8 (brain)	8.7
	437528	N59646	Hs.169745	crumbs (Drosophila) homolog 1	8.7
75	440152	AB002376	Hs.7006	KIAA0378 protein	8.7 8.7
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	8.6
	400780			and the same of th	8.6
	434891	AA814309	Hs. 123583	ESTs	8.6
80	449277	AA001064	Hs.172976	ESTs	8.6
30	415709	AA649850	Hs.278558	ESTs	8.5
	439947	AB006627 D36075	Hs.6788	astrotaciin	8.5
	447197 433042	R36075 AW193534	Ma 201005	gb:yh88b01.s1 Soares placenta Nb2HP Homo	8.5
		ATT 133334	Hs.281895	Homo sapiens cDNA FLJ11660 ffs, clone HE	8.4

	440070	400475			
	416370	N90470	Hs.203697	ESTs, Weakly similar to 138022 hypotheti	8.4
	452785 415798	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	8.4
	426271	R87548 AF026547	Hs.78854	ATPase, Na+/K+ transporting, beta 2 poly	8.3
5	408947	AL080093	Hs.169047 Hs.49117	chondroitin sulfate proteoglycan 3 (neur	8.3
•	419863	AW952691	Hs.93485	Homo sapiens mRNA; cDNA DKFZp564N1662 (I	8.3
	433447	U29195	Hs.3281	Homo sapiens mRNA; cDNA DKFZp761D191 (tr neuronal pentravin II	8.3
	431467	N71831	Hs.258398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	8.3 8.3
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	8.3
10	414300	AJ304870	Hs.188680	ESTs	8.2
	407728	AW071502	Hs.175931	ESTs	8.2
	422798	R92347	Hs.34574	ESTs., Weakly similar to ALU1_HUMAN ALU S	8.2
	419704	AA429104	Hs.45057	ESTs	8.2
10	429007	D80642		gb:HUM092E098 Human fetal brain (TFujiwa	8.1
15	442710	AI015631	Hs.23210	ESTs	8.1
	425048	H05468	Hs.164502	ESTs	8.1
	429149	AW193360	Hs.197962	ESTs. Wealtly similar to I38022 hypotheti	8.0
	445740	T78281	Hs.13226	Homo sapiens clone 25181 mRNA sequence	8.0
20	418771	AA807881	Hs.25329	ESTs	7.9
20	422728 425984	AW937826 AW836277	Hs.103262 Hs.165636	ESTs, Wealdy similar to ZN91_HUMAN ZINC	7.9
	448408	AA322866	Hs.21107	hypothetical protein DKFZp761C07121 neuroligin	7.9
	455364	H72176	Hs.4273	hypothetical protein FLJ13159	7.9
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	7.9
25	435501	AW051819	Hs.129908	KIAA0591 protein	7.9 7.8
	423600	AI633559	Hs.310359	ESTs	7.8
	450625	AW970107		gb:EST382188 MAGE resequences, MAGK Homo	7.8
	415314	N88802	Hs.5422	glycoprotein M68	7.7
20	420036	R60336	Hs.52792	Homo sepiens mRNA; cDNA DKFZp586I1823 (f	7.7
30	427687	AW003867	Hs.1570	histamine receptor H1	7.7
	449328	AI962493	Hs.197647	EST ₅	7.7
	419249	X14767	Hs.89768	gamma-eminobutyric acid (GABA) A recepto	7.7
	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	7.7
35	419103 438779	Z40229	Hs.96423	hypothetical protein FLJ23033	7.6
23	433532	NM_003787 AW975357	Hs.6414	nucleolar protein 4	7.6
	448555	AI536697	Hs.159863	gb:EST387475 MAGE resequences, MAGN Horno ESTs	7.6
	439662	H97552	Hs.269060	ESTs	7.5
	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (f	7.5 7.5
40	410099	AA081630	Hs.169387	KIAA0036 gene product	7.5 7.5
	431592	R69016	Hs.213194	hypothetical protein MGC10895	7.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.4
	405819			• • • • • • • • • • • • • • • • • • • •	7.4
4.5	407886	AW969688	Hs.100826	ESTs	7.4
45	437416	AL359605	Hs.283851	Homo sapiens mRNA; cDNA DKFZp547G036 (fr	7.4
	437698	R61837	Hs.7990	ESTs, Moderately similar to 184505 catci	7.4
	408604	D51408	Hs.21925	ESTs	7.4
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	7.3
50	447499	AW262580	Hs.147674	protocadherin beta 16	7.3
50	454036 409746	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	7.3
	410037	NM_004794	Hs.56294	RAB33A, member RAS oncogene family	7.2
	419318	AB020725 AW969742	Hs.58009 Hs.291005	KIAA0918 protein ESTs	7.2
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	7.2
55	442026	AI243749	Hs.8074	brain-specific angiogenesis inhibitor 3	7.2
	448243	AW369771	Hs.52620	Integrin, bela 8	7.2
	436281	AW411194	Hs.85195	myeloid leukemia factor 1	7.2 7.2
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	7.2
C O	407182	AA312551	Hs.230157	ESTs	7.1
60	415293	R49462	Hs.106541	ESTs	7.1
	422764	AJ767727	Hs.47522	ESTS	7.1
	451592	AJ805416	Hs.213897	ESTs	7.1
	429469	M64590	Hs.27	glycine dehydrogenase (decerboxylating;	7.0
65	415734	NM_014747	Hs.78748	KIAA0237 gene product	7.0
05	434149 436726	Z43829 AA324975	Hs.19574	hypothetical protein MGC5469	7.0
	417632	R20855	Hs.128993	ESTs, Wealty similar to T00079 hypotheti	7.0
	422421	AA325138	Hs.5422 Hs.235873	glycoprotein M68 hypothetical protein FLJ22672	7.0
	435267	N23797	Hs.110114	ESTs	6.9
70	437117	AL049256	Hs.122593	ESTs	6.9 6.9
	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	6.9
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	6.9
	445745	AB007924	Hs.13245	KIAA0455 gene product	6.9
75	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.9
75	428588	F12101	Hs. 185701	Homo sapiens mRNA full length insert cDN	6.8
	421723	AA620400	Hs.300717	sodium channel, voltage-gated, type III,	6.8
	447342	Al199268	Hs.19322	Homo sapiens, Similar to RIKEN cONA 2010	6.7
	443297	AI049864	Hs.133029	ESTs	6.7
80	443992	AW022228	Hs.322922	ESTs .	6.7
50	453096 453857	AW294631	Hs.11325	ESTs	6.7
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	6.7
	429609	AI525743 AF002246	Hs.160603	ESTs	6.6
	723003	PW 002240	Hs.210863	cell adhesion molecule with homology to	6.6

	100000				
	435056 453431	AW023337	Hs.5422	glycoprotein M68	6.5
	444190	AF094754 AI878918	Hs.32973 Hs.10526	glycine receptor, beta	6.5
	418110	R43523	Hs.217754	cysteine and glycine-rich protein 2 hypothetical protein FLJ22202	6.5
5	413988	M81883	Hs.324784	giutamate decarboxylase 1 (brain, 67kD)	6.5 6.5
_	420805	L10333	Hs.99947	rescutor 1	6.4
	429125	AA446854	Hs.271004	ESTs, Wealthy similar to 138022 hypotheti	6.4
	435256	AF193766	Hs.13872	cytokine-like protein C17	6.4
10	407866	AW088232	Hs.89506	paired box gene 6 (aniridia, keratitis)	6.3
10	440700	AW952281	Hs.296184	guanine nucleotide binding protein (G pr	6.3
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	6.3
	422949 445102	AA319435 AW204610	Hs.22270	gb:EST21657 Adrenal gland turnor Homo sap	6.2
	452401	NM_007115	Hs.29352	ESTs turnor necrosis factor, alpha-induced pro	6.2
15	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	6.2 6.2
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	6.2
	416871	H98716		gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	6.1
	416702	AA186428	Hs.85591	ESTs	6.1
20	419347	C15944	Hs.90005	superiorcervical ganglia, neural specifi	6.1
20	424997	AL138167	Hs.96920	ESTB	6.1
	438660 453649	U95740 Y07494	Hs.6349	Homo sapiens, clone IMAGE:3010666, mRNA,	6.1
	449444	AW818436	Hs.34114 Hs.23590	ATPase, Na+/K+ transporting, alpha 2 (+) solute carrier family 16 (monocarboxylic	6.1
	414117	W88559	Hs.1787	proteolipid protain 1 (Pelizaeus-Merzbac	6.1 6.0
25	425517	AF121179		gb:AF121179 Homo sepiens liver (Chang L-	6.0
	427457	AW779105	Hs.164682	ESTs	6.0
	437034	AA742643		gb:rry91c01.s1 NCI_CGAP_GC81 Homo saplens	6.0
	444170	AW613879	Hs.102408	ESTs	6.0
30	457183	H91882	Hs.118569	DVI-binding protein IDAX (inhibition of	6.0
50	448999 454048	AF 179274 H05626	Hs.22791	transmembrane protein with EGF-like and	6.0
	439772	AL365406	Hs.6921 Hs.10268	ESTs Homo sapiens mRNA full length insert cDN	6.0
	448944	AB014605	Hs.22599	strophin-1 interacting protein 1; activi	5.9 5.9
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	5.9
35	415486	H12214	Hs.13284	ESTs, Weakly similar to 2109260A B cell	5.9
	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	5.9
	447350	Al375572	Hs.172634	ESTs	5.9
	451783	R42554	Hs.210862	T-box, brain, 1	5.9
40	447101 440492	N72185	Hs.44189	ESTs	5.9
70	440274	R39127 R24595	Hs.21433 Hs.7122	hypothetical protein DKFZp547J036	5.9
	438461	AW075485	Hs.286049	scrapie responsive protein 1 phosphoserine aminotransferase	5.9
	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	5.9 5.8
	437035	AI571514	Hs.133022	ESTs	5.7
45	412225	AW902042		gb:QV0-NN1022-170400-193-c02 NN1022 Homo	5.7
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.7
	444218	AF070641	Hs.10684	Homo sapiens clone 24421 mRNA sequence	5.7
	445828 447198	F05802 D61523	Hs.81907	ESTS	5.7
50	427897	NM_017413	Hs.283435 Hs.303084	ESTs apelin; peptide ligand for APJ receptor	5.7
	448499	BE613280	Hs.77550	hypothetical protein MGC1780	5.7 5.7
	443672	AA323362	Hs.9667	butyrobetaine (garnma), 2-oxoglutarate di	5.6
	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP1	5.6
66	435718	R06569	Hs.269534	ESTs	5.6
55	449340	AW235786	Hs.195359	hypothetical protein MGC10954	5.6
	424481 451996	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	5.6
	422411	AW514021 AW749443	Hs.245510 Hs.22511	ESTs	5.6
	438328	Al492261	Hs.32450	ESTs ESTs	5.6 5.6
60	433244	AB040943	Hs.271285	KIAA1510 protein	5.6
	435191	R15912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	5.5
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	5.5
	400859				5.5
65	413625	AW451103	Hs.71371	ESTs	5.5
Ų,	421863 434933	AI952677	Hs.108972	Homo sapiens mRNA; cONA DKFZp434P228 (fr	5.5
	438702	R91095 AI879064	Hs.4276 Hs.54618	KIAA1701 protein ESTs	5.5
	452055	Al377431	Hs.141693		5.5
	430979	AJ479755	Hs.129010		5.5 5.5
70	412709	AL022327	Hs.74518	KIAA0027 protein	5.5
	439920	H05430	Hs.288433	neurotrimin	5.5
	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	5.4
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	5.4
75	419235 418030	AW470411	Hs.288433 Hs.83321		5.4
, 5	410330	8E207573 AW023630	Hs.46786	neuromedin 8 ESTs	5.4
	410781	AI375672	Hs.165028		5.4 5.4
	420658	AW965215	Hs.336656		5.4 5.4
00	421308	AA687322	Hs.192843		5.4
80	443740	R56434	Hs.21062	ESTs	5.4
	426457	AW894667	Hs.169965		5.4
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	5.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	5.4

	400000	ANA 000000	11- 4740-4		
	426600 424432	NM_003378 AB037821	Hs.171014 Hs.146858	VGF nerve growth factor inducible	5.4
	429250	H56585	Hs.198308	protocadherin 10 byptophan rich basic protein	5.4 5.4
_	443785	AW449952	Hs.190125	basic-helix-loop-helix-PAS protein	5.4
5	435282	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	5.4
	404584				5.3
	430091	AB032958	Hs.233023	KIAA1132 protein	5.3
	439845 424001	AL355743 W67883	Hs.56663 Hs.137476	Homo sapiens EST from clone 41214, full	5.3
10	425073	W39609	Hs.22003	paternally expressed 10 solute carrier family 6 (neurotransmitte	5.3 5.3
	426625	T78300	Hs.300642	serologically defined colon cancer antiq	5.3
	428137	AA421792	Hs.170999	ESTs	5.3
	428579	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sap	5.3
15	438176	AW138970	Hs.122113	ESTs	5.3
13	440138	A8033023 AW965599	Hs.318127	hypothetical protein FLJ10201	5.3
	451018 416340	N31772	Hs.247324 Hs.79226	mitochondrial ribosomal protein S14	5.3
	435244	N77221	Hs.187824	fasciculation and elongation protein zet ESTs	5.3 5.3
	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	5.3
20	424624	A8032947	Hs.151301	Ca2-dependent activator protein for sec	5.3
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	5.3
	430437	Al768801	Hs.169943	Homo sapiens cDNA FLJ13569 fs, clone PL	5.3
	414825 453941	X06370 U39817	Hs.77432 Hs.36820	epidermal growth factor receptor (avian	5.2
25	424998	U58515	Hs.154138	Bloom syndrome chilinase 3-like 2	5.2 5.2
	423419	R55336	Hs.23539	ESTs	5.2
	424922	BE386547	Hs.217112	hypothetical protein MGC10825	5.2
	447359	NM_012093	Hs.18268	adenylate kinase 5	5.2
30	408206	AF041853	Hs.43670	kinesin family member 3A	5.2
30	421013 429443	M52397 AB028967	Hs.1345	mutated in colorectal cancers	5.2
	434367	AB020700	Hs.202687 Hs.3830	potassium voltage-gated channel, Shal-re KIAA0893 protein	5.2
	444861	R45789	Hs.76118	ubiquitin carboxyl-terminal esterase L1	5.2 5.2
2.5	446142	AI754693	Hs.145968	ESTs	5.2
35	448816	AB033052	Hs.22151	KIAA1226 protein	5.2
	451050	AW937420	Hs.69662	ESTs	5.2
	451106 439285	BE382701 AL133916	Hs.25960 Hs.172572	v-myc avian myelocytomatosis viral relat	5.2
	418737	AF154335	Hs.79691	hypothetical protein FLJ20093 UM domain protein	5.2
40	424800	AL035588	Hs.153203	MyoD family inhibitor	5.2 5.2
	443695	AW204099	Hs.337720	ESTs, Wealty similar to AF126780 1 retin	5.2
	415257	F03016	Hs.27513	ESTs	5.2
	433929	Al375499	Hs.27379	ESTs	5.1
45	415651 451027	AI207162 AW519204	Hs.3815 Hs.40808	stathmin-like-protein RB3	5.1
73	409172	Z99399	Hs.118145	ESTs ESTs	5.1
	423343	AA324643	Hs.246106	ESTs	5.1 5.1
	429172	AA447417	Hs.285491	ESTs	5.1
50	437268	AJ754847	Hs.227571	regulator of G-protein signalling 4	5.1
30	451270	AW341392	Hs.235795	ESTs	5.1
	452904 420560	AL157581 AW207748	Hs.30957 Hs.59115	Homo sapiens mRNA; cDNA DKFZp434E0626 (1	5.1
	418097	R45137	Hs.21868	ESTS ESTS	5.1 5.1
	442910	AJ385130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	5.1
55	434849	AW292765	Hs.8053	ESTs	5.1
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	5.1
	414217	AI309298 S72043	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	5.1
	412068 413627	8F182082	Hs.73133 Hs.246973	metallothionein 3 (growth inhibitory fac	5.0
60	418661	NM_001949	Hs.1189	ESTs E2F transcription factor 3	5.0 5.0
-	422438	AA445925	Hs.270896	ESTs, Moderately similar to Z195_HUMAN Z	5.0 5.0
	423728	AW891294	Hs. 132136	solute carrier family 4, sodium bicarbon	5.0
	431431	AL096711	Hs.252953	Human DNA sequence from clone RP3-403A15	5.0
65	435087	AW975241	Hs.23567	ESTs	5.0
03	452097 410434	AB002364 AF051152	Hs.27916	a disintegrin-like and metalloprotease (toll-like receptor 2	5.0
	408692	AL040127	Hs.63668 Hs.34074	dipeptidylpeptidase VI	4.9
	407808	AA663559	Hs.279789	histone deacetylase 3	4.9 4.9
70	418940	H17739	Hs.288513	Human DNA sequence from clone RP5-899C14	4.9
70	425977	R15138	Hs.165570	Homo sapiens clone 25052 mRNA sequence	4.9
	426814	AF036943	Hs.172619	myelin transcription factor 1-like	4.9
	447112 449574	H17800 F05048	Hs.7154	ESTs	4.9
	453652	AW009640	Hs.175373 Hs.28368	ESTs ESTs, Moderately similar to \$65657 alpha	4.9
75	423869	BE409301	Hs.134012		4.9 4.9
	413248	T64858	Hs.21433	hypothetical protein DKFZo547J036	4.9
	449176	AI633545	Hs.198072	ESTs	4.9
	448451	AW015994		gb:UI-H-BIOp-abh-g-09-0-UILs1 NCI_CGAP_S	4.8
80	402604 436039	AW023323	Hs.121070	661.	4.8
	448769	N66037	Hs.38173	ESTs ESTs	4.8
	423678	AW963357	Hs.7847	ESTs	4.8 4.8
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	4.8

	425870	R13406	Hs.56782	ESTs	4.8
	408777	U71204	Hs.47626	Ric (Drosophila)-like, expressed in neur	4.8
	413409 413823	AI638418 AA825721	Hs.78580 Hs.246973	OEAD/H (Asp-Gtu-Ala-Asp/His) box polypep ESTs	4.8
5	417246	A1760098	Hs.21411	ESTs	4.8
-	420900	AL045633	Hs.44269	ESTs	4.8
	424153	AA451737	Hs.141496	MAGE-like 2	4.8 4.8
	443539	AI076182	Hs.134074	ESTs, Moderately similar to ALU6_HUMAN A	4.8
	448750	U95020	Hs.21903	calcium channel, voltage-dependent, beta	4.8
10	454030	AW021429	Hs.231980	ESTs	4.8
	424458	M29273	Hs.1780	myelin associated glycoprotein	4.8
	444119	R41231	Hs.184261	ESTs, Wealthy similar to T26686 hypotheti	4.8
	407792	AJ077715	Hs.39384	putative secreted ligand homologous to f	4.8
15	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	4.7
13	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	4.7
	429956 435060	AI374651 AI422719	Hs.22542 Hs.233349	ESTs	4.7
	436203	BE384982	Hs.5076	ESTs, Wealdy similar to fork head like p Homo sapiens cDNA: FLJ22128 fts, clone H	4.7
	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	4.7 4.7
20	422222	Al699372	Hs.193247	hypothetical protein DKFZp434A171	4.7
	431733	AW298410	Hs.21475	ESTs	4.7
	449353	AA001220	Hs.271369	ESTs	4.7
	452022	AW072330	Hs.293875	ESTs	4.7
25	454269	AI961060	Hs.129908	KIAA0591 protein	4.7
25	404541				4.7
	428189	AA424030	Hs.46627	ESTs	4.7
	409125 458435	R17268 AJ418718	Hs.259873	axonal transport of synaptic vesicles	4.7
	425745	U44060	Hs.144121 Hs.14427	ESTs, Wealdy similar to T46916 hypotheti	4.6
30	413492	D87470	Hs.75400	Homo sapiens cDNA: FLJ21800 fis, clone H KIAA0280 protein	4.6
•	419629	AB020695	Hs.91662	KIAA0888 protein	4.6 4.6
	407638	AJ404672	Hs.334483	hypothetical protein FLJ23571	4.6
	438140	W87355	Hs.269587	ESTs	4.6
~ -	439169	AI912122	Hs.41095	ESTs	4.6
35	443150	Al034467	Hs.34650	ESTS	4.6
	451073	AJ758905	Hs.206063	ESTs	4.6
	451659	BE379761	Hs.14248	ESTs	4.6
	452106	A1141031	Hs.21342	ESTs	4.6
40	451407	AA131376	Hs.326401	fibroblast growth factor 12B	4.6
70	448765 430147	R15337 R60704	Hs.21958 Hs.234434	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.6
	437204	AL110216	Hs.12285	hairy/enhancer-of-spfit related with YRP ESTs, Weakly similar to ISS214 salivary	4.6
	431117	AF003522	Hs.250500	delta (Orosophila)-like 1	4.6
	422175	N79885	Hs.6382	ESTs, Highly similar to T00391 hypotheti	4.5 4.5
45	407889	R34556	Hs.30800	ESTs, Weakly similar to S65657 alpha-1C-	4.5
	419343	AA456245	Hs.85603	down-regulated by Ctnnb1, a	4.5
	421790	AW896201	Hs.22654	sodium channel, voltage-gated, type I, a	4.5
	429399	AA452244	Hs.16727	ESTs	4,5
50	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	4.5
30	453118	AW195849	Hs.252757	ESTs	4.5
	443455 442613	AB001025	Hs.9349	ryanodine receptor 3	4.4
	429643	AJ004002 AA455889	Hs.130522 Hs.167279	Ky channel-interacting protein 1	4.4
	416209	AA236776	Hs.79078	FYVE-finger-containing Rab5 effector pro MAD2 (mitotic arrest deficient, yeast, h	4.4
55	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	4.4
	435202	AJ971313	Hs.170204	KIAA0551 protein	4.4 4.4
	437498	AA452378	Hs.170144	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	4.4
	451254	AJ571016	Hs.172967	ESTS	4.4
60	439039	AI656707	Hs.48713	ESTs	4.4
60	439979	AW500291	Hs.6823	hypothetical protein FLJ10430	4,4
	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	4.4
	424983	A1742434	Hs.169911	ESTs	4.4
	410611 402605	AW954134	Hs.20924	KIAA1628 protein	4.4
65	409248	AB033035	Hs.51965	KIAA1209 protein	4,4
	442222	AJ061301	Hs.164773	ESTs	4.4 4.4
	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	4.4
	454293	H49739	Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	4.4
70	442832	AW206560	Hs.253569	ESTs	4.4
70	407304	AA\$65832		gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens	4.4
	423279	AW959861	Hs.290943	ESTs	4.3
	427194	AA399018	Hs.250835	ESTs	4.3
	419723	AL120193	Hs.92614	longevity assurance (LAG1, S. cerevisiae	4.3
75	445810	AW265700	Hs.155660	ESTS	4.3
, 5	409734 410389	8E161664	Hs.56155	hypothetical protein	4.3
	411571	AW954049 AA122393	Hs.8177 Hs.70811	ESTs, Weakly similar to PIHUB6 salivary	4.3
	433024	AA573847	Hs.26549	hypothetical protein FLJ20516 KIAA1708 protein	4.3
^^	453202	AW085781	Hs.26270	hypothetical protein FLJ11588	4.3
80	425264	AA353953	Hs.20369	ESTs, Wealthy similar to gonadotropin ind	4.3 4.3
	416427	BE244050	Hs.79307	Rac/Cdc42 guarins exchange factor (GEF)	4.3
	431789	H19500	Hs.269222	mitogen-activated protein kinase 4	4.3
	444600	R41398	Hs.6996	ESTS	4.3

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	454042	H22570	Hs.172572	hypothetical protein FLJ20093	4.3
	441899	AI372588	Hs.8022	TU3A protein	4.3
	425256	BE297611	Hs.155392	collapsin response mediator protein 1	4.3
5	410358 430291	AW975168 AV660345	Hs.13337	ESTs, Wealthy similar to unnamed protein	4.2
_	433597	AA708205	Hs.238126 Hs.100343	CGI-49 protein ESTs	4.2 4.2
	444127	N63620	Hs.13281	ESTs	4.2
	448507	AL133109	Hs.21333	Homo sapiens mRNA; cDNA DKFZp566N1047 (I	4.2
10	413589 408577	AW452631 H50572	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	4.2
10	409719	Al769160	Hs.19515 Hs.108681	ESTs, Highly similar to NRG3_HUMAN PRO-N Homo sepiens brain turnor associated prot	4.2 4.2
	428536	AI143139	Hs.2288	visintn-like 1	4.2
	429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein	4.2
15	432865	A1753709	Hs.152484	ESTs, Wealty similar to 138022 hypotheti	4.2
13	447138 450648	AI439112 AI703366	Hs.93828 Hs.26768	ESTs, Wealdy similar to 2109260A B cell ESTs	4.2 4.2
	451459	AI797515	Hs.270560	ESTs. Moderately similar to ALU7_HUMAN A	4.2
	421686	AB011156	Hs.106794	KIAA0584 protein	4.2
20	452776	AA194540	Hs.13522	ESTs, Weakly similar to 138022 hypotheti	4.2
20	436421 423858	AI678031 AL137326	Hs.122813 Hs.133483	ESTs, Weakly similar to ZN22_HUMAN ZINC	4.2
	434001	AW950905	Hs.3697	Homo sapiens mRNA; cDNA DKFZp43480650 (f serine (or cysteine) proteinase inhibito	4.2 4.2
	437380	AL359577	Hs.112198	Homo sapiens mRNA; cDNA DKFZp547M073 (fr	4.2
25	432328	A1572739	Hs.195471	6-phosphofructo-2-kinase/tructose-2,6-bi	4.1
25	439607 424028	8E540565 AF055084	Hs.159460 Hs.153692	ESTs	4.1
	446936	H10207	Hs.47314	Homo sapiens cDNA FLJ14354 fis, clone Y7 ESTs	4.3 4.1
	424240	AB023185	Hs.143535	calcium/calmodufin-dependent protein kin	4.1
20	412446	AJ768015	Hs.92127	ESTs	4.1
30	409953	AA332277	Hs.57691	cadherin 18, type 2	4.1
	416220 419683	N49776 AA248897	Hs.170994 Hs.48784	hypothetical protein MGC10946 ESTs	4.1 4.1
	426071	AW138057	Hs.163835	ESTs	4.1
26	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZpS64H172 (fr	4,1
35	432809	AA565509	Hs.131703	ESTs	4.1
	440105 452039	AA694010 AI922988	Hs.6932 Hs.172510	Homo sapiens clone 23809 mRNA sequence ESTs	4.1 4.1
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	4.1
. 40	457561	AA331517	Hs.286055	chimerin (chimaerin) 2	4.1
40	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	4.1
	433932 435637	AW954599 AJ783629	Hs.169330 Hs.26766	neuronal protein ESTs	4.1 4.1
	439231	AW581935	Hs.141480	Homo saplens mRNA; cDNA DKFZp434N079 (fr	4.1
4.5	450530	NM_006668	Hs.25121	cytochrome P450, subfamily 46 (cholester	4.1
45	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	4.1
	407881 410486	AW072003 AW235094	Hs.40968 Hs.69233	heparan sulfate (glucosamine) 3-O-sulfot	4.1
	413916	N49813	Hs.75615	zinc finger protein apolipoprotein C-II	4.0 4.0
	438703	AI803373	Hs.31599	ESTs	4.0
50	424726	AK001007	Hs.138760	Homo sapiens cDNA FLJ10145 fis, clone HE	4.0
	405771 418841	NM_002332	Hs.89137	low density Epoprotein-related protein	4.0 4.0
	421764	AI681535	Hs.148135	serine/threonine kinase 33	4.0
	424176	AL137273	Hs.142307	hypothetical protein	4.0
55	425773	N21279	Hs.237749	ESTs	4.0
	427304 428882	AA761526 AA436915	Hs.163853 Hs.131748	ESTs ESTs, Moderately similar to ALU7_HUMAN A	4.0 4.0
	452834	AJ638627	Hs.105685		4.0
60	453745	AA952989	Hs.63908	hypothetical protein MGC14726	4.0
60	405239	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	4.0
	413801 429698	M62246 A1685086	Hs.35406 Hs.26339	ESTs, Highly similar to unnamed protein ESTs, Wealdy similar to S21348 probable	4.0
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	4.0 4.0
	439199	R40373	Hs.26299	ESTs	4.0
65	439450	RS1613	Hs.125304		4.0
	446782 419687	A1653048	Hs.144006		4.0
	402408	A1638859	Hs.227699	ESTs, Weakly similar to T2D3_HUMAN TRANS	3.9 3.9
70	453362	H14988	Hs. 107375	ESTs	3.9
70	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	3.9
	420578 425010	AAB13546 T16837	Hs.99034 Hs.4241	GTP-binding protein Rho? ESTs	3.9
	444230	H95537	Hs.146067		3.9 3.9
	441736	AW292779	Hs.169799		3.9
75	418951	F07809	Hs.89506	paired box gene 6 (aniridia, keratitis)	3.9
	406311 408460	4405477	Un sacce	FOT	3.9
	410658	AA054726 AW105231	Hs.285574 Hs.192035		3.9 3.9
^^	414599	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	3.9
80	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	3.9
	429477	AI275514	Hs.6658	ESTs	3.9
	433766 436190	AA609234 AK001059	Hs.112669	gb:Homo sapiens cDNA FLJ10197 fis, clone	3.9 3.9
	-50.00			BAT WILD BETWEEN COLAN L. P. 10121 122' (2016)	3.9

	447004	R41754	He CADE	F67.	
	447891 450221	AA328102	Hs.6496 Hs.24541	ESTs	3.9 3.9
	404283	70020102	113.24041	cytoskeleton associated protein 2	3.9
-	453919	AW959912	Hs.7076	KIAA1705 protein	19
5	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	3.9
	412754	AW160375	Hs.74565	armyloid beta (A4) precursor-like protein	3.9
	445314 435652	A1689948 N32388	Hs.65489 Hs.334370	Homo sapiens cDNA: FLJ21517 fs, clone C	3.9
	407378	AA299264	Hs.57776	uncharacterized hypothalamus protein HBE ESTs, Moderately similar to IS8022 hypot	19 19
10	438054	AA776626	Hs.62183	ESTs	3.9
	438420	AA443966	Hs.31595	ESTs	3.9
	445133	AW157648	Hs.153506	ESTs	3.9
	432590 453331	A1609273 A1240665	Hs.110783 Hs.8895	ESTs ESTs	3.9
15	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	3.9 3.8
	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL	3.8
	451489	NM_005503	Hs.26468	arryloid beta (A4) precursor protein-bind	3.8
	447247 448302	AW369351	Hs.287955	Homo sepiens cDNA FLJ13090 fs, done NT	3.8
20	415669	AI480208 NM_005025	Hs.182906 Hs.78589	Homo sepiens mRNA for KIAA1872 protein, serine (or cysteine) proteinase inhibito	3.8
	417355	D13168	Hs.82002	endothelin receptor type B	3.8 3.8
	446727	AB011095	Hs.16032	KIAA0523 protein	3.8
	424340	AA339036	Hs.7033	ESTs	3.8
25	423346 412788	AI267677 AA120960	Hs.127416 Hs.198416	synaptojanin 1	3.8
	404593	AA120300	FIS. 1904 10	ESTs	3.8 3.8
	416856	N27833	Hs.269028	ESTs, Wealty similar to 138022 hypotheti	3.8
	429896	AA460367	Hs.224223	ESTs, Moderately similar to 138022 hypot	3.8
30	439619	AW975998	Hs.58595	ESTs, Wealthy similar to 138022 hypotheti	3.8
30	439634 440322	W79377 AA879430	Hs.167	microtubule-associated protein 2	3.8
	447761	AF061573	Hs.19492	gb:oj91d08.41 Soares_NFL_T_GBC_S1 Homo s protocadherin 8	3.8 3.8
	452453	Al902519		gb:QV-BT009-101198-051 BT009 Homo sapien	3.8
35	439671	AW162840	Hs.6841	tunesin family member 5C	3.8
33	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	3.8
	459278 447028	AW294659 AI973128	Hs.34054 Hs.167257	Homo sapiens cDNA: FLJ22488 fis, clone H brain link protein-1	3.8
	449458	AJ805078	Hs.208261	ESTs	3.8 3.8
40	445888	AF070564	Hs.13415	Homo sapiens clone 24571 mRNA sequence	3.8
40	407385	AA610150	Hs.272072	ESTs, Weakly similar to 138022 hypotheti	3.8
	428841 430643	Al418430 AW970065	Hs.104935 Hs.287425	ESTs	3.8
	422263	AA307639	Hs.129908	MEGF10 protein KIAA0591 protein	3.8 3.8
	451625	R56793	Hs.106576	alanine-glyoxylate aminotransferase 2-ti	3.8
45	439236	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN!	3.8
	441928	AI370188	Hs.211454	ESTs	3.8
	441797 414922	AI936933 D00723	Hs.214635 Hs.77631	ESTs glycine cleavage system protein H (amino	3.7
	425588	F07396	Hs.46751	ESTs	3.7 3.7
50	437007	AA741300	Hs.202599	ESTs. Weakly similar to 138022 hypotheti	3.7
	435793	AB037734	Hs.4993	KIAA1313 protein	3.7
	443682 425741	AI383061 AF052152	Hs.47248 Hs.159412	ESTs, Highly similar to similar to Cdc14	3.7
	418211	BE244748	Hs.247474	Horno sapiens clone 24528 mRNA sequence hypothetical protein FLJ21032	3.7 3.7
55	440080	AW051597	Hs.143707	ESTs	3.7
	452898	AA814497	Hs.78792	ESTs	3.7
	435575 409234	AF213457 AI879419	Hs.44234 Hs.27206	triggering receptor expressed on myeloid	3.7
	420489	AA815089	Hs.193513	EST8 ESTs	3.7 3.7
60	426890	AA393167	Hs.41294	ESTs	3.7
	438849	W28948	Hs.10762	ESTs	3.7
	441869 448796	NM_003947 AA147829	Hs.8004	hunfingtin-associated protein interactin	3.7
	459318	NM_000038	Hs.301431	endothetial zinc finger protein induced gb:Homo sapiens adenomatosis polyposis c	3.7
65	459518	AJ937419	Hs.294069	Homo sapiens cDNA FLJ 13384 fis, clone Pt.	3.7 3.7
	434444	AJ765276	Hs.101257	hypothetical protein MGC3295	3.7
	421183	AL135740	Hs.102447	TSC-22-like	3.7
	410555 421637	U92649 AF035290	Hs.64311 Hs.106300	a disintegrin and metalloproteinase doma	3.7
70	418522	AA605038	Hs.7149	Homo sapiens clone 23556 mRNA sequence Homo sapiens cDNA: FLJ21950 fis, clone H	3.7
	420807	AA280627	Hs.57846	ESTs	3.7 3.7
	449961	AW265634	Hs.133100		3.7
	422634	NM_016010		CGI-62 protein	3.7
75	421030 427099	AW161357 AB032953	Hs.101174 Hs.173560		3.7
	452355	N54926	Hs.29202	G protein-coupled receptor 34	3.7 3.7
	440483	AI200836	Hs.150386	ESTs	3.7
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	3.7
80	423756 425187	AA828125 AW014488	Nº 33500	gb:od71a09.s1 NCI_CGAP_Ov2 Homo sapiens	3.6
_ •	434859	BE255080	Hs.22509 Hs.299315	ESTs collapsin response mediator protein-5; C	3.6
	413199	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	3.6 3.6
	445729	H21066	Hs.13223	Homo saplens mRNA full length insert cON	3.6

	416120	H46739		gb:yo14h02.s1 Soares adult brain N2b5HB5	2.5
	429239	AA448419	Hs.45209	ESTs	3.6 3.6
	419086	NM_000216	Hs.89591	Kalimann syndrome 1 sequence	3.6
5	446659	AI335361	Hs.226376	ESTs	3.6
5	426757	AW205640	Hs.158206	ESTs	3.6
	418819 458332	AA228776	Hs. 191721	ESTs	3.6
	408826	AI000341 AF216077	Hs.220491 Hs.48376	ESTs Homo sapiens clone HB-2 mRNA sequence	3.6
	410343	AA084273	Hs.76561	ESTs, Weakly similar to \$47072 finger or	3.6 3.6
10	410507	AA355288	Hs.40834	transitional epithelia response protein	3.6
	422977	AA631498		gb:np83h04.s1 NCI_CGAP_Thy1 Homo sepiens	3.6
	425305	AA363025	Hs.155572	Human clone 23801 mRNA sequence	3.6
	428002	AA418703	44. 8804	gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	3.6
15	428505 430530	AL035461 AA480870	Hs.2281 Hs.47660	chromogranin B (secretogranin 1)	3.6
	436425	AI913146	Hs.318725	ESTs CGI-72 protein	3.6
	438078	AI016377	Hs.131693	ESTs	3.6 3.6
	442927	AI024347	Hs.131519	ESTs	3.6
20	446242	N66336	Hs.7360	ESTs	3.6
20	448831	AL080123	Hs.22182	zinc finger protein 23 (KOX 16)	3.6
	450474 452198	AW872844 AI097560	Hs.201919 Hs.61210	ESTS	3.6
	455800	R22479	Hs.167073	ESTs, Wealdy similar to 138022 hypotheti Homo sapiens cDNA FLJ13047 fis, clone NT	3.6
	436443	AW138211	Hs.128746	ESTs	3.6 3.6
25	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	36
	456038	AA203285	Hs.294141	ESTs, Wealthy similar to atternatively sp	3.6
	408902	AW014859	Hs.5510	ESTs .	3.6
	442950 423905	AI500417 AW579960	Hs.46764 Hs.135150	ESTs	3.6
30	425478	AB007953	Hs.268840	lung type-I cell membrane-associated gly ESTs	3.6
•	453884	AA355925	Hs.35232	KIAA0186 gene product	3.6 3.6
	404721		- A.0020C	Tar Victor gone product	3.6
	408453	AI369838	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	3.6
25	440553	AA889416	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	3.5
35	446372	AB020644	Hs. 14945	long fally acyl-CoA synthetase 2 gene	3.5
	413999 421458	N48124	Hs.34460	ESTs	3.5
	425017	NM_003654 AL119305	Hs.104576 Hs.288405	carbohydrate (keratan suffate Gal-6) sul ESTs	3.5
	435958	H98180	Hs.117975	ESTs	3.5
40	415101	R45531	Hs. 144534	ESTs	3.5 3.5
	451320	AW118072	Hs.89981	diacylglycerol kinase, zeta (104kD)	3.5
	430290	A1734110	Hs.136355	ESTS	3.5
	416836	D54745	Hs.80247	cholecystokinin	3.5
45	414821 419412	M63835 AW161058	Hs.77424 Hs.90297	Fc tragment of IgG, high affinity la, re	3.5
	437860	AA333063	Hs.279898	synuclein, beta Homo sapiens cDNA: FLJ23165 fis, clone L	3.5
	452689	F33868	Hs.284176	transferin	3.5 3.5
	.416661	AA834543	Hs.79440	IGF-II mRNA-binding protein 3	3.5
50	427491	R43279	Hs.22574	ESTs. Wealdy similar to 138022 hypotheti	3.5
30	428037	N47474	Hs.89230	potassium intermediate/small conductance	3.5
	444584 408296	AJ 168422 AL 117452	Lb. 44155	gb:ok30e11.x1 Soares_NSF_F8_9W_OT_PA_P_S	3.5
	453775	NM_002916	Hs.44155 Hs.35120	DKFZP585G1517 protein replication factor C (activator 1) 4 (37	3.5
	412659	AW753865	Hs.74376	offactomedin related ER localized protei	3.5 3.5
55	429077	AB028983	Hs.2352	adenylata cyclase 2 (brain)	3.5
	436887	AW953157	Hs.193235	hypothetical protein DKFZpS47D155	3.5
	450784	AW246803	Hs.47289	ESTS	3.5
	446827	AW451243	Hs.157069	ESTS	3.5
60	436434 412777	N50465 Al335773	Hs.92927 Hs.270123	putative 47 kDa protein	3.5
	438476	AA326108	Hs.33829	ESTs bHLH protein DEC2	3.5 3.5
	408601	U47928	Hs.86122	protein A	3.5 3.4
	429401	AW295102	Hs.99272	ESTs, Weakly similar to S32567 A4 protei	3.4
65	448425	A1500359	Hs.233401	ESTs	3.4
05	418727 451729	AA227609	Hs.94834	ESTs	3.4
	435910	AW160725 AI084152	Hs.312469 Hs.21782	ESTs	3.4
	434577	R37316	Hs.179769	ESTs, Wealdy similar to ALU7_HUMAN ALU S Homo sapiens cDNA: FLJ22487 ffs, clone H	3.4
	41459B	AI094221	Hs.135150	tung type-I cell membrane-associated gly	3.4 3.4
70	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	3.4
	413293	AL047483	Hs.302498	GTP-binding protein homotogous to Saccha	3.4
	423992 426249	AW898292	Hs.137206	Homo sapiens mRNA; cDNA DKFZp564H1663 (1	3.4
	426249 426968	F05422 U07616	Hs.168352	nucleoporin-like protein 1	3.4
75	430388	AA356923	Hs.173034 Hs.240770	amphiphysin (Stiff-Mann syndrome with br nuclear cap binding protein subunit 2, 2	3.4
•	435081	AI651474	Hs. 163944	ESTs	3.4
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	3.4 3.4
	449714	AB033015	Hs.23941	KIAA1189 protein	3.4
80	443392	AI055821	Hs.293420	ESTs	3.4
00	410082	AA081594 NM_013280	Hs.158311	Musashi (Orosophila) homolog 1	3.4
	445337 408493	BE206854	Hs.12523 Hs.46039	fibronectin leucine rich transmembrane p	3.4
	432731	R31178	Hs.287820	phosphoglycerate mutase 2 (muscle) fibronectin 1	3.4
					3.4

	448758	AB018311	Hs.21917	KIAA0768 protein	3.4
	432613	AW081698	Hs.80712	KIAA0202 protein	3.4
	434164	AW207019	Hs.148135	serine/threonine kinase 33	3.4
5.	425294 410108	AF033827	Hs.155553	HNK-1 sulfotransferase	3.4
5	406815	AA081659 AA833930	Hs.318775 Hs.288036	OSBP-related protein 6	3.4
	402855	~~633330	13.200030	RNA isopentanylpyrophosphate transferas	3.4
	422170	AJ791949	Hs.112432	anti-Multerian hormone	3.3
	445034	AW293376	Hs.143659	ESTs	3.3 3.3
10	42437B	W28020	Hs.167988	neural cell adhesion molecule 1	3.3
	423611	AB011163	Hs.129908	KIAA0591 protein	3.3
	435593	R88872	Hs.4964	DIGFZP586J1624 protein	33
	404819				3.3
• •	436607	AW561783	Hs.211061	ESTs	3.3
15	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (F	3.3
	452693	T79153	Hs.48589	zinc finger protein 228	3.3
	454996	AW850180		gb:IL3-CT0219-271099-022-C09 CT0219 Homo	3.3
	406927	M26460		gb:Homo sapiens (clone 104) retinoblasto	3.3
20	409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp43400515 (I	3.3
20	415238	R37780	Hs.21422	ESTs	3.3
	417845 421192	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (I	3.3
	426695	AA833718 AW118191	Hs.204529	KIAA1806 protein	3.3
	438885	AI886558	Hs.112729 Hs.184987	ESTs ESTs	3.3
25	451762	AF222980	Hs.26985	disrupted in schizophrenia 1	3.3
	452103	R42764	Hs.339654	ESTs, Wealty similar to 138022 hypotheti	3.3 3.3
	453590	AF150278	Hs.33578	KIAA0820 protein	3.3
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	3.3
30	457285	A1038858	Hs.130522	Ky channel-interacting protein 1	3.3
30	436045	AB037723	Hs.5028	DKFZP56400423 protein	3.3
	437470	AL390147	Hs.134742	hypothetical protein DKFZp5470065	3.3
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	3.3
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	3.3
35	432656	NM_000246	Hs.3076	MHC class II transactivator	3.3
75	443898 423582	AW804296 BE000831	Hs.9950	Sec61 gamma	3.3
	445953	AI612775	Hs.23837 Hs.145710	Homo sapiens cDNA FLJ11812 fis, done HE ESTs	3.3
	427940	AA417812	Hs.38775	ESTS	3.3
	414683	S78296	Hs.76888	hypothetical protein MGC12702	3.3 3.3
40	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.3
	420649	A1866964	Hs.124704	ESTs. Moderately similar to \$65657 alpha	3.3
	419498	AL036591	Hs.20887	hypothetical protein FLJ10392	3.3
	457579	AB030816	Hs.36761	HRAS-like suppressor	3.3
45	436556	AI384997	Hs.7572	ESTs	3.2
73	424369 457065	R87622 AI476318	Hs.26714	KIAA1831 protein	3.2
	440210	AW674562	Hs.192480 Hs.125296	ESTs ESTs	3.2
	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	3.2
	434353	AA630863	Hs.131375	ESTs, Moderately similar to ALUB_HUMAN I	3.2 3.2
50	414430	AJ346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.2
	439924	AI985897	Hs.125293	ESTs	3.2
	411505	AF155659	Hs.70565	molybdenum cofactor synthesis 2	3.2
	423175	W27595	Hs.18553	hypothetical protein FLJ 14627	3.2
55	415115	AA214228	Hs.127751	hypothetical protein	3.2
55	407878	D87468	Hs.40888	activity-regulated cytoskeleton-associat	3.2
	410274 437762	AA381807	Hs.61762	hypoxia-inducible protein 2	3.2
	438944	T78028 AA302517	Hs.154679 Hs.92732	synaptotagmin I KIAA1444 protein	3.2
	450313	At038989	Hs.332633	Bardet-Biedl syndrome 2	3.2
60	409459	D86407	Hs.54481	low density lipoprotein receptor-related	3.2 3.2
	410953	AW811766	Hs.334858	hypothetical protein MGC12250	3.2
	418527	AA450386	Hs.7149	Homo sapiena cDNA: FLJ21950 fis, clone H	3.2
	420081	AW510776	Hs.94958	tubulin lyrosine ligase-like 1	3.2
65	429496	AA453800	Hs.192793	ESTs	3.2
03	430099	AW194988	Hs.20537	hypothetical protein FLJ13942	3.2
	434928 435532	AW015595	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA	3.2
	438306	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	3.2
	439274	AW188266 AF086092	Hs.163645 Hs.48372	ESTS	3.2
70	440847	AA907511	Hs.130178	ESTs ESTs	3.2
· -	447750	AI422234	Hs. 143434		3.2 3.2
	455350	AW901809		gb:QV0-NN1020-170400-195-h02 NN1020 Homo	3.2
	430890	X54232	Hs.2699	glypican 1	3.2
76	420568	F09247	Hs.247735	protocadherin alpha 10	3.2
75	410768	AF038185	Hs.66187	Homo sapiens clone 23700 mRNA sequence	3.2
	427450		Hs.178121	KIAAD626 gene product	3.2
	430456	AA314998	Hs.241503		3.2
	430181 418512	AF065314 AW498974	Hs.234785 Hs.89981		3.2
80	419912	AF249745	Hs.6066	diacylglycerol kinase, zeta (104k0) Rho guanine nucleotide exchange factor (3.2
_	450689	AI369275	Hs.243010		3.2 3.2
	424899	AL119387	Hs.119062	ESTs	3.2
	436277	R88520	Hs.120917		3.2

	451455	AI937227	Hs.8821	hepcidin antimicrobial peptide	3.2
	445078 447746	AI869975 AW015920	Hs.4775 Hs.161359	junctophikn 3	3.2
	435458	F11872	Hs.4892	ESTs Homo sapiens clone 24841 mRNA sequence	3.2 3.2
5	427729	AB033100	Hs.300646	KIAA protein (similar to mouse paladin)	3.2
	417417	F05745	Hs.89512	ATPase, Ca→ transporting, plasma membra	3.1
	438810	AW897846	Hs.6421	hypothetical protein DKFZp761N09121	3.1
	439570 432527	T79925 AW975028	Hs.269165 Hs.102754	ESTs, Wealdy similar to ALU1_HUMAN ALU S ESTs	3.1
10	416801	X98834	Hs.79971	sal (Orosophila)-like 2	3.1 3.1
- •	421988	AW450481	Hs.161333	ESTS	3.1
	426509	M31166	Hs.2050	pentaxin-related gene, rapidly induced b	3.1
	408785	AA773187	Hs.294027	ESTS	3.1
15	433494 412723	AB029396 AA648459	Hs.3353 Hs.335951	beta-1,3-glucuronytransferase 1 (glucur hypothetical protein AF301222	3.1
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	31 31
	439456	A1752409	Hs. 109314	hypothetical protein FLJ20980	31
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	3.1
20	452780	BE171598	Hs.13522	ESTs, Wealdy similar to 138022 hypotheti	3.1
20	438192 424939	A1859065 AK000059	Hs.337620 Hs.153881	Homo sapians AFG3L1 isoform 1 mRNA, part Homo sapians NY-REN-62 antigen mRNA, par	3.1 3.1
	403053	R58624	Hs.2186	eukaryotic translation elongation factor	3.1
	404299				3.1
25	407864	AF059291	Hs.40539	chromosome 8 open reading frame 1	3.1
23	4101B1 418852	AI468210 BE537037	Hs.261285 Hs.273294	pleiotropic regulator 1 (PRL1, Arabidops	3.1
	449101	AA205847	Hs.23016	hypothetical protein FL/20069 G protein-coupled receptor	3.1 3.1
	453240	AI969564	Hs.166254	hypothetical protein DKFZp566I133	3.1
20	440486	BE243513	Hs.7212	hypothetical protein PP1044	3.1
30	408096	BE250162	Hs.83765	dihydrofolate reductase	3.1
	439864 414706	AI720078 AW340125	Hs.291997 Hs.76989	ESTs, Weakly similar to A47582 8-cell gr KtAA0097 gene product	3.1
	436315	BE390513	Hs.27935	hypothetical protein MGC4837	3.1 3.1
26	426855	AL117427	Hs.172778	Homo sapiens mRNA; cDNA DKFZp566P013 (fr	3.1
35	425683	AB037813	Hs.159200	hypothetical protein DKFZp762K222	3.1
	410126	BE169274	Hs.169387	KIAA0036 gene product	3.1
	435312 425491	AJ243396 AA883316	Hs.4865 Hs.255221	voltage-gated sodium channel beta-3 subu ESTs	3.1 3.1
	456273	AF154846	Hs.1148	zinc Enger protein	3.1
40	412140	AA219691	Hs.73625	RAB8 interacting, kinesin-like (rabkines	3.1
	445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	3.1
	432154 453128	AI701523 AW026516	Hs.112577	ESTs	3.1
	438458	AW975186	Hs.31791	acylphosphatase 2, muscle type gb:EST387294 MAGE resequences, MAGN Homo	3.1 3.1
45	448616	AF035621	Hs.21611	kinesin family member 3C	3.0
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	3.0
	443906 417318	AA348031	Hs.7913	ESTS	3.0
	452619	AW953937 AW298597	Hs.12891 Hs.61884	ESTs Homo sapiens, clone IMAGE:4298026, mRNA,	3.0 3.0
50	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	3.0
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	3.0
	426327	W03242	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	3.0
	451468 422758	AW503398 AF152329	Hs.293663 Hs.284180	ESTs, Moderately similar to I38022 hypot protocadherin gamma subfamily C, 3	3.0
55	421633	AF121860	Hs. 106260	sorting nextin 10	3.0 3.0
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.0
	418932	L34059	Hs.89484	cadherin 4, type 1, R-cadherin (retinal)	3.0
	416805 419518	F13271 U79289	Hs.79981	Human clone 23560 mRNA sequence	3.0
60	422709	AA315331	Hs.90798 Hs.153485	Human clone 23695 mRNA sequence ESTs	. 3.0 3.0
	423135	N67655	Hs.26411	ESTs	3.0
	424901	Z11933	Hs. 182505	POU domain, class 3, transcription facto	3.0
	426617 427386	W58006	Hs.266258	endonuclease G-like 1	3.0
65	429859	AW836261 NM_007050	Hs.337717 Hs.225952	ESTs protein tyrosine phosphatase, receptor t	3.0
	435071	D60683	Hs.35495	ESTs	3.0 3.0
	435092	AL137310	Hs.4749	Homo sapiens mRNA; cDNA DKFZp761E13121 (3.0
	436211	AK001581	Hs.334828	hypothetical protein FLI10719; KIAA1794	3.0
70	436936 445855	AL134451 BE247129	Hs.197478	ESTs	3.0
	452294	AJ871925	Hs.145569 Hs.117895	ESTs ESTs, Moderately similar to A47582 8-cel	3.0 3.0
	433980	AA137152	Hs.286049	phosphoserine aminotransferase	3.0
	430228	AW950939	Hs.6382	ESTs, Highly similar to T00391 hypotheti	3.0
75	451026	AA013218	Hs.157492		3.0
, ,	435232 439566	NM_001262 AF086387	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1 gb:Homo sapiens full length insert cDNA	3.0
	425782	U66468	Hs.159525		3.0 3.0
	416586	D44643	Hs.14144	secreted modular calcium-binding protein	3.0
80	416874	H98752	Hs.42568	ESTs	30
30	410386 411411	W26187 AA345241	Hs.3327 Hs.55950	Homo septens cDNA: FLJ22219 fis, clone H ESTs, Weakly similar to KIAA1330 protein	3.0
	424066	Z99348	Hs.112461		3.0 3.0
	404048				3.0

	429163	AA884766		mbm20-10-10-10-10-10-10-10-10-10-10-10-10-10	••
	454117	BE410100	Hs.40368	gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s adaptor-related protein complex 1, sigma	3.0 3.0
	418196	Al745649	Hs.26549	KIAA1708 protein	3.0
_	434131	AI858275	Hs.143659	EST ₈	3.0
5	441255	R06350	Hs.171635	ESTs	2.9
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALUS_HUMAN ALU S	2.9
	453905 416602	NM_002314	Hs.36566 Hs.79389	UM domain kingse 1	2.9
	431173	NM_006159 AW971198	Hs.294068	nel (chicken)-like 2 ESTs	2.9 2.9
10	425599	AW366745	Hs.214140	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
	436401	AI087958	Hs.29088	ESTs	29
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	2.9
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	29
15	412490	AW803564	Hs.288850	Homo sepiens cDNA: FLJ22528 fis, clone H	2.9
13	433149 434811	BE257672 AW971205	Hs.42949 Hs.114280	hypothetical protein HES6 ESTs	29
	425897	AA935315	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	2.9 2.9
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	29
~~	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	2.9
20	411124	AW196937	Hs.53929	ESTs, Weakly similar to ALUB_HUMAN !!!!	2.9
	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.9
	427651 441707	AW405731 R42637	Hs.18498 Hs.21963	Homo sapiens cDNA FLJ12277 fis, clone MA	29
	435741	AJ240668	Hs.113099	hypothetical protein DKFZp761B0514 ESTs	2.9 2.9
25	437273	AL137451	Hs.120873	ESTs, Highly similar to T46266 hypotheti	2.9
	422939	AW394055	Hs.98427	ESTs, Weakly similar to I38022 hypotheti	29
	439376	AA883521	Hs.222064	ESTs	29
	439935	\$75105	Hs.301676	gtutamate receptor, lonotropic, kainate	2.9
30	437267 453740	AW511443	Hs.258110	ESTs	29
50	400250	AL120295	Hs.311809	ESTs, Moderately similar to PC4259 ferri	29
	400992				2.9 2.9
	408814	N62499	Hs.176227	hypothetical protein FU11155	2.9
3.5	411849	AW964970	Hs.18861	ESTs, Moderately similar to KIAA1276 pro	29
35	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-assoc	2.9
	423751	AW235633	Hs.46525	ESTS	2.9
	426910 450203	AA470023 AF097994	Hs.190089 Hs.301528	ESTs, Moderately similar to ALU1_HUMAN A	2.9
	459311	R40192	Hs.21527	L-kynurenine/alpha-aminoadipate aminotra Human DNA sequence from clone GS1-115M3	2.9 2.9
40	425304	AA453844	Hs.31339	fibroblast growth factor 11	2.9
	428500	AI815395	Hs.184641	fatty acid desaturase 2	2.9
	421641	AI638184	Hs. 106334	Homo sapiens clone 23836 mRNA sequence	2.9
	421141	AW117261	Hs.125914	ESTs	2.9
45	407870 456723	AB032990	Hs.40719	hypothetical protein KIAA1164	2.9
73	436456	Z43902 AW292677	Hs.4748 Hs.248122	adenylate cyclase activating polypeptide G protein-coupled receptor 24	2.9
	421483	NM_003388	Hs.104717	hypothetical protein MGC11333	2.9 2.9
	412190	R16180	Hs.274461	ESTs	2.9
50	446131	NM_000929	Hs.290	phospholipase A2, group V	2.9
50	441668	AI611973	Hs.127525	ESTs	2.9
	437387	AI198874	Hs.28847	AD026 protein	2.9
	423420 427958	AI571364 AA418000	Hs.128382 Hs.98280	Homo sapiens mRNA; cONA DKFZp76111224 (f	2.9
_	429084	AJ001443	Hs.195614	potassium intermediate/small conductance splicing factor 3b, subunit 3, 130kD	2.9 2.9
55	447067	R42098	Hs.21964	ESTs	2.9
	430887	N66801	Hs.260287	KIAA1841 protein	2.9
	441824	AB007871	Hs.7977	KIAA0411 gene product	2.9
	424126	AA335635	Hs.96917	ESTs	2.9
60	408739 447422	W01556 BE618703	Hs.238797	ESTs, Moderately similar to 138022 hypot	2.9
-	435615	Y15065	Hs.98258 Hs.4975	orthopedia (Drosphita) homolog potassium voltage-gated channel, KQT-tik	2.9 2.9
	446997	AA383439	Hs.16758	Spir-1 protein	2.9
	433573	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	2.9
45	408447	AK002089	Hs.45080	Homo sapiens cDNA FLJ11227 fis, clone PL	2.9
65	419588	AI088485	Hs.144759	ESTs, Weakly similar to 138022 hypotheti	2.8
	417022	NM_014737	Hs.80905	Ras association (RalGOS/AF-6) domain fam	2.8
	408432 420320	AW195262 AB002361	Hs.96633	gb:xn67b05.x1 NCI_CGAP_CML1 Homo sepiens KIAA0363 protein	2.8
	425241	AA324524	Hs.155247	aldolase C, fructose-bisphosphate	2.8 2.8
70	428670	AA431682	Hs.134832	ESTs	2.8
	424415	NM_001975			2.8
	409185	AW961601	Hs.252406		2.8
	411555	AF113537	Hs.70669	HMP19 protein	2.8
75	426847	\$78723 AMO72612	Hs.298623		2.8
13	458809 420071	AW972512 AB028985	Hs.20985 Hs.94806	sin3-associated polypeptide, 30kD	2.8
	424572	M19850	Hs.150741	ATP-binding cassette, sub-family A (ABC1 2,3-cyclic nucleotide 3 phosphodieste	2.8 2.8
	444670	H58373	Hs.332938		2.8
00	411089	AA456454	Hs.183418		2.8
80	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (2.8
	440637	AW900115	Hs.7309	Homo sapiens clone 23741 mRNA sequence	2.6
	408554 403056	AA836381 R58624	Hs.315111 Hs.2186	nuclear receptor co-repressor/HDAC3 comp	28
	-03030	100024	F13.2100	eukaryotic translation elongation factor	2.6

	423449	ALEGRANA	Hs.33067	ECT-	
	423449 424188	AJ497900 AW954552	Hs.142634	ESTs zinc finger protein	2.8 2.8
	429006	AA443143	Hs.50929	hypothetical protein FLJ13842	2.6 2.8
_	434981	AW182577	Hs.293077	ESTs	2.8
5	437435	AA249439	Hs.27027	hypothetical protein DKFZp762H1311	2.8
	442748 443312	AID16713	Hs.135787	ESTS	2.8
	450940	N52025 AJ744943	Hs.46516 Hs.143209	ESTs ESTs, Wealdy similar to 138022 hypothed	2.8 2.8
	452738	AL133800	Hs.7088	hypothetical protein MGC12435	2.6
10	409182	AA064970	Hs.118145	ESTs	2.8
	439793	AA018825	Hs.7934	Kruppel-like factor 4 (gut)	2.8
	432683 434269	AW995441	Hs.10475	ESTs	2.8
	429500	AK001991 X78565	Hs.3781 Hs.289114	similar to murine leucine-rich repeat pr hexabrachion (tenascin C, cytotactin)	2.8 2.8
15	433290	R20077	Hs.302185	Homo sapiens clone 23618 mRNA sequence	2.8
	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	28
	435977	AL138079	Hs.5012	brain-specific membrane-anchored protein	2.8
	430294 425168	AI538226 R96366	Hs.32976	guanine nucleotide binding protein 4	2.8
20	428180	AI129767	Hs.182974	gb:yq37d04.s1 Soares fetal liver spieen guanine nucleotide binding protein (G pr	2.8 2.8
	409348	AI401535	Hs.146090	EST:	28
	409887	AL137534	Hs.56876	Homo sapiens mRNA; cDNA DKFZp434H1419 (f	2.8
	457211 430039	AW972565	Hs.32399	ESTs, Wealdy similar to S51797 vasodilat	2.8
25	417642	BE253012 BE302665	Hs.153400 Hs.105461	ESTs, Wealdy similar to ALU1_HUMAN ALU S hypothetical protein FLJ20357	2.8 2.8
	419169	AW851980	Hs.262346	ESTs, Wealthy similar to S72482 hypotheti	2.8
	434008	AA740878	Hs.112982	ESTs	2.8
	446776 408838	AW293417	Hs.155455	ESTs FST-	2.8
30	422565	AI669535 BE259035	Hs.40369 Hs.118400	ESTs singed (Orosophila)-like (sea urchin fas	2.8 2.8
	447397	BE247676	Hs.18442	E-1 enzyme	2.8
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	2.8
	424330	AW073953	Hs.333396	Homo sapiens cDNA FLJ13596 fls, clone PL	2.8
35	446377 458924	AW014022 BE242158	Hs.170953 Hs.24427	ESTs DKFZP56601646 protein	2.8 2.8
	447710	Al420523	Hs.328241	F5Ts	29
	404049				28
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	28
40	426400 413264	M78361 W26456	Hs.169743 Hs.134757	Homo sapiens clone 25121 neuronal ollact hypothetical protein FLJ20033	28 28
• •	458997	AW937420	Hs.69662	EST ₈	27
	422854	AA318323		gb:EST20390 Retina II Homo sepiens cONA	2.7
	430526	AF181862	Hs.242407	G protein-coupled receptor, family C, gr	2.7
45	452023 432022	AB032999 AL162042	Hs.27566 Hs.272348	KIAA1173 protein Homo sapiens mRNA; cDNA DKFZp761L1212 (I	2.7 2.7
	452438	BE514230	Hs.29595	JM4 protein	27
	435408	H07897	Hs.4302	ESTs, Weakly similar to T29299 hypotheti	2.7
	418791 438821	AA935633 AA826425	Hs.194628 Hs.291829	EST ₅ EST ₅	2.7
50	423454	NM_016240	Hs.128856	CSR1 protein	2.7 2.7
	442091	AW770493	Hs.182874	guanina nucleotide binding protein (G pr	2.7
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fls, clone H	2.7
	412436 432821	AA665089 BE170702	Hs.279005	gb:nu76d01.s1 NCI_CGAP_AV1 Homo sepiens	2.7
55	416404	AA180138	Hs.107924	solute cerrier family 21 (organic anion ESTs	2.7 2.7
	441364	AW450466	Hs.126830	ESTs, Wealdy similar to Y038_YEAST HYPOT	2.7
	450202	AW969756	Hs.34145	ESTs, Wealdy similar to B49647 GTP-bindi	2.7
	426304 428722	AA374532 U76456	Hs.124673 Hs.190787	Homo sapiens cDNA FLJ11477 ffs, clone HE tissue inhibitor of metalloproteinase 4	27
60	449701	AW952323	Hs.129908	KIAA0591 protein	2.7 2.7
	420372	AW960049	Hs.293660	Homo sepiens, clone IMAGE:3535476, mRNA,	2.7
	410318 414603	AA084050	Hs.269259	ESTs, Wealty similar to \$23650 retroviru	2.7
	416098	R58394 H18577	Hs.25119 Hs.88974	ESTs, Weakly similar to YEXO_YEAST HYPOT	27
65	420895	AW149342	Hs.24444	cytochrome b-245, beta polypeptide (chro Homo sapiens cDNA: FLJ22165 fis, clone H	2.7 2.7
	424856	AA347746	Hs.9521	ESTs. Wealty similar to ZN43_HUMAN ZINC	2.7
	436304	AA339622	Hs.108887	ESTs	2.7
	44 1027 452545	AI911412 N31940	Hs.125444 Hs.14434	ESTs	2.7
70	454201	AB023191	Hs.44131	ESTs, Wealdy similar to I38022 hypotheti KIAA0974 protein	2.7 2.7
	448560	BE613183	Hs.23213	ESTs	27
	426807	AA385315	Hs.156682		2.7
	425825 440351	AI929508 AF030933	Hs.159590 Hs.7179	2 7	2.7
75	425390	AI092634	Hs.158114	RAD1 (S. pombe) homolog protein tyrosine phosphatase, non-recept	2.7
	427624	AA406245	Hs.24895	ESTs	2.7 2.7
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo saplen	2.7
	422491	AA338548	Hs.117546		2.7
80	424560 432415	AA158727 T16971	Hs.150555 Hs.289014		27
	414865	AA157155	Hs.274414		2.7 2.7
	415827	H17462	Hs.23079	ESTs	2.7
	445568	H00918	Hs.268744	KIAA1796 protein	2.7

	433315	R96754	Hs.239706	GRB2-associated binding protein 1	2.7
	428862 447959	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	2.7
	426420	A1452784 BE383808	Hs.270270 Hs.322430	ESTs, Weakly similar to 2109260A B cell NDRG family, member 4	2.7 2.7
5	436899	AA764852	Hs.291567	ESTs	27
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	2.7
	426501	AW043782	Hs.293616	ESTs	2.7
	449092	U91641	Hs.22985	alpha2,8-slalytransterase	2.7
10	427311 453313	AB020672 BE005771	Hs.175411 Hs.153746	KIAA0865 protein	2.7
. •	404029	DE003///	IIS. 155/40	hypothetical protein FLJ22490	2.7 2.7
	416289	W26333	Hs.337438	ESTs	27
	439108	AW163034	Hs.6467	synaptogyrin 3	2.6
15	418746	AI955289	Hs.300759	ribosomal protein L38	2.6
13	412046 435040	Y07847 A1932350	Hs.73088 Hs.152825	RAS-related on chromsome 22	2.6
	453083	U87223	Hs.31622	ESTs contactin associated protein 1	2.6 2.6
	428167	AA770021	Hs.16332	ESTs	26
20	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-0) s	2.6
20	443715	AI583187	Hs.9700	cyclin E1	2.6
	421247 424687	BE391727 J05070	Hs.102910	general transcription factor (IH, polype	2.6
	415056	AB004662	Hs.151738 Hs.77867	matrix metalloproteinase 9 (gelatinase B adenosine A1 receptor	2.6 2.5
	451697	AW449774	Hs.296380	POM (POM121 rat homolog) and ZP3 fusion	2.6
25	433701	AW445023	Hs.15155	ESTS	2.6
	457358	AI479755	Hs.129010	ESTs	26
	430347 418027	NM_002039 AB037807	Hs.239706	GRB2-associated binding protein 1	2.6
	440491	R35252	Hs.83293 Hs.24944	hypothetical protein ESTs, Wealdy similar to 2109260A B cell	26 26
30	425171	AW732240	Hs.16365	ESTs	2.6
	459335	AW298545	Hs.250726	EST	26
	425402	AI215881	Hs.24970	ESTs, Wealthy similar to B34323 GTP-bindi	2.6
	453169 433647	AB037815 AA603367	Hs.32156	KIAA1394 protein	2.6
35	450414	AI907735	Hs.222294 Hs.21446	ESTs KIAA1716 protein	2.6 2.6
	446233	AJ282028	Hs.25205	ESTs	2.6
	415446	F08898	Hs.66075	ESTS	2.6
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	2.6
40	413012	D83777	Hs.75137	KIAA0193 gene product	2.6
40	428671 427158	BE297851 AA935603	Hs.189482 Hs.166231	zinc finger protein 179 ESTs	2.6 2.6
	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	2.6 2.6
	459516	AI049662	Hs.246858	EST	2.6
45	402693				2.6
43	408039 422896	AA131424 AW961489	Hs.50340	ESTs	2.6
	423130	AW897588	Hs.154116 Hs.21213	ESTs ESTs	2.6 2.6
	438796	W67821	Hs.109590	genethonin 1	26
50	439871	R88518	Hs.46736	hypothetical protein FLJ23476	26
50	440192	AA872282	Hs.190598	ESTs	2.6
	419708 449436	AK000753 AA860329	Hs.92374	hypothetical protein	2.6
	436870	AW204219	Hs.279307 Hs.155560	hypothetical protein DKFZp434l2117 calnexin	2.6 2.6
	448424	AW009892	Hs.31924	ESTs	2.6
55	401324				2.6
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	2.6
	433943 428001	AA992805 H97428	Hs.44865 Hs.219907	lymphoid enhancer-binding factor 1	26
	429139	F09092	Hs.66087	ESTs, Moderately similar to Transforming ESTs	2.6 2.6
60	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	2.6
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.6
	444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	2.6
	412049 441783	N53437 BE313412	Hs.18268 Hs.7961	edenytate kinase 5 Homo sapiens clone 25012 mRNA sequence	2.6
65	425287	R88249	Hs.155524	peanut (Drosophila)-like 2	2.6 2.6
	432149	AW614326	Hs.157022	ESTs. Weakly similar to T34549 probable	2.6
	452234	AW084176	Hs.223296	ESTs, Weakly similar to 138022 hypotheti	2.6
	453478	AF083898	Hs.33021	neuro-oncological ventral antigen 2	2.6
70	418962 418858	AA714835 AW961605	Hs.271863 Hs.21145	ESTs hypothetical protein RG083M05.2	2.6
. •	443257	AJ334040	Hs.11614	HSPC065 protein	2.6 2.6
	428748	AW593206	Hs.98785	Ksp37 protein	2.6
	444984	H15474	Hs.132898	fatty acid desaturase 1	2.6
75	433404	T32982	Hs.102720	ESTs	2.6
, ,	434779 420582	AF153815 RE047878	Hs.50151	potassium inwardly-rectifying channel, s	2.6
	452856	BE047878 AF034799	Hs.99093 Hs.30881	Homo sapiens chromosome 19, cosmid R2837 protein tyrosine phosphatase, receptor t	2.6
	436440	AI471862	Hs.196008	Homo sapiens cDNA FLJ11723 fls, clone HE	2.6 2.6
<u>و</u> ۸	438527	AI969251	Hs.115325	RAB7, member RAS oncogene family-like 1	26
80	433216	AF217412	Hs.47320	neuroligin 3	2.6
	435380 428966	AA679001 AF059214	Hs.192221 Hs.194687	ESTs	26
	439653	AW021103	Hs.6631	cholesterol 25-hydroxylase hypothetical protein FLJ20373	26
	,,,,,,				2.6

	419304	AI271326	Hs.145101	ESTs, Wealty similar to T45070 protein k	2.6
	422991	H10940	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	2.6
	448548	R13209	Hs.21413	solute carrier family 12, (potassium-chi	2.0
5	435370 408875	AI964074 NM_015434	Hs.225838 Hs.48604	ESTs DKFZP434B168 protein	2.0
•	457005	AJ007421	Hs.172597	sal (Orosophila)-filte 3	2.
	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	2.
	438549	8E386801	Hs.21858	trinucleotide repeat containing 3	2.9
10	427951 411800	AI826125 N39342	Hs.43546 Hs.103042	ESTs microtubule-essociated protein 18	2:
	457683	AI821877	Hs.140002	ESTs, Moderately similar to ALU7_HUMAN A	2.
	451422	AB002336	Hs.26395	erythrocyte membrane protein band 4.1-5	2.
	430713	AA351647	Hs.2642	eukaryotic translation elongation factor	2
15	428826 428963	AL048842	Hs.194019	attractin	2.
	428903	AW382682 D50402	Hs.258208 Hs.182611	Homo sapiens, clone MGC:15606, mRNA, com solute carrier family 11 (proton-coupled	2
	429550	AW293055	Hs.119357	ESTs	2:
	438662	AA223599	Hs.6351	cleavage and polyadenylation specific (a	2.
20	435760	AF231922	Hs.213004	chromosome 21 open reading frame 62	2.
.0	427513 430061	AJ476318 AB037817	Hs.192480 Hs.230188	ESTs KIAA1396 protein	2.
	435923	BE301930	Hs.5010	Homo sapiens clone 24672 mRNA sequence	2. 2.
	417123	BE326521	Hs.159450	ESTs	2
15	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	2.
25	412980	AI815750	Hs.20977	hypothetical protein MGC3129 similar to	2
	427209 424327	H06509 AA431707	Hs.92423 Hs.31209	KIAA1566 protein ESTs	2. 2.
	436340	R42246	Hs.21606	ESTS	2.
	450650	T65617	Hs.101257	hypothetical protein MGC3295	2.
30	439444	A1277652	Hs.54578	ESTs, Weakly similar to 138022 hypotheti	2.
	400777 439478	AF049460	W- CC24	Address of a table and a second and a	2
	450407	NM 000810	Hs.6574 Hs.24969	deformed epidermal autoregulatory factor gamma-aminobulyric acid (GABA) A recepto	2.
	450385	AI531024	Hs.24948	synuclein, alpha interacting protein (sy	2
35	432558	R97268	Hs.177269	ESTs	2.
	400860				2
	410361 416063	BE391804 BE047699	Hs.62661 Hs.93454	guanylate binding protein 1, interferon- ESTs	2.
	414998	NM_002543	Hs.77729	ests oxidised low density lipoprotein (lectin	2.
10	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	2
	417791	AW965339	Hs.111471	ESTs	2
	418079	R40058	Hs.6911	ESTs	. 2
	408495 442104	W68796 L20971	Hs.237731	ESTs	2
45	437370	AL359567	Hs. 188 Hs. 161962	phosphodiesterase 48, cAMP-specific (dun Homo sapiens mRNA; cDNA DKFZp547D023 (fr	2
	429803	W81489	Hs.223025	RAB31, member RAS oncogene family	2
	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	2
	427413	BE547647	Hs.177781	hypothetical protein MGC5618	2
50	408955 415261	BE315170 T40928	Hs.8087 Hs.8346	NAG-5 protein ESTs	2
	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	2
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	2
	418388	R72332	Hs.29258	Homo sapiens cDNA FLJ11364 ffs, clone HE	2
55	421002 423244	AF116030	Hs.100932	transcription factor 17	2
"	423553	AL039379 AA405635	Hs.209602 Hs.96854	ESTs, Wealtly similar to ubiquitous TPR m ESTs, Wealtly similar to DYLX_HUMAN CYTOP	2
	427981	AWZ93165	Hs.143134	ESTs	á
	428301	AW628666	Hs.98440	ESTs, Weakly similar to 138022 hypotheti	- 3
60	428508	BE252383	Hs.184668	SBBI31 protein	2
50	428858 428943	AA436760 AW086180	Hs.37636	gb:zv67d11.r1 Soares_total_fetus_Nb2HF8_	- 3
	432427	AL037630	Hs.6638	ESTs, Weakly similar to KIAA1392 protein Homo sapiens cDNA FLJ11602 fis, clone HE	
	435347	AW014873	Hs.116963	ESTs	- 3
65	437949	U78519	Hs.41654	ESTs, Weakly similar to A46010 X-linked	- 3
65	438208	AL041224	Hs.65379	ESTs	
	440285 441523	U29589 AW514263	Hs.7138	cholinergic receptor, muscarinic 3	- 3
	441805	AA285136	Hs.301771 Hs.301914	ESTs, Weakly similar to ALUF_HUMAN !!!! neuronal specific transcription factor D	
~^	442337	Al371029	Hs.129257		
70	442789	AW904361	Hs.131191	ESTs, Wealdy similar to ALU7_HUMAN ALU S	:
	445556	AI910241	Hs.12887	actin-related protein 3-beta	:
	449086 459583	AI628357 AI907673	Hs.208037		
	472007	VI201013		gb:IL-BT152-080399-004 BT152 Homo sapien	:
75	TABLE 2	4B:			
	Pkey:			set identifier number	
	CAT nun		ne cluster num nbank accessio		
	Accessio	n. Gel	INSIN HOCESSI	an numbers	
80	Pkey	CAT Numbe			
	408432	1058667_1		R27868 AW811262	
	412225	1284108_1 129439_1	AW902042		
	412436	152493_1	~~0000089	AA135130 AA484059 AA102419 AW877765	

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	416120	1571266_1	H45739 H515	13 H19779		
	416871	1626761_1				
	416913	163001_1	AW934714 BI	161007 BE162500 AW74990	AW749864 BE162498 BE161005 AA190449	AW513465 BE161006 BE162499
5	422864	222336_1			690 AA436954 Z43802 F11753 T65491 D81	1821
,	422949	223184_1		6456 AA319377 AW961532 To		
	422977	223410_1	AW853758 H)	W 14222 WY 199033 WYROSSRP WRYSTOPR WY	NS70223 AAS74389 AAS82438 A1745346 AW964510 AA319642
	423756	231725_1		834883 AA330555		
	425158	247552_1		3929 AA351636 H78818 AA47	7084 728957 HR0194	
10	425517	252729_1		162736 AA358827	00122001100101	
	426413	266650_1		V954494 AI022688		
	428002	285602_1	AA418703 AA	418711 BE071915 BE071920	3E071912	
	428679	294049_1	AA431765 AA			
15	428858	296453_1		V237453 BE327496 N47347 N	6967	
1.5	429007	298301_1		3145 AL119015 AW904500		
	429163 433532	300543_1		V974271 AA592975 AA447312		
	436190	368950_1 41555_1	AK001059 A	A598607 AA742735		
	437034	431713_1		V808575 AW976668		,
20	438458	457837_1		A807807 D29548		•
	438993	467651_1		V834879 AI926361		
	439566	47387_1		77884 W72711		
	440322	491966_1			BE070484 BE070397 BE070395 BE070201 I	BE070198 BE070404 BE070270 BE070400
25	444584	611496_1	AJ168422 D8			
23	447197 448451	711623_1	R36075 AI36		rou 300	
	450625	764066_1 84032_1		39898 AW000978 AI598202 A A513951 AA010406	221706	
	452453	918300_1		02518 Al902516		
	454996	1248640_1				
30	455350	1283853_1		W901787 AW901795 AW9017	2 AW901744 AW901753 AW901807 AW901	1798
		_				
	TABLE 24					
	Pkey:			esponding to an Eos probeset		
35	Ref:	S	equence source. 1	he 7 digit numbers in this colu	on are Genbank Identifier (GI) numbers. "Dur	nham, et al.* refers to the publication entitled "The DNA
55	Strand:	SI In	nsmun to exnaupe	chromosome 22° Dunham, et a d from which exons were preda	. (1999) <u>Nature</u> 402:489-495.	
	Nt_positio	n: In		positions of predicted exons.	ieu.	
				produce of produces course.		
40	Pkey	Ref	Strand	Nt_position		
40	400777	8131663	Plus	70745-71121		
	400780	8131663	Minus	118372-118619		
	400859	9757499	Minus	91888-92018,98131-98294,9		
	400860 400992	9757499	Minus	151830-152104,152649-1527	14	
45	401324	8096828 9863791	Plus Plus	140390-140822 234057-234174		
	402408	9796239	Minus	110326-110491		
	402604	9909420	Plus	20393-20767		
	402605	9909420	Minus	47680-47973		
60	402693	8569863	Minus	82366-82515		
50	402855	9662953	Minus	59763-59909		
	404029	7671252	Plus	108716-111112		
	404048 404049	3688074 3688074	Minus	54421-56808		
	404283	2276311	Minus Minus	75765-78155 99460-99564		
55	404299	5738652	Minus	3826-4025		
	404541	8318559	Plus	103456-103664		
	404584	9857511	Plus	138651-139153		
	404593	9944088	Minus	74922-75788		
60	404721	9856648	Minus	173763-174294		
UU	404819	4678240	Plus		i736-16859,16941-17075,17170-17287,1738	9-17529,18261-18357,18443-18578
	405238 405771	7249119	Minus Plus	51728-51836		
	405819	7018349 4007557	Plus	91191-91254,91510-91589 2830-2967		
	406311	9211559	Minus	137114-139033		
65						
	TABLE 2	SA: ABOUT	1202 GENES UP-	REGULATED IN GLIOBLASTO	MA COMPARED TO NORMAL ADULT CEN	TRAL NERVOUS SYSTEM (CNS)
	1 able 25/	A lists about	1202 genes up-reg	ulated in güoblastoma compare	d to normal adult central pervous system (CN	S) These were selected from 59580 nmhesets on the
70	Anymetri	WEOS HUO3 (SeneChip array sur	ch that the ratio of "average" gl	blastoma to "average" normal adult CNS tiss	tues was greater than or equal to 2.0. The "average"
70	gnouast	ma ieves wæ	set to the /5" per	centre amongst various gliobia	stoma tumors. The "average" normal adult Ci	NS tissue level was set to the 95th percentile amongst various
	subtracta	el from hosh s	he numerator and	the denominator before the rat	ers of non-specific myondization, the 10" perc	pentile value amongst various non-malignant tissues was
	Pkey:	1	Inique Fos probes	et identifier number	was evaluation.	
	ExAcon:			n number, Genbank accession	number	
75	Unigenet		Jingene number			
	Unigene		Inigene gene title			
	R1:	,	Ratio of 75th percer	tille turnor to 95° percentile no	nal adult nervous system tissue	
	Dia.	Eu saa-	Unincests	Heissen Title		
80	Pkey 452461	ExAcca N78223	UnigenelD Hs.108106	Unigene Title transcription factor	R1	
- •	435895	AF03733		carbonic anhydrase XII	15.3	
	453941	U39817	Hs.36820	Bloom syndrome	14.3	
	443247	BE61438			12.0	
						•

	****	122524	14. 0050		
	428330 447342	L22524 Al199268	Hs.2256 Hs.19322	matrix metalloproteinase 7 (matrilysin,	12.0
	422163	AF027208	Hs.112360	Homo sapiens, Similar to RIKEN cDNA 2010 prominin (mouse)-like 1	11.7
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	11.4 11.2
5	424800	ALD35588	Hs. 153203	MyoD family inhibitor	10.2
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (10.0
	444190	AJ878918	Hs.10526	cysteine and glycine-rich protein 2	9.9
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	9.9
10	449340	AW235786	Hs.195359	hypothetical protein MGC10954	9.8
10	409731	AA125985	Hs.56145	frymosin, beta, identified in neuroblast	9.4
	439978 411411	BE139460 AA345241	Hs.124673	Homo sapiens cDNA FLJ11477 ffs, clone HE	8.9
	456516	BE172704	Hs.55950 Hs.222746	ESTs, Weakly similar to KIAA1330 protein KIAA1610 protein	8.9
	420092	AA814043	Hs.88045	ESTS	8.2 7.9
15	422631	BE218919	Hs.118793	hypothetical protein FLJ 10688	7.9
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	7.9
	438527	AI969251	Hs.115325	RAB7, member RAS oncogene family-like 1	7.9
	427581	NM_014788	Hs.179703	KIAA0129 gene product	7.8
20	418661	NM_001949	Hs.1189	E2F transcription factor 3	7.8
20	440684	AI253123	Hs.127356	ESTs, Highly similar to S21424 nestin (H	7.8
	429643 409638	AA455889 AW450420	Hs.167279	FYVE-finger-containing RabS effector pro	7.7
	444665	BE613126	Hs.21335 Hs.47783	ESTs B aggressive lymphoma gene	7.5
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	7.5 7.5
25	412777	Al335773	Hs.270123	ESTs	7.4
	436607	AW661783	Hs.211061	ESTs	7.3
	432058	AW665996	Hs.130729	ESTs. Weakly similar to ALU1_HUMAN ALU S	7.3
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	7.3
30	428976	AL037824	Hs.194695	ras homolog gene family, member I	7.2
30	433244	AB040943	Hs.271285	KIAA1510 protein	7.1
	436726 408432	AA324975 AW195262	Hs.128993	ESTs, Weakly similar to T00079 hypotheti	7.1
	434164	AW207019	Hs.148135	gb:xn67b05:x1 NCI_CGAP_CML1 Homo sapiens serine/threonine kinase 33	7.1
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	7.0 7.0
35	439726	AW449893	Hs.293707	ESTs. Weakly similar to 138598 zinc fing	7.0
	432656	NM_000246	Hs.3076	MHC class II transactivator	6.8
	431117	AF003522	Hs.250500	delta (Drosophila)-lika 1	6.8
	453387	AI990741	Hs.252809	ESTs	6.8
40	418821	AA436002	Hs.183161	ESTs	6.6
40	437034 411252	AA742643 AB018549	Hs.69328	gb:ny91c01.s1 NCI_CGAP_GC81 Homo sapiens MD-2 protein	8.6
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	6.5
	452953	AI932884	Hs.271741	ESTs. Weakly similar to A46010 X-linked	6.4 6.3
	433532	AW975367	113.211741	gb:EST387475 MAGE resequences, MAGN Homo	6.3
45	420311	AW445044	Hs.38207	Human DNA sequence from clone RP4-530115	6.3
	418097	R45137	Hs.21868	ESTs	6.2
	407304	AA565832		gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens	6.2
	435256	AF193766	Hs.13872	cytokine-like protein C17	6.1
50	449448	D60730	Hs.57471	ESTs	6.1
50	403790 425517	AF121179		abiAC131170 Hama resistant Electronia	6.0
	420674	NM_000055	Hs.1327	gb:AF121179 Homo sepiens liver (Chang L- bulyrytcholinesterase	6.0 6.0
	435542	AA687376	Hs.269533	ESTs	5.9
	418216	AA662240	Hs.283099	AF15q14 protein	5.8
55	439086	AF085947		gb:Homo sepiens full length insert cDNA	5.8
	408037	AW271720	Hs.42233	hypothetical protein FLJ10300	5.7
	412225	AW902042		gb:QV0-NN1022-170400-193-c02 NN1022 Homo	5.7
	436109 435005	AA922153	Hs.132760	hypothetical protein MGC15729	5.7
60	429149	U80743 AW193360	Hs.306094 Hs.197962	trinucleotide repeat containing 12 ESTs, Wealdy similar to 138022 hypotheti	5.7 5.7
	418113	AJ272141	Hs.B3484	SRY (sex determining region Y)-box 4	5.7 5.6
	405558		•		5.6
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	5.6
65	442547	AA306997	Hs.217484	ESTs, Wealty similar to ALU1_HUMAN ALU S	5.6
03	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprole	5.5
	420560 408096	AW207748 BE250162	Hs.59115	ESTs Churchelete and colors	5.5
	443539	AI076182	Hs.83765	dihydrofolate reductase	5.5
	426318	AA375125	Hs.134074 Hs.147112	ESTs, Moderately similar to ALU6_HUMAN A Homo sapiens cDNA: FLJ22322 fs, clone H	5.4
70	429115	AA446728	Hs.289020	Homo sapiens cDNA FLJ 14098 fs, clone MA	5.4 5.3
	453900	AW003582	Hs.226414	ESTs. Weakly similar to ALUS_HUMAN ALU S	5.3
	444168	AW379879		gb:RC1-HT0256-081199-011-f01 HT0256 Homo	5.3
	432789	D26351	Hs.3104	KIAA0042 gene product	5.3
75	437036	AI571514	Hs.133022		5.2
13	421247	BE391727	Hs.102910		5.2
	441523 451106	AW514263	Hs.301771		5.2
	457211	BE382701 AW972565	Hs.25960 Hs.32399	v-myc avian myelocytomatosis viral relat ESTs, Weakly similar to S51797 vasodilat	5.1
	454157	AW162906	Hs.312481	ESTs. Wealthy similar to S65668 hydrogen	5.1 5.1
80	423343	AA324643	Hs.246106	ESTs	5.1
	425292	NM_005824		37 kDa leucine-rich repeat (LRR) protein	5.1
	406679	AA070788		gb:zm66b07.r1 Stratagene neuroepithelium	5.1
	442671	A1005668	Hs.134779	EST	5.1
				200	

	433001	AF217513	Hs.279905	done HQ0310 PR00310p1	5.0
	418819	AA228776	Hs.191721	ESTs	5.0
	432946	U60899	Hs.279854	mannosidase, alpha, class 28, member 1	4.9
5	420730	NM_002691	Hs.99890	polymerase (DNA directed), delta 1, cata	4.9
)	441217	AJ922183	Hs.213246	ESTs	4.9
	453385	AW296101	Hs.252806	ESTs	4.8
	418203	X54942	Hs.83758	CDC28 protein kinase 2	4.7
	450813	AI739625	Hs.203376	ESTs	4.7
• •	444006	8E395085	Hs.10086	type i transmembrane protein Fn14	4.7
10	412530	AA766268	Hs.266273	hypothetical protein FLJ 13346	4.7
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	4.7
	429786	AL080232	Hs.220696	Homo sapiens mRNA; cDNA DKFZp586A061 (tr	4.7
	405771				4.6
	457065	Al476318	Hs.192480	ESTs	4.6
15	436190	AK001059		gb:Homo sapiens cDNA FLJ10197 fis, clone	4.6
	400859				4.6
	435267	N23797	Hs.110114	ESTs	4.6
	443454	AI057494	Hs.133421	ESTs	4.5
	452811	AA937079	Hs.118983	hypothetical protein FLJ12150	4.5
20	437267	AW511443	Hs.258110	ESTs	4.5
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	
	454269	AI961060	Hs.129908	KIAA0591 protein	4.5
	422106	D84239	Hs.111732	Fc fragment of IgG binding protein	4.5
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	4.5
25	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	4.5
	423756	AA828125	16.100023		4.5
	417308	H80720	Hs.81892	gb:od71a09.s1 NCI_CGAP_Ov2 Homo sapiens KIAA0101 gene product	4.5
	422170	AJ791949	Hs.112432	anti-Mullerian hormone	4.5
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	4.4
30	406568	AF088886	Hs.11590	cathepsin F	4.4
	426812	AF 105365	Hs.172613	solute carrier family 12 (potassium/chio	4.4
	402516	A 105505	113.112013	some carrier rainity 12 (porassiunivers)	4.4
	432865	AI753709	Hs.152484	CCT- Market al aller to 100000 to annie all	4.4
	413625	AW451103	Hs.71371	ESTs, Wealdy similar to I38022 hypotheti	4.4
35	436098	R20597	Hs.9739	ESTs	4.4
55	418333	W92113	LI2:31.73	glycerol-3-phosphate dehydrogenase 1 (so	4.4
	416933		14- 00000	gb:zh48e01.r1 Soares_fetal_liver_spleen_	4.4
	438192	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	4.4
	457374	AI859065	Hs.337620	Homo sapiens AFG3L1 Isoform 1 mRNA, part	4.3
40	433159	AA493662	U- 150507	gb:nh05d12s1 NCI_CGAP_Thy1 Homo sapiens	4.3
-10	444386	AB035898 BE065183	Hs.150587	kinesin-like protein 2	4.3
	453202		11- 00000	gb:RC1-BT0314-020200-012-c04 BT0314 Homo	4.3
		AW085781	Hs.26270	hypothetical protein FLJ11588	4.3
	441020	W79283	Hs.35962	ESTs	4.3
45	414733	BE514535	Hs.77171	minichromosome maintenance deficient (S.	4.3
73	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	4.3
	405701				4.3
	451659	BE379761	Hs.14248	ESTs	4.3
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	4.2
50	433323	AA805132	Hs.30701	ESTs	4.2
30	439811	AA135332	Hs.71608	ESTs	4.2
	415406	T26510		gb:AB282F8R Infant brain, LLNL array of	4.2
	436282	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4,1
	441269	AW015206	Hs.178784	ESTs	4,1
55	418727	AA227609	Hs.94834	ESTs	4.1
در	433006	8E242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	4.1
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	4,1
	430786	AA486144	Hs.31293	EST ₆	4.1
	445372	N36417	Hs.144928	ESTs	4.1
60	410555	U92649	Hs.64311	a disintagrin and metalloproteinase doma	4.0
UU	457465	AW301344	Hs.122908	ONA replication factor	4.0
	422094	AF129535	Hs.272027	F-box only protein 5	4.0
	442029	AW956698	Hs.14456	neural precursor cell expressed, develop	4.0
	459321	AW044477	Hs.299538	ESTs	4.0
65	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	4.0
UJ	420567	AK000812	Hs.98874	similar to proline-rich protein 48	4.0
	447004	AW296968	Hs.157539	ESTs	4.0
	448295	AJ381911	Hs.334859	KIAA1814 protein	3.9
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	3.9
70	440704	M69241	Hs.162	Insufin-like growth factor binding prote	3.9
70	453096	AW294631	Hs.11325	ESTs .	3.9
	457026	AA397620	Hs.48692	ESTs	3.9
	404642				3.9
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	3.9
75	430132	AA204685	Hs.234149	hypothetical protein FLJ20647	3.9
75	437718	AI927288	Hs.196779	ESTs	3.9
	438490	AW\$93272	Hs.301299	ESTs	3.9
	429919	AA460692	Hs.278945	hypothetical protein FLJ23024	3.9
	413604	R51767		gb;yg73g11.r1 Soares Infant brain 1NIB H	3.9
٥٨	425599	AW366745	Hs.214140	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.9
80	448796	AA147829	Hs.301431	endothelial zinc finger protein induced	3.9
	449300	AI656959	Hs.222165	ESTs	3.6
	452203	X57522	Hs.158164	transporter 1, ATP-binding cassette, sub	3.8
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	3.8

	404295				••
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	3.8 3.8
	428728	NM_016625	Hs.191381	hypothetical protein	3.8
5	409142 430172	AL136877 AA468591	Hs.50758 Hs.161889	SMC4 (structural maintenance of chromoso	3.8
,	447499	AW262580	Hs.147674	ESTs protocadherin beta 16	3.8
	405884			Protocoling in post 10	3.8 3.8
	437235	AW137B17	Hs.244353	ESTs	3.7
10	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	3.7
10	444143 425529	AW747996 NM_014656	Hs.160999 Hs.158282	ESTs, Moderately similar to A56194 throm KIAA0040 gene product	3.7
	425502	R98895	Hs.125823	ESTs	3.7 3.7
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.7
15	402424				3.7
13	429469 434072	M64590 H70854	Hs.27 Hs.283059	glycine dehydrogenase (decarboxylating;	3.7
	414872	U82010	Hs.77513	Homo sapiens PRO1082 mRNA, complete cds COX10 (yeast) homolog, cytochrome c oxid	3.7 3.7
	426071	AW138057	Hs.163835	ESTs	3.7
20	419078	M93119	Hs.89584	insulinama-associated 1	3.7
20	428037 416547	N47474 H62914	Hs.89230 Hs.268946	potassium intermediate/small conductance	3.7
	436899	AA764852	Hs.291567	ESTs. Wealtly similar to PC4259 ferritin ESTs	3.7 3.6
	436722	AW975977		gb:EST388086 MAGE resequences, MAGN Homo	3.6
25	440652	AJ215751	Hs.143977	ESTs	3.6
23	428450 452103	NM_014791	Hs.184339	KIAAD175 gene product	3.6
	409048	R42764 H59990	Hs.339654 Hs.37699	ESTs, Wealdy similar to 138022 hypotheti ESTs	3.6
	439546	AF088056	1.0.01000	gb:Homo sapiens full length insert cONA	3.6 3.6
20	443544	AI076315	Hs.16359	ESTs	3.6
30	418478 435889	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.6
	420301	AJ249107 AA767526	Hs.269901 Hs.22030	ESTS	3.6
_	438078	AI016377	Hs.131693	paired box gene 5 (B-cell lineage specif ESTs	3.6 3.6
26	408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	3.6
35	416871	H98716	11. 420000	gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	3.5
	424085 446291	NM_002914 BE397753	Hs.139226 Hs.14623	replication factor C (activator 1) 2 (40	3.5
	432281	AK001239	Hs.274263	interferon, gamma-inducible protein 30 hypothetical protein FLJ 10377	3.5 3.5
40	436123	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	3.5
40	411256	AW834039		gb:QV0-TT0010-091199-053-e09 TT0010 Homo	3.5
	419239 435065	AA468183 BE084391	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	3.5
	435532	AW291488	Hs.117305	gb:RC4-BT0310-110300-015-b08 BT0310 Homo Homo sapiens, clone IMAGE:3682908, mRNA	3.5
4.5	447101	N72185	Hs.44189	ESTs	3.5 3.5
45	410530	M25809	Hs.64173	ATPase, H+ transporting, lysosomal (vacu	3.5
	422156 453616	N34524	Un 22040	gb:yy56d10.s1 Soares_multiple_sclerosis_	3.5
	439743	NM_003462 AL389956	Hs.33846 Hs.283858	dynein, axonemal, light intermediate pol Homo sapiens mRNA full length insert cDN	3.5
60	453884	AA355925	Hs.36232	KIAA0188 gene product	3.5 3.5
50	424954	NM_000546	Hs.1846	turnor protein pS3 (Li-Fraumeni syndrome)	3.5
	420721 426764	AA927802	Hs.159471	ZAP3 protein	3.5
	420649	AA732524 AI866964	Hs.151464 Hs.124704	ESTs, Weakly similar to ALUC_HUMAN !!!! ESTs, Moderately similar to S65657 alpha	3.4
	448831	AL080123	Hs.22182	zinc finger protein 23 (KOX 16)	3.4 3.4
55	444371	BE540274	Hs.239	forkhead box M1	3.4
	402604 442407	AMACRERA	11. 2025		3.4
	414300	AW469584 AL304870	Hs.32353 Hs.188680	mitogen-activated protein kinase kinase ESTs	3.4
C C	444670	H58373	Hs.332938	hypothetical protein MGC5370	3.4 3.4
60	414550	BE379808		gb:601159567T1 NIH_MGC_53 Homo saplens c	3.4
	452211 414416	AI985513	Hs.233420	ESTs	3.4
	449961	AW409985 AW265634	Hs.76084 Hs.133100	hypothetical protein MGC2721 ESTs	3.4
	413257	8E075035	118.155100	gb:PM3-BT0584-260300-002-g05 BT0584 Homo	3.4 3.4
65	453857	AL080235	Hs.35861	DKFZP586E1621 protein	3.4
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	3.4
	422848 446189	BE513934 H85224	Hs.1583 Hs.214013	neutrophil cytosolic factor 1 (47kD, chr ESTs	3.4
	437385	AA757055	Hs.164060	EST\$	3.4 3.4
70	453652	AW009640	Hs.28368	ESTs, Moderately similar to \$65657 atpha	3.4
	408298	AJ745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	3,4
	455778 417546	BE088748 H65569	Hs.18845	gb:CM2-BT0693-210300-123-d09 BT0693 Homo	3.3
_	412471	M63193	Hs.73946	ESTs endothelial cell growth factor 1 (plate)	3.3
75	454631	AW811324		gb:/L3-ST0141-131099-017-A02 ST0141 Homo	3.3 3.3
	454294	AB000734	Hs.50640	JAK binding protein	3.3
	457131	AC002310	Hs.301463	Human Chromosome 18 BAC clone CIT987SK-A	3.3
	410102 449676	AW248508 AW380579	Hs.279727 Hs.209657	Homo sapiens cDNA FLJ14035 fis, clone HE	3.3
80	436211	AK001581	Hs.334828	ESTs hypothetical protein FLJ 10719; KIAA1794	3.3
	453746	AL120611		gb:DKFZp761H119_r1 761 (synonym; harmy2)	3.3 3.3
	452799	A1948829	Hs.213788	ESTs	3.3
	435380	AA579001	Hs.192221	ESTs .	3.3



	426746	J03626	Hs.2057	undine monophosphate synthetase (protat	. 13
	453362	H14988	Hs.107375	ESTs	3.3
	456473 416426	AI202788 AA180256	Hs.25682 Hs.210473	Homo sapiens mRNA for KIAA1863 protein.	3.3
5	445777	AI580371	Hs.145384	Homo sapiens cDNA FLJ14872 fs. clone PL ESTs	33
	423757	AL049337	Hs.132571	Homo sapiens mRNA; cDNA DKFZp564P016 (fr	3.3 3.3
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ 20099 fls, clone CO	3.3
	404299				3.3
10	404108 425189	H16622		phymacon of Course infant havin 1800 M	3.3
	449318	AW236021	Hs.78531	gb:ym26c07.r1 Soares infant brein 1NIB H Homo sapiens, Similar to RIKEN cDNA 5730	3.3 3.3
	450193	AI916071	Hs.15607	Homo sapiens Fanconi anemia complementat	12
	427725	U66839	Hs.180533	mitogen-activated protein kinase kinase	3.2
15	424051 418968	AL110203	Hs.138411	Homo seplens mRNA; cDNA DKFZp586J1922 (f	3.2
1.5	449248	NM_000078 M33782	Hs.89538 Hs.23391	cholesteryl ester transfer protein, plas Homo sepiens, Similar to transcription f	3.2
	439416	W58294	Hs.56254	ESTs	3.2 3.2
	401596	AA172106	Hs.110950	Rag C protein	3.2
20	408380	AF123050	Hs.44532	diubiquitin	3.2
20	450325 428730	AI935962 AA625947	Hs.26289 Hs.25750	ESTs ESTs	3.2
	457536	AA305233	Hs.278712	eutaryotic translation initiation factor	3.2
	426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (e	3.2 3.2
25	442710	Al015631	Hs.23210	ESTs	3.2
23	435232 430970	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	3.2
	416192	AJ018210 NM_005036	Hs.144083 Hs.998	ESTs	3.2
	446676	H09380	Hs.300965	peroxisome proliferative activated recep ESTs	3.2 3.2
20	451459	AJ797515	Hs.270560	ESTs, Moderately similar to ALU7_HUMAN A	3.2
30	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	3.2
	413840 448751	AI301558 BE551203	Hs.146381 Hs.201792	RNA binding motif protein, X chromosome	3.2
	432593	AW301003	Hs.51483	ESTs ESTs. Wealthy similar to hypothetical pro	12
~ ~	458786	AI457098	Hs.280848	ESTs	3.2 3.2
35	455909	BE156417	Hs.278798	ESTs	3.2
	419311	AA689591		gb:nv66a12s1 NCI_CGAP_GCB1 Homo sapiens	3.2
	439710 434559	AF086543 AF147315		gb:Homo sapiens full length insert cDNA	3.2
	455800	R22479	Hs.167073	gb:Homo sapiens full length insert cDNA Homo sapiens cDNA FLJ13047 fis, clone NT	3.1 3.1
40	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.1
	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	3.1
	437860 434182	AA333063 W20309	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	3.1
	417900	BE250127	Hs.118520 Hs.82906	G-protein gamma-12 subunit CDC20 (cell division cycle 20, S, cerevi	3.1
45	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12876 fis, clone NT	3.1 3.1
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	3.1
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo saplen	3.1
	447959 404589	AJ452784	Hs.270270	ESTs, Wealdy similar to 2109260A B cell	3.1
50	421764	AI681535	Hs.148135	serine/threonine kinase 33	3.1 3.1
	419986	AJ345455	Hs.78915	GA-binding protein transcription factor.	3.1
	416941	BE000150	Hs.48778	niban protein	3,1
	414761 449611	AU077228 AI970394	Hs.77256 Hs.197075	enhancer of zeste (Orosophila) homolog 2 ESTs	3.1
55	434746	AA648368	Hs.295368	ESTs	3.1 3.1
	434274	AA828539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	3.1
	427899	AA829286	Hs.332053	serum armytoid A1	3.1
	417642 452472	BE302665	Hs.105461	hypothetical protein FLJ20357	3.1
60	446131	AW957300 NM_000929	Hs.294142 Hs.290	ESTs, Weakly similar to C55663 oligodend phospholipase A2, group V	3.1
	440052	A1633744	Hs.195648	ESTs, Weakly similar to 138022 hypotheti	3.1 3.1
	426531	AA381071		gb:EST94100 Activated T-cells XII Homo s	3.1
	422158 406267	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.1
65	447039	AV661798	Hs.282915	ESTs	3.1
	404802	777007750	115.202313	COIS	3.1 3.1
	406927	M26460		gb:Homo sapiens (clone 104) retinoblasto	3.1
	419314	AW971924	Hs.87280	ESTs	3.0
70	435894 432140	A\$076667 AK000404	Hs.188011	ESTs	3.0
. •	443426	AF098158	Hs.272688 Hs.9329	hypothetical protein FLJ20397 chromosome 20 open reading frame 1	3.0
	425202	AW962282	Hs.152049	ESTs, Weakly similar to 138022 hypotheti	3.0 3.0
	407047	X65965		gb:H.sapiens SOD-2 gene for manganese su	3.0
75	418241	M26682	Hs.1149	LIM domain only 1 (rhombotin 1)	3.0
, ,	446599 412950	297832 BE018581	Hs.15476 Hs.245342	differentially expressed in FOCP (mouse	3.0
	428670	AA431682	Hs.134832	hypothetical protein FLJ14642 ESTs	3.0
	446975	BE246446	Hs.16695	ubiquitin-activating enzyme E1-like	3.0 3.0
80	437756	AA767537	Hs.197096	ESTs	3.0
00	416084 402374	L16991 AL135225	Hs.79006 Hs.301865	deoxythymidylate kinase (thymidylate kin	3.0
	443885	H91806	Hs.15284	dopachrome tautomerase (dopachrome delta ESTs	3.0
	434008	AA740878	Hs.112982	ESTs	3.0 3.0

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	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	3.0
	414239	AJ288330	Hs.182330	ESTs	3.0
	421013	M52397	Hs.1345	Mutated in colorectal cancers	
	424635				3.0
5		AA420687	Hs,115455	Homo sapiens cDNA FLJ14259 fis, clone PL	3.0
3	410276	A1554545	Hs.68301	ESTs	3.0
	433865	N29862	Hs.44104	ESTs	3.0
	406028				3.0
	401626				
		1110000		***	3.0
10	415949	H10562	Hs.21691	ESTs	3.0
10	418583	AA604379	Hs.86211	hypothetical protein	3.0
	417933	X02308	Hs.82962	thymidylate synthetase	3.0
	434577	R37316	Hs.179769		
				Homo sapiens cDNA: FLJ22487 fis, clone H	3.0
	430437	Al768801	Hs.169943	Homo sapiens cDNA FLJ 13569 fis, clone PL	3.0
1.5	427940	AA417812	Hs.38775	ESTs	29
15	456060	C14904	Hs.45184	Homo sapiens cDNA FLJ12284 fis, clone MA	29
	421988	AW450481	Hs.161333	ESTs	2.9
	448775	AB025237	Hs.388	nudix (nucleoside diphosphata linked moi	
	438598	AI805943			29
			Hs.326067	hypothetical protein MGC5178	2.9
20	429612	AF062649	Hs.252587	pituitary turnor-transforming 1	29
20	451189	AA016019	Hs.40905	ESTs	29
	401558				29
	426207	BE390657	Hs.30026	HSPC182 protein	
	404721		14.00020	nor orde protest	29
					2.9
26	401384				29
25	417288	Al984792	Hs.108812	hypothetical protein FLJ22004	2.9
	427648	AI376722	Hs.180062	proteasome (prosome, macropain) subunit.	2.9
	435928	H84345	Hs.183961	ESTs	
	431740	N75450			2.9
			Hs.183412	ESTs, Moderately similar to AF116721 67	29
20	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	2.9
30	439972	AI348100	Hs.124662	ESTs	2.9
	433112	AA973801	Hs.144553	ESTs, Weakly similar to unnamed protein	2.9
	423751	AW235633	Hs.46525	ESTs	2.9
	406748	AW339106	Hs.217493	annexin A2	
					29
25	422154	179045	Hs.126927	ESTs	2.9
35	405588				2.9
	440911	AA909536	Hs.143562	ESTs	2.9
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	2.9
	445043	AW014413	Hs.196066		
				ESTs	29
40	410114	AW590540	Hs.271280	ESTS	29
40	419217	AA504571		gb:aa60e12.r1 NCI_CGAP_GCB1 Homo sapiens	2.9
	415849	R20529	Hs.6806	ESTs	2.9
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	2.9
	453331	AI240665	Hs.8895	ESTs	
					2.9
15	432065	AA401039	Hs.2903	protein phosphatase 4 (formerly X), cata	2.9
45	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	29
	454377	AA076811		gb:7803C12 Chromosome 7 Fetal Brain cDNA	2.9
	421491	H99999	Hs.42736	ESTs	29
	452291	AF015592	Hs.28853		
	415446	F08898		CDC7 (cell division cycle 7, S. cerevisi	2.8
50			Hs.66075	ESTs	2.8
50	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	2.8
	427221	L15409	Hs.174007	von Hippel-Lindau syndrome	2.8
	422493	AW474183	Hs.250173	hypothetical protein FLI13158	2.8
	419451	AJ907117	Hs.90535	syntaxin binding protein 2	
	448789	BE539108	Hs.22051		2.8
55				hypothetical protein MGC15548	2.8
55	424126	AA335635	Hs.96917	ESTs	2.8
	458695	AV660159	Hs.282284	ESTs, Wealdy similar to 138022 hypotheti	2.8
	418973	AA233056	Hs.191518	ESTs	2.8
	440471	AA886146	Hs.307944	ESTs	2.8
	421016	AA504583	Hs.101047		
60	433647	AA603367		transcription factor 3 (E2A immunoglobul	2.8
55			Hs.222294	ESTs	2.8
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	2.8
	421723	AA620400	Hs.300717	sodium channel, voltage-gated, type III,	2.8
	434964	A1638850	Hs.130746	ESTs	2.8
	432022	AL162042	Hs.272348	Homo sapiens mRNA; cDNA DKFZo761L1212 (f	
65	400517	AF242388	Hs.149585		2.8
00				lengsin	2.8
	433023	AW864793	Hs.87409	thrombospondin 1	2.8
	448734	8E614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	2.8
	406736	AI254733	Hs.182426	ribosomal protein S2	2.8
	409207	AW373564	Hs.194637	BANP homolog, SMAR1 homolog	
70	440196				2.8
, 0		N72847	Hs.125221	EST8	2.8
	403961				28
	425193	. AW965689	Hs.22509	ESTs .	2.6
	425268	AI807883	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	2.8
	440483	AI200836	Hs.150386	EST8	
75	412391	AW947710	110.130300		2.8
				gb:RC0-MT0004-130300-011-e07 MT0004 Homo	2.8
	448769	N66037	Hs.38173	ESTs	2.8
	411632	AW854829		gb:QV2-CT0261-201099-011-01 CT0261 Homa	2.8
	438221	A1798853	Hs.122224	ESTs, Wealdy similar to ALU5_HUMAN ALU S	2.8
_	457578	AA578027		gb:n/20h01.s1 NCI_CGAP_HSC1 Homo sapiens	
80	455510	AA422029	Wr 14384A		2.8
			Hs.143640	ESTs, Weakly similar to hyperpolarizatio	2.8
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	2.8
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	2.8
	433800	AJ034361	Hs.135150	lung type-I cell membrane-associated gly	2.8
					2.0

	439662	H97552	Hs.269060	ESTs	2.8
	425694	U51333	Hs.159237	hexokinase 3 (white cell)	2.8
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin	2.8
5	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	2.8
3	447752	M73700	Hs.105938	lactotransferrin	2.8
	408761 453350	AA057264 AI917771	Hs.238936	ESTs, Wealdy similar to (defline not ava	2.8
	456529	AW891965	Hs.61790 Hs.279789	hypothetical protein FLI23338 histone deacetylase 3	27
	439538	AAB37323	Hs.164047	ESTs	2.7 2.7
10	458814	AM98957	Hs.170861	ESTs, Wealthy similar to Z195_HUMAN ZINC	27
	456029	BE255990	Hs.218329	hypothetical protein	27
	451129	BE072881		gb:RC2-8T0548-200300-012-e09 BT0548 Homo	27
	456412	AW749617	Hs.280776	tankyrase, TRF1-interacting ankyrin-reta	27
15	453536	AA137000	Hs.62578	ESTs	2.7
13	438378 425745	AW970529	Hs.88434	hypothetical protein FLJ21816	2.7
	446322	U44060 N23033	Hs.14427 Hs.155814	Homo sapiens cDNA: FLJ21800 fis, clone H	27
	451592	A1805416	Hs.213897	ESTs ESTa	27
	429466	M85835	Hs.12827	ESTS	27 27
20	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	27
	455514	AW983871		gb:RC1-HN0003-220300-021-h07 HN0003 Homo	2.7
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	27
	444207	AJ565004	Hs.79572	cathepsin D (lysosomal aspartyl protease	2.7
25	427421 449655	AA402414	Hs.3059	coatomer protein complex, subunit beta	2.7
23	422648	AJ021987 D86983	Hs.59970	ESTs	2.7
	428494	AA233439	Hs.118893 Hs.184634	Melanoma associated gene hypothetical protein FLJ20005	2.7
	406895	X60648	Hs. 172550	polypyrimidine tract binding protein (he	2.7
	453255	AA278167	Hs.19215	Homo sapiens, clone IMAGE:3605822, mRNA	2.7 2.7
30	427348	NM_014137	Hs.177258	PRO0650 protein	2.7
	435370	AI964074	Hs.225838	EST8	2.7
	407862	BE548267	Hs.50724	Homo sepiens cDNA FLJ10934 fis, clone OV	2.7
	411874	AA096106	Hs.20403	ESTs	2.7
35	421192 435899	AA833718 W89093	Hs.204529	KIAA1806 protein	2.7
55	414503	R58394	Hs.189914 Hs.25119	ESTs ESTs, Weakly similar to YEXQ_YEAST HYPOT	2.7
	453462	AL037291	Hs.236605	ESTs, Moderately similar to ALU4_HUMAN A	2.7 2.7
	436554	AI985810	Hs.301173	ESTs	2.7
40	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.7
40	403881			•	2.7
	431779	AW971178	Hs.268571	apolipoprotein C-I	2.7
	404984	05544434			2.7
	448275 446839	BES14434 BE091926	Hs.20830	kinesin-like 2	2.7
45	411927	BE274009	Hs.16244 Hs.772	mitotic spindle coiled-coil related prot	27
	404756	565, 4003	113.172	glycogen synthase 1 (muscle)	2.7 2.7
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	2.7
	422176	H80977		gb:yu89a11.s1 Soares fetal liver spleen	2.7
50	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	2.7
50	436532	AA721522		gb:nv54h12r1 NCI_CGAP_Ew1 Homo sapiens	2.7
	412833 457245	AW950547	Hs.298262	ribosomal protein \$19	2.7
	446861	A1745498 A1696519	Hs.204579 Hs.14427	ESTs	2,7
	453263	R91778	Hs.99369	Homo sapiens cONA: FLJ21800 fis, clone H ESTs	27
55	459385	BE380047	1.0.0000	gb:601159362F2 NIH_MGC_53 Homo sapiens c	2.7 2.7
	438764	AA824524	Hs.336452	ESTA	2.7
	429285	AI971081	Hs.20432	ESTs, Weakly similar to 138022 hypotheti	2.7
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	2.7
60	430037	BE409649	Hs.227789	mitogen-activated protein kinase-activat	2.7
oo	449892 454201	N73608	Hs.50309	ESTs	2.7
	452279	AB023191 AA286844	Hs.44131 Hs.61260	KIAA0974 protein	2.7
	427954	J03060	Hs.247551	hypothetical protein FLJ13164 metaxin 1	2.7 2.7
	400371	U80740		Thomas T	2.7
65	452449	AW068658	Hs.20943	ESTs .	2.7
	431114	AA492400	Hs.291015	ESTs .	2.7
	417088	M54915	Hs.81170	pim-1 oncogene	2.7
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	2.7
70	403680 454579	AW813110			2.7
	411968	AV013110 AJ207410	Hs.69280	gb:CM4-ST0189-051099-021-f05 ST0189 Homo Homo sapiens, clone IMAGE:3536299, mRNA,	2.7
	422240	R60594	Hs.29002	KIAA1706 protein	2.6
	424368	AB037766	Hs.146085	KIAA1345 protein	2.6 2.6
76	405808				26
75	419700	AF084935	Hs.92357	galactokinase 1	26
	435972	W95088	Hs.114198	ESTs	2.6
	453568	870782	Hs.557	adrenergic, alpha-1D-, receptor	2.6
	443725 444156	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
80	428209	AW500059 AA424197	Hs.85437 Hs.98947	ESTs, Highly similar to AF219140 1 gastr	2.6
	437640	AA764893	Hs.272155	ESTs, Wealdy similar to S33496 trypsin [ESTs, Wealdy similar to I38022 trypotheti	2.6
	453948	AJ970797	Hs.64859	ESTs. Wesley surings to 150022 hypother	2.6 2.6
	415402	AA164687	Hs.177576	mannosyl (alpha-1,3-)-glycoprotein beta-	2.6
					,
				340	•

	404000				
	425397	J04088	Hs.156346	topoisomerase (DNA) II atpha (170kD)	2.6
	418228	AA962181	Hs.111219	ESTs, Moderately similar to ALU1_HUMAN A	2.6
	401324				2.6
_	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	2.6
5	443210	AI692649	Hs.9451	hypothetical protein MGC13168	2.6
	457244	AA581385	Hs. 152473	ESTs, Weakly similar to I38022 hypotheti	
	417144	AA382104	Hs.81337		2.6
	433933	AI754389		lectin, galactoside-binding, soluble, 9	2.6
			Hs.133494	Homo sapiens done TCCCIA00164 mRNA sequ	26
10	437437	AA226869	Hs.16520	hypothetical protein DKFZp762L0311	2.6
10	434206	AW136973	Hs.288516	ESTs. Weakly similar to \$69890 mitogen I	2.6
	400992				2.6
	455530	AW984744		gb:RC1-HN0015-040400-011-d03 HN0015 Homo	26
	436139	AA765786	Hs.120936	ESTs	26
	448330	AL038449	Hs.207163	ESTs	26
15	412942	AL120344	Hs.75074	mitogen-activated protein kinase-activat	2.6
	432753	NM_014075	Hs.336938	Homo sapiens PRO0593 mRNA, complete cds	
	433430	AI863735	Hs.186755	ESTs	2.6
	436693	AW973223			2.6
			Hs.303197	B-cell CLUlymphoma 7C	2.6
20	429482	AF076974	Hs.203952	transformation/transcription domain-asso	2.6
20	432715	AA247152	Hs.200483	ESTs, Wealty similar to KIAA1074 protein	2.6
	414217	AJ309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	28
	434165	AA971328	Hs.95361	myosin VIIA (Usher syndrome 1B (autosoma	2.6
	414835	AA156720	Hs.185342	ESTs	2.6
~ -	424489	T48851	Hs.149250	O-siglec precursor,	2.6
25	436496	AA281959	Hs.5210	glia maturation factor, gamma	2.6
	403797			But have been topics, Actual	
	434573	AW372340	Hs.159717	ESTs	26
	418841	NM_002332	Hs.89137		2.6
	415785			low density (poprotein-related protein	2.6
30		R82419	Hs.23603	ESTs, Moderately similar to ALU8_HUMAN A	2.6
50	450608	AA010365	Hs.193229	ESTs .	2.6
	425304	AA463844	Hs.31339	fibroblast growth factor 11	26
	432268	BE311856	Hs.274230	3-phosphoadenosine 5-phosphosulfate sy	2.6
	410507	AA355288	Hs.40834	transitional epithelia response protein	2.6
25	427343	AJ880044	Hs.176977	protein kinase C binding protein 2	26
35	420917	AW135716	Hs.117330	ESTs	26
	414399	L47345	Hs.155202	transcription elongation factor 8 (SIII)	2.6
	446089	AI860021	Hs.270651	ESTs, Moderately similar to A47582 B-cel	
	440829	AF136407	Hs.7446		26
	408475	AA315514	Hs.47986	chromosome 6 open reading frame 5	2.6
40	450946	AA374569	Hs.127698	hypothetical protein MGC10940	2.6
70				ESTs, Moderately similar to 2109260A B c	26
	421462	AF016495	Hs.104624	aquaporin 9	2.6
	434846	AW295389	Hs.119768	ESTs	26
	422887	A1751848	Hs.49215	ESTs	2.6
40	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	2.6
45	437389	AL359587	Hs.271586	hypothetical protein DKFZp762M115	2.5
	408981	AW500797	Hs.49427	Gem-interacting protein	25
	432180	Y18418	Hs.272822	RuvB (E coli homolog)-like 1	
	418079	R40058	Hs.6911	ESTs	2.5
	437820	AA769062	Hs.323836		2.5
50	439685	AW956781	Hs.293937	ESTs, Wealty similar to attematively sp	2.5
50	425681			ESTs, Wealthy similar to FXD2_HUMAN FORKH	2.5
		AB018297	Hs.159183	KIAA0754 protein	2.5
	435177	AI018174	Hs.42936	ESTs	2.5
	437323	AA371145	Hs.226627	leptin receptor	2.5
C C	422114	AW194851	Hs.111801	arsenate resistance protein ARS2	2.5
55	448478	AI523218	Hs.203456	ESTs	2.5
	426623	AA382826	Hs.132793	ESTs	2.5
	448764	AI568607	Hs.182112	ESTs	2.5
	458385	AI051489	Hs.246214	ESTs	
	403726	N28939	Hs.13434	Homo sapiens clone 24418 mRNA sequence	2.5
60	444888	AI651039	Hs.148559	ESTs	2.5
	456179	H75490	Hs.271930		2.5
	424840	D79987	Hs.153479	ESTs	2.5
	406273			extre spindle poles, S. cerevisiae, homo	25
		NM_000919	Hs.83920	peptidylglycine alpha-amidating monocxyg	2.5
65	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.5
00	445936	BE543594	Hs.61478	hypothetical protein FLJ22329	2.5
	454967	AW848276		gb:IL3-CT0214-150200-074-E06 CT0214 Homo	2.5
	442303	AA989289	Hs.129169	ESTs	2.5
	456583	AF179897	Hs.104105	Meis (mouse) homolog 2	2.5
70	434263	N34895	Hs.44648	ESTs	2.5
70	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	
	424528	AW073971	Hs. 238954	ESTs, Weakly similar to KIAA1204 protein	2.5
	406038	Y14443	Hs.88219	zinc finger protein 200	2.5
	413495	Y12395			2.5
	423098	AA321980	Hs.315177	interferon-related developmental regulat	2.5
75			Hs.204682	ESTs	2.5
, 5	410817	A1262789	Hs.93659	protein disulfide isomerase related prot	2.5
	439841	AF038961	Hs.6710	mannose-P-defichel utilization defect 1	2.5
	453828	AW970960	Hs.293821	ESTs	2.5
	445034	AW293376	Hs.143659	ESTs	2.5
00	449620	BE407797	Hs.23794	checkpoint with forkhead and ring finger	
80	406876	AJ382286	Hs.180842	ribosomai protein L13	2.5
	412370	AW946614		ab-RC2-ET0021-280400.014 cas ===================================	2.5
	423642	AW452650	He 167140	gb:RC2-ET0021-280400-011-c05 ET0021 Homo	2.5
	430357		Hs.157148	hypothetical protein MGC13204	2.5
	~000	AW976789	Hs.165607	ESTs	25

	414853	U31116	Hs.77501	**************************************	• •
	416097	8E387371	Hs.118964	sarcoglycan, beta (43kD dystrophin-assoc hypothetical protein FLJ20085	2.5 2.5
	428619	AK002140	Hs.187378	hypothetical protein FLJ11278	25 25
_	413976	BE295452	Hs.75655	procollagen-proline, 2-oxoglutarate 4-di	25
5	445223	AW291553	Hs.254983	ESTs	2.5
	423925	X03833	Hs.1722	interleukin 1, alpha	2.5
	410165	BE560228	Hs.71869	apoptosis-associated speck-like protein	2.5
	406474				2.5
10	433908	AW298141	Hs.157975	ESTs	25
10	439755	AW748482	Hs.77873	B7 homotog 3	2.5
	437528	N\$9646	Hs.169745	crumbs (Drosophila) homolog 1	2.5
	420734	AW972872	Hs.293736	ESTs	2.5
	415346 419337	243108	N. 000070	gb:HSC13E071 normalized infant brain cDN	2.5
15	444606	AW291112 R09478	Hs.209978	ESTS	2.5
13	430061	AB037817	Hs.16041 Hs.230188	ESTs NIAA1396 protein	2.5
	413407	A1356293	Hs.75339		2.5
	411955	BE467339	Hs.280115	inositol polyphosphate phosphatase-like ESTs	2.5 2.5
	409278	AA346683	Hs.52763	anaphase-promoting complex subunit 7	2.5 2.5
20	403142		. 5.52. 00	are preserved by currency poor in 1	2.5
	401714				2.5
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	25
	416505	H66470	Hs.16004	ESTs	2.5
25	431518	AA743462	Hs.165337	ESTs	2.5
25	448623	BE613468	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	2.5
	428301	AW628666	Hs.98440	ESTs, Weakly similar to 138022 hypotheti	2.5
	404366				2.5
	449733	R74546	Hs.29438	Homo sapiens cDNA FLJ12094 fis, clone HE	2.5
30	459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapien	2.5
30	402856	AW939659		gh:RC0-DT0076-110100-031-c09 DT0076 Homo	2.5
	420751	J03019	Hs.99913	adrenergic, beta-1-, receptor	24
	436805	AA731533	Hs.270751	ESTs	2.4
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	2.4
35	453 496 453 853	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	24
55	407909	AL040600 AW103986	Hs.188083	EST8	2.4
	454630	BE142075		gb:xd63e06.x1 NCI_CGAP_Ov23 Homo sapiens	24
	451026	AA013218	Hs.157492	gb:CM3-HT0137-170999-012-f02 HT0137 Homo	2.4
	420779	L12398	Hs.99922	cer-d4 (mouse) homolog	2.4
40	438322	AA804170	Hs.221349	doparnine receptor D4 ESTs	2.4
	455908	BE158306	19.551943	gb:QV0-HT0367-150200-114-hD4 HT0367 Homo	2.4
	419625	U91616	Hs.91640	nuclear factor of kappa light polypeptid	2.4 2.4
	440773	AA352702	Hs.332541	Homo sapiens, Similar to RIKEN cDNA 2700	2.4
	450823	T81223	Hs.22011	complement-c1g tumor necrosis factor-ref	2.4
45	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	2.4
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	2.4
	451802	AI817711	Hs.209374	ESTs	2.4
	419417	R92491	Hs.39429	ESTs	2.4
60	407094	AF000574	Hs.22405	leukocyte immunoglobutin-tika receptor,	2.4
50	423567	BE252949	Hs.69331	hypothesical protein FLJ13633	2.4
	427501	AI369280	Hs.131743	ESTs	2.4
	451773	Z42044	Hs.26996	KIAA1278 protein	2.4
	435845	AA732297	Hs.113928	ESTs	2.4
55	431584	AW295121	Hs.266263	Homo sepiens cDNA FLJ14115 fis. clone MA	2.4
55	440614	AA781530	Hs.127236	hypothetical protein FLJ12879	2,4
	423721	AF176911	Hs.132004	cardiotrophin-like cytokine; neurotrophi	2.4
	452125 419508	BE312642 AW997938	Hs.28077	GOP-mannose pyrophosphorylase B	2.4
	453446	BE299996	Hs.90786	ATP-binding cassette, sub-family C (CFTR of)-50094457451 NIN MCC 17 Home regions a	24
60	419792	AA250890	Hs.190037	gb:500944574F1 NIH_MGC_17 Homo sepiens c ESTs	2.4
	452786	R61362	Hs.106642	ESTs. Weakly similar to T09052 hypotheti	2.4
	410447	AW816134		gb:MR3-ST0220-290100-016-e04 ST0220 Homo	2.4 2.4
	438662	AA223599	Hs.6351	cleavage and polyadenylation specific fa	24
	402408			go om polymonymont opount to	2.4
65	443950	NM_001425	Hs.9999	epithefial membrane protein 3	2.4
	414625	AA335738	Hs.76686	glutathione peroxidase 1	2.4
	403048			•	2.4
	432088	AA525454		gb:rri85c09.s1 NCI_CGAP_Pr20 Homo sapiens	2.4
70	431692	AL021331	Hs.267749	unc93 (C.elegans) homotog A	24
70	455023	AW850907		gb:IL3-CT0220-310100-065-H11 CT0220 Homo	24
	426249	F05422	Hs.168352	nucleoporin-like protein 1	2.4
	448795	AJ797713	Hs.156471	ESTs	24
	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.4
75	414252	AA346483	Hs.126191	ESTs	2.4
13	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	24
	427550	BE242818	Hs.179606	nuclear RNA helicase, DECO variant of DE	2.4
	404020		14. 45.455	At 1 AAA 1	2.4
	407846	AA426202	Hs.40403	Cop/p300-Interacting transactivator, wit	2.4
80	417222	AJ525424	Hs.42053	hypothetical protein MGC2383	2.4
50	443639 452706	BE269042 AW449390	Hs.9661	proteasome (prosome, macropain) subunit,	2.4
	492706	V1144373A	Hs.257150	ESTs, Moderately similar to SUR1_HUMAN S	2.4
	428882	AA435915	Hs.131748	ESTs Madagash similar to ALLIT MINAMA	2.4
			143.731740	ESTs, Moderately similar to ALU7_HUMAN A	2.4

	436277	R88520	Hs.120917	ESTs	2.4
	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	2.4
	405353				24
_	409193	AA131483		gb:zo08e05.r1 Stratagene neuroepithelium	2.4
5	431431	AL096711	Hs.252953	Human DNA sequence from clone RP3-403A15	2.4
	407889	R34556	Hs.30800	ESTs, Wealdy similar to S65657 alpha-1C-	24
	453335	AW857376	Hs.169238	fucosyftransferase 3 (galactoside 3(4)-L	24
	450621	AW297288	Hs.55918	hypothetical protein FL/11354	24
10	419652	AL157485	Hs.91973	hypothetical protein	24
10	421151	BE174431	Hs.63386	ESTs	2.4
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	2.4
	420681	AA847602	Hs.106510	ESTs, Moderately similar to ALU2_HUMAN A	2.4
	405288				24
15	453527	R49570	Hs.180236	EST ₆	2.4
כו	429875	AJ091815		gb:qa58b06.s1 Soares_NhHMPu_S1 Homo sapi	24
	436360	Al962796	Hs.136754	ESTs	24
	418592	X99226	Hs.284153	Fancoril anemia, complementation group A	2.4
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	24
20	449539	W80363	Hs.58446	ESTs .	2.4
20	419870	AW403911	Hs.266175	phosphoprotein associated with GEMs	24
	404584				2.4
	454276	AW294996	Hs.255374	ESTs	2.4
	423746	AW361817	Hs.132370	NADPH coldase 1	24
25	415558	AA885143	Hs.125719	ESTs	24
23	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	2.4
	406953	L36847	11. 44049	gb:Human (clone p17/90) rearranged iduro	2.4
	444471	AB020684	Hs.11217	KIAA0877 protein	2.4
	451031	Al360187	Hs.4254	ESTs	2.4
30	455302	AW997641		9b:RC6-BN0062-170200-011-D06 BN0052 Homo	2.4
50	449063	AJ627352	Hs.236547	Homo sapiens, clone IMAGE:2905978, mRNA	2.4
	401048	*********			2.4
	434420 425848	AA688278	Hs.194864	hypothetical protein FLJ22578	2.4
		BE242709	Hs.159637	valyl-tRNA synthetase 2	2.4
35	449086	A1628357	Hs.208037	ESTs	2.4
55	415238 448337	R37780	Hs.21422	ESTS	2.4
		AW206453	Hs.3782	ESTs	24
	416991	N36389	Hs.141296	KIAA0226 gene product	2.3
	412600	L28824	Hs.74101	spleen tyrosine kinase	2.3
40	418385 440769	AW590613	Hs.301040	Homo sepiens, clone IMAGE:3357127, mRNA,	2.3
70	450437	BE561793	Hs.21446	KIAA1716 protein	2.3
		X13956	Hs.24998	hypothetical protein MGC10471	2.3
	412035	N78559	Hs.293629	hypothetical protein MGC3121	2.3
	406739	A1566709	Hs.182426	ribosomal protein S2	2.3
45	418506	AA084248	Hs.B5339	G protein-coupled receptor 39	2.3
72	410286	AI739159	Hs.61898	DKFZP586N2124 protein	2.3
	443740 405605	R56434	Hs.21062	ESTs	2.3
	416913	AUAD24744		1 004 PT004 44444	2.3
	426509	AW934714 M31166	11- 0050	gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.3
50	445828	F05802	Hs.2050	pentaxin-related gene, rapidly induced b	2.3
50	457195		Hs.81907	ESTs	2.3
	420372	AB011099	Hs.196647	KIAA0527 protein	23
	423198	AW960049	Hs.293660	Homo sapiens, clone IMAGE:3535476, mRNA,	2.3
	457730	M81933 AW753613	Hs.1634	cell division cycle 25A	2.3
55	412014	AI620650	Hs.43761	gb:RC1-CT0268-060100-013-e01 CT0268 Homo	2.3
	447131	NM_004585	Hs.17466	ESTs, Weakly similar to A46010 X-linked	2.3
	446288	AW189209	Hs.149708	retinoic acid receptor responder (tazaro	2.3
	436954	AA740151	Hs.130425	ESTs EST-	2.3
	411658	AW855598	10.100123	ESTs gb:CM1-CT0278-031199-032-e08 CT0278 Homo	2.3
60	404240			80.000.0010011199-095-600 C10519 NOMO	2.3
	456094	H95091		gb:yw57a09.r1 Soares_ptacenta_8to9weeks_	23
	416951	AA190926	Hs.190785	ESTs, Moderately similar to S65657 alpha	2.3
	406737	AJ356586	507 50	gb:qy15h09.x1 NCI_CGAP_Brn23 Homo sapien	23
	458453	AI097452	Hs.135095	ESTs	2.3
65	452330	AI879127	Hs.191979	KIAA1733 protein	2.3
	408523	AW833259	Hs.314287	ESTS	2.3
	455470	AW947992	110.011201	gb:PM0-MT0011-240300-001-c09 MT0011 Hama	2.3
	436323	R17697	Hs.140963	ESTs. Weakly similar to (38022 hypotheti	2.3
	450000	AI952797	Hs.10888	hypothetical protein FLI21709	2.3
70	416171	H23896	Hs.125790	leucine-rich repeat-containing 2	23
-	419134	T89863	Hs.221771	ESTs	23
	445933	AV655733	Hs.293860	spinster-like protein	2.3
	422089	AA523172	Hs.103135	ESTs. Weakly similar to SFR4_HUMAN SPLIC	23 23
	449911	AI262106	Hs.12653	ESTs	
75	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	2.3 2.3
	411742	AW247593	Hs.71819	eukaryolic translation initiation factor	2.3 2.3
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-lik	
	423491	AA191765	Hs.129673	eukaryotic translation initiation factor	2.3 2.3
00	407182	AA312551	Hs.230157	ESTs	2.3
80	411448	AA178955	Hs.271439	ESTs, Weakly similar to 138022 hypotheti	2.3
	438644	AJ126162	Hs.129037	ESTs	2.3
	432691	U29725	Hs.3080	mitogen-activated protein kinase 7	2.3
	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	2.3
					2.5

	411125	AA151647	Hs.68877	machinen h 245 steha cabinastica	
	404054	20131047	12.00017	cylochrome b-245, alpha polypeptide	2.3
	430458	AA479300	Hs.225706	ESTs, Wealdy similar to 138022 hypotheti	2.3 2.3
_	440210	AW874562	Hs.125296	ESTs	23
5	445727	AB011095	Hs.16032	KIAA0523 protein	2.3
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	23
	438379	N23018	Hs.171391	C-terminal binding protein 2	23
	449919	A1674685	Hs.200141	ESTs	23
10	415293 441126	R49462	Hs.106541	ESTs	2.3
10	408203	NM_000429 AA053137	Hs.323715 Hs.42390	methionine adenosytransferase I, alpha	23
	434941	AW073202	Hs.334825	nasopharyngeal carcinoma susceptibility Homo sapiens cDNA FLJ14752 fis, clone NT	2.3
	450748	A1733093	Hs.130016	ESTs	23 23
	404185				23
15	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	2.3
	451370	AJ791929	Hs.300782	ESTs	2.3
	400034				2.3
	407723	AW071161	Hs.252873	ESTs	23
20	431320 429271	AW969474 AF039850	Hs.183070	ESTs	2.3
20	453707	AW003879	Hs.198515 Hs.126522	dead ringer (Drosophila)-like 1	2.3
	419225	U70073	113.120022	Homo sapiens, ctone MGC:16722, mRNA, com gb:HSU70073 Human Homo sapiens cDNA cton	23
	444556	AJ277924	Hs.145199	ESTs	23 23
25	405741				23
25	400917				23
	432567	AA736777	Hs.293770	EST8	23
	437949	U78519	Hs.41654	ESTs, Weakly similar to A46010 X-linked	2.3
	450514 418400	AC005785 BE243026	Hs.25059	A kinase (PRKA) anchor protein 8	2.3
30	444019	BE173977	Hs.301989 Hs.10098	KIAA0246 protein putative nucleolar RNA helicase	2.3
	406326	02110311	113.10030	Printing increase Law lieuresid	2.3
	412077	NS1107	Hs.47199	ESTs, Weakly similar to FLJ00004 protein	2.3 2.3
	427647	W19744	Hs. 180059	Homo sapiens cONA FLJ20553 fis, clone KA	23
25	414528	AA148950	Hs.188836	ESTs	2.3
35	414854	BE546797	Hs.51483	ESTs, Weakly similar to hypothetical pro	2.3
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	2.3
	439467 402627	AW292275	Hs.158365	ESTs	2.3
	451711	AK000461	Hs.26890	and and syndrome sharmonana malan and	23
40	424308	AW975531	Hs.154443	cat eye syndrome chromosome region, cand minichromosome maintenance deficient (S.	23
	423869	BE409301	Hs.134012	C1g-related factor	2.3 2.3
	405915				2.3
	431503	NM_012129	Hs.258576	claudin 12	2.3
45	423306	W88562	Hs. 108198	ESTs .	2.3
43	443232	AF161521	Hs.9081	phenylalanyl-IRNA synthetase beta-subuni	2.3
	433064 434437	D79991	Hs.30002	SH3-containing protein SH3GLB2; KIAA1848	2.3
	435191	AJ912566 BE407866	Hs.187813 Hs.170253	ESTs	23
	420006	H14429	Hs.94300	hypothetical protein FLJ23282 serologically defined colon cancer antig	23
50	447942	F12628	Hs.334786	hypothetical protein MGC16040	2.3 2.3
	403166			,,	2.3
	422119	A1277829	Hs.111862	KIAA0590 gene product	2.3
	403751				2.3
55	426451	A1908165	Hs.169946	GATA-binding protein 3	23
	427413 409091	BE547647 AW970386	Hs.177781 Hs.269423	hypothetical protein MGC5618	23
	440491	R35252	Hs.24944	ESTs ESTs, Wealdy similar to 2109260A B cell	2.3
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.3 2.3
40	405747				23
60	438210	AA780519	Hs.311601	EST	2.3
	404652	ACOFFORD	44- 44		2.3
	423524 426793	AF055989 X89887	Hs.129738 Hs.172350	potassium voltage-gated channel, Shaw-re	22
	444424	AJ654684	Hs.196377	HIR (histone cell cycle regulation defec ESTs	2.2
65	434031	BE384165	Hs.23723	pseudouridytate synthase 1	2.2
	427650	AW501245	Hs.252259	ribosomal protein S3	2.2 2.2
	435220	D50030	Hs.104	HGF activator	2.2
	438279	AAB05166	Hs.154762	HIV-1 rev binding protein 2	2.2
70	424668	D83702	Hs.151573	cryptochrome 1 (photolyase-like)	2.2
70	429961	BE246829	Hs.226770	OXFZP566C0424 protein	2.2
	442065 415198	AI831229 AW009480	Hs.128417	hypothetical protein FLJ 14009	2.2
	420538	AL117455	Hs.943 Hs.275438	natural killer cell transcript 4 histone deacetytese 7A	2.2
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	2.2
75	443753	AW387578	Hs.134749	ESTs	22
	423243	AA351938	Hs.23964	sin3-associated polypeptide, 18kD	22
	446572	AV659151	Hs.282961	ESTs .	22
	412247	AF022375	Hs.73793	vascular endothelial growth factor	2.2
80	421040	AA715026	Hs.135280	ESTs	2.2
	426212 455584	871824 BE007420	Hs.167988	neural cell adhesion molecule 1	2.2
	406851	AA609784	Hs.180255	gb:PM3-BN0142-200300-001-c04 BN0142 Homo major histocompatibility complex, class	2.2
	444153	AK001610	Hs.10414	hypothetical protein FLJ 10748	2.2 2.2
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5 10 15 20 25 30	418672 456261 415737 447554 405159 42177 446139 458339 401876 425079 41837 439664 431474 431474 431474 431474 431474 431474 431474 42262 441502 442504 44302 445502 44502 445566 427695 42564 43141 443070 445566 427695 42564 435666 427695 42564 435666 427695 42564 435666 427695 42564 435666 427695 42664 435666 427695 42664 435666 427695 42664 435666 427695 42664 435666 437695 436666 437695 436666 437695 436666 437695 436666 436666 437695 4366666 436666 436666 436666 436666 436666 436666 436666 436666 4366666 436666 436666 436666 436666 436666 436666 436666 436666 4366666 436666 436666 436666 436666 436666 436666 436666 436666 4366666 436666 436666 436666 436666 436666 436666 436666 436666 4366666 436666 436666 436666 436666 436666 436666 436666 436666 4366666 436666 436666 436666 436666 436666 436666 436666 436666 4366666 436666 436666 436666 436666 436666 436666 436666 436666 43666666 436666 436666 436666 436666 436666 436666 436666 436666 4366666 436666 436666 436666 436666 436666 436666 436666 436666 4366666 436666 436666 436666 436666 436666 436666 436666 436666 436666 436666 436666 436666 436666 436666 436666 436666 436666 4366666 436666 436666 436666 436666 436666 436666 436666 436666 43666	L4284 AA210718 AA210718 AA167626 AJ391598 AW661820 H77395 AW976853 AF086387 H09963 AA361743 AB015419 AL133990 NM_002265 AV647184 AW294544 NM_00947 AF035537 M32074 AA370599 AI302654 AW467376 AA368546 AW117261 BE388662 H95741 R88483 AA380153	Hs. 159743 Hs. 104157 Hs. 118743 Hs. 38119 Hs. 211413 Hs. 39749 Hs. 172843 Hs. 2257 Hs. 179881 Hs. 247710 Hs. 190642 Hs. 38070 Hs. 143601 Hs. 125785 Hs. 74519 Hs. 115521 Hs. 144055 Hs. 208024 Hs. 125914 Hs. 8984 Hs. 17914	ESTs ESTs, Weakly similar to KIAA0694 protein ESTs ESTs, Weakly similar to ALU1_HUMAN ALU S ESTs ESTs ESTs ESTs By:Homo sepiens full length insert cDNA vitronectin (serum spreading factor, som core-blinding factor, beta subunit preproprotactin-releasing peptide ESTs lymphoid nuclear protein related to AF4 hypothetical protein hCLA-tso ESTs, Weakly similar to CORB MOUSE CORNI primace, pohypeptide 2A (S&LO) REV3 (yeast homolog)-like, cstalytic sub gb:Human retinoic acid receptor gamma 2 ESTs ESTs ESTs ESTs ESTs ESTs Ig superfamily protein ESTs Homo sapiens chromosome 14 BAC 98L12	22 22 22 22 22 22 22 22 22 22 22 22 22
10 15 20 25 30	415737 447557 442757 442177 446139 401876 438339 401876 439566 439567 441837 430647 407739 424244 407739 424244 407170 405902 437902 447504 44767 44770 445554 44301 445554 44554	AJ391598 AW561820 H77395 AW976853 AF086387 H09963 AA361743 AB015419 AL133990 AL133990 AMM_002285 AV647184 AW294544 AW294544 AW294544 AW300537 M32074 AA770599 AL302654 AW467376 AA368546 AW317261 BE388662 H95741 R88483 AA380153	Hs.118743 Hs.36119 Hs.211413 Hs.3749 Hs.172843 Hs.2257 Hs.179881 Hs.247710 Hs.190642 Hs.38070 Hs.143601 Hs.125765 Hs.74519 Hs.115521 Hs.144055 Hs.208024 Hs.129640 Hs.129914 Hs.8984 Hs.129914 Hs.8984 Hs.17914	ESTs ESTs, Weakly similar to ALU1_HUMAN ALU S ESTs ESTs ESTs ESTs gb:Homo sapiens full length insert cDNA vitronectin (serum spreading factor, som core-binding factor, beta subunit preproprotactin-releasing peptide ESTs lymphoid nuclear protein related to AF4 hypothetical protein hCLA-tso ESTs, Weakly similar to CORB MOUSE CORNI primase, polypeptide 24 (58kD) REV3 (yeast homolog)-like, catalytic sub gb:Human retinoic acid receptor gamma 2 ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2
10 15 20 25 30	405159 442173 446139 458339 401876 419566 425079 441837 43064 431474 407739 42424 438057 412712 40502 401012 446505 442769 44254 443070 446566 427695 43790 446563 43790 446563 43790 446563 43790 446563 43790 43	AW561820 H77395 AW976853 AF086387 H09963 AA361743 AB015419 AL133990 NM_002285 AV647184 AW294544 NM_000947 AF035537 M32074 AA770599 AM302654 AW467376 AA368546 AW417261 BE388662 H95741 R88483 AA380153	Hs.211413 Hs.39749 Hs.172843 Hs.172843 Hs.2257 Hs.179881 Hs.247710 Hs.190642 Hs.38070 Hs.143601 Hs.143601 Hs.14561 Hs.14555 Hs.74519 Hs.115521 Hs.144055 Hs.28064 Hs.125914 Hs.8984 Hs.8984 Hs.19914	ESTs ESTs gb:Homo sapiens full length insert cDNA vitronectin (serum spreading factor, som core-blinding factor, beta subunit preproprodactin-releasing peptide ESTs hymphoid nuclear protein related to AF4 hypothetical protein hCLA-iso ESTs, Weakly similar to CORB MOUSE CORNI primace, polypeptide 24, (58LO) REV3 (yeast homolog)-like, cistalytic sub gb:Human retinoic acid receptor gamma 2 ESTs ESTs ESTs ESTs Ig superfamily protein ESTs	22 22 22 22 22 22 22 22 22 22 22 22 22
15 20 25 30	442177 4461339 401876 439566 439566 439566 431474 407739 424244 438057 412715 422385 401012 446502 437902 437902 447503 443070 445554 443070 445566 443073 445563 431468 415133 431468 415133	H77395 AW976853 AF086387 H09963 AA361743 AB015419 AL133990 NM_002285 AV647184 AW294544 NM_000947 AF035537 M32074 AA770599 AL302654 AW467376 AA386546 AW117261 BE388662 H95741 R88483 AA380153	Hs.39749 Hs.172843 Hs.172843 Hs.2257 Hs.179881 Hs.190642 Hs.38070 Hs.143601 Hs.125765 Hs.74519 Hs.115521 Hs.144055 Hs.208024 Hs.129640 Hs.8904 Hs.8984 Hs.17914	ESTs gb:Homo saciens full length insert cDNA vitronectin (serum spreading factor, som core-binding factor, bette subuntit preproprotactin-releasing peptide ESTs hymphoid nuclear protein related to AF4 hypothetical protein hCLA-tso ESTs, Weathy similar to CORB MOUSE CORNI primace, polypeptide 2A (58kO) REV3 (yeast homolog)-like, catalytic sub gb:Human retinoic acid receptor gamma 2 ESTs ESTs ESTs ESTs Ig superfamily protein ESTs	22 22 22 22 22 22 22 22 22 22 22 22 22
15 20 25 30	446139 458339 458339 439566 425079 441837 430644 431474 407739 407739 412715 422365 404170 405902 401012 445502 443021 42144 443021 42144 443021 42146 443070 445566 427695 427695 437319	H77395 AW976853 AF086387 H09963 AA361743 AB015419 AL133990 NM_002285 AV647184 AW294544 NM_000947 AF035537 M32074 AA770599 AL302654 AW467376 AA386546 AW117261 BE388662 H95741 R88483 AA380153	Hs.39749 Hs.172843 Hs.172843 Hs.2257 Hs.179881 Hs.190642 Hs.38070 Hs.143601 Hs.125765 Hs.74519 Hs.115521 Hs.144055 Hs.208024 Hs.129640 Hs.8904 Hs.8984 Hs.17914	ESTs gb:Homo saciens full length insert cDNA vitronectin (serum spreading factor, som core-binding factor, bette subuntit preproprotactin-releasing peptide ESTs hymphoid nuclear protein related to AF4 hypothetical protein hCLA-tso ESTs, Weathy similar to CORB MOUSE CORNI primace, polypeptide 2A (58kO) REV3 (yeast homolog)-like, catalytic sub gb:Human retinoic acid receptor gamma 2 ESTs ESTs ESTs ESTs Ig superfamily protein ESTs	22 22 22 22 22 22 22 22 22 22 22 22 22
15 20 25 30	401976 439566 439567 441837 430644 431474 437739 424244 438057 412715 422385 401012 445502 437902 447503 445554 443021 445554 443021 445556 447695 447695 447695 447695 447695 447695 447695 447695 447695 447695 447695 447695	AF085387 H09963 AA361743 AB015419 AL133990 NM_002285 AV647184 AW294544 NM_000947 AF035537 M32074 AA770599 AI302654 AW457376 AA368546 AW117261 BE388662 H95741 R88483 AA380153	Hs. 2257 Hs. 179881 Hs. 247710 Hs. 190642 Hs. 38070 Hs. 143601 Hs. 125785 Hs. 74519 Hs. 115521 Hs. 144055 Hs. 208024 Hs. 129640 Hs. 125914 Hs. 8984 Hs. 17914	gb:Homo sapiens full length insert cDNA vitronectin (serum spreading factor, som core-binding factor, beta subunit preproprotactin-releasing peptide ESTs hmphoid nuclear protein related to AF4 hypothetical protein hCLA-tso ESTs, Weathy similar to CORB MOUSE CORNI primase, polypeptide 2A (58kD) REV3 (yeast homolog)-like, catalytic sub gb:Human retinoic acid receptor gamma 2 ESTs ESTs ESTs Is g superfamily protein ESTs	22 22 22 22 22 22 22 22 22 22 22 22 22
15 20 25 30	439566 425073 431644 431474 437739 424244 438057 412715 422365 404170 405902 437902 401012 445502 443021 421141 443070 445566 427695 427693 431469 415183 437319	H09963 AA361743 AB015419 AL133990 NM_002285 AV647184 AW294544 NM_000947 AF035537 M32074 AA770599 AA302654 AW467376 AA368546 AW117261 BE388662 H95741 R88483 AA380153	Hs.179881 Hs.247710 Hs.190642 Hs.38070 Hs.143601 Hs.125785 Hs.74519 Hs.115521 Hs.144055 Hs.208024 Hs.129640 Hs.8904 Hs.8904 Hs.8984 Hs.17914	vitronectin (serum spreading factor, som corn-binding factor, beta subunit preproprotactin-releasing peptide ESTs hymphoid nuclear protein related to AF4 hypothetical protein NCLA-Iso ESTs, Weathy similar to CORB MOUSE CORNI primase, potypeptide 2A (S&LO) REV3 (yeast homolog)-like, estalytic sub gb:Human retinoic acid receptor gamma 2 ESTs ESTs Ig superfamily protein ESTs	22 22 22 22 22 22 22 22 22 22 22 22 22
20 25 30	425079 441837 430644 431474 407739 424244 438067 412716 406902 401012 446592 443021 44254 443070 446566 427693 431469 415183 4311469 415183 437319	H09963 AA361743 AB015419 AL133990 NM_002285 AV647184 AW294544 NM_000947 AF035537 M32074 AA770599 AA302654 AW467376 AA368546 AW117261 BE388662 H95741 R88483 AA380153	Hs.179881 Hs.247710 Hs.190642 Hs.38070 Hs.143601 Hs.125785 Hs.74519 Hs.115521 Hs.144055 Hs.208024 Hs.129640 Hs.8904 Hs.8904 Hs.8984 Hs.17914	vitronectin (serum spreading factor, som corn-binding factor, beta subunit preproprotactin-releasing peptide ESTs hymphoid nuclear protein related to AF4 hypothetical protein NCLA-Iso ESTs, Weathy similar to CORB MOUSE CORNI primase, potypeptide 2A (S&LO) REV3 (yeast homolog)-like, estalytic sub gb:Human retinoic acid receptor gamma 2 ESTs ESTs Ig superfamily protein ESTs	22 22 22 22 22 22 22 22 22 22 22 22 22
20 25 30	441837 430644 431474 437139 424244 438057 412715 422385 404170 405902 437902 442554 443021 445554 443021 445556 443021 441010 445556 447695 447695 447695 447693 44	AA361743 AB015419 AL133990 NM_002285 AV647184 AW294544 NM_000947 AF035537 M32074 AA770599 AI302654 AW487376 AA368546 AW117261 BE388662 H95741 R88483 AA380153	Hs.179881 Hs.247710 Hs.190642 Hs.38070 Hs.143601 Hs.125785 Hs.74519 Hs.115521 Hs.144055 Hs.208024 Hs.129640 Hs.8904 Hs.8904 Hs.8984 Hs.17914	core-binding factor, beta subunti preproprolactin-releasing peptide ESTs hmphoid nuclear protein related to AF4 hypothetical protein hCLA-iso ESTs, Weakly similar to CORB MOUSE CORNI primase, polypeptide 2A (58kD) REV3 (yeast homolog)-like, estalytic sub gb:Human retinoic acid receptor gamma 2 ESTs ESTs ESTs	22 22 22 22 22 22 22 22 22 22 22 22 22
20 25 30	431474 407734 42424 438057 412715 402365 404170 406902 401012 446504 443021 443070 446566 427693 431469 415183 431469 415183	AL133990 NM_002285 NM_002285 NM_00287 NM294544 NM_000947 AF035537 M32074 AA770599 AA770599 AA302654 AW467376 AA368546 AW117261 BE388662 H95741 R88483 AA380153	Hs. 190642 Hs. 38070 Hs. 143601 Hs. 125785 Hs. 74519 Hs. 115521 Hs. 144055 Hs. 208024 Hs. 125914 Hs. 8984 Hs. 8984 Hs. 1914	ESTs bymphoid nuclear protein related to AF4 hypothetical protein hCLA-iso ESTs, Wealdy similar to CORB MOUSE CORNI primase, polypeptide 2A (58kD) REV3 (yeast homolog)-like, catalytic sub gb:Human retinoic acid receptor gamma 2 ESTs ESTs ESTs Ig superfamily protein ESTs	22 22 22 22 22 22 22 22 22 22 22 22 22
20 25 30	407739 42424 438057 412715 405902 437902 437902 445502 442554 443021 443021 443021 443021 44556 427693 431468 415183 437319	NM_002285 AV647184 AW294544 NM_000947 AF035537 M32074 AA770599 AI302654 AW487376 AA368546 AW117261 BE386662 H95741 R88483 AA330153	Hs.38070 Hs.143601 Hs.125785 Hs.74519 Hs.115521 Hs.115521 Hs.1208024 Hs.129640 Hs.8904 Hs.8984 Hs.8984 Hs.8984	hymphoid nuclear protein related to AF4 hypothetical protein hCLA-tso ESTs, Weathy similar to CORB MOUSE CORNI primase, polypeptide 2A (58kD) REV3 (yeast homolog)-like, catalytic sub gb:Human retinoic acid receptor gamma 2 ESTs ESTs ESTs ESTs ESTs ESTs ES ts ES ts ES ts ES ts ES ts ES ts ES ts ES ts	2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2
25 30	42424 43805 412715 422385 404170 405902 437902 401012 445502 445502 443070 445566 427695 427695 437319	AV647184 AW7294544 NM_000947 AF035537 M32074 AA770599 AI302654 AW467376 AA368546 AW117261 BE388662 HS5741 R88483 AA380153	Hs.143601 Hs.125785 Hs.74519 Hs.115521 Hs.144055 Hs.208024 Hs.129640 Hs.8904 Hs.125914 Hs.125914 Hs.17914	hypothetical protein hCLA-iso ESTs, Wealdy similar to CORB MOUSE CORNI primase, polypeptide 2A (58k0) REV3 (yeast homolog)-like, catalytic sub gb:Human retinoic acid receptor gamma 2 ESTs ESTs ESTs Ig superfamily protein ESTs	2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2
25 30	412715 42235 404170 406902 437902 401012 446502 442554 443021 421141 443070 446569 427695 426503 431468 416185 437319	NM_000947 AF035537 M32074 AA770599 AI302654 AW467376 AA368546 AW117261 BE388662 HS5741 R88483 AA380153	Hs.144055 Hs.144055 Hs.208024 Hs.129640 Hs.129914 Hs.125914 Hs.125914 Hs.17914	ESTs, Weatry similar to CORB MOUSE CORNI primace, polypepide 2A (58k0) REV3 (yeast homolog)-like, catalytic sub gb:Human retinoic acid receptor gamma 2 ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTS ESTS	2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2
25 30	422385 404170 406902 437902 401012 446502 442554 443021 421141 443070 446566 427695 426503 431468 415185 437319	AF035537 M32074 AA770599 A302654 AW467376 AA368546 AW117261 BE386662 H35741 R85743 AA380153	Hs.115521 Hs.144055 Hs.208024 Hs.129640 Hs.8904 Hs.15914 Hs.8984 Hs.17914	REV3 (yeas) homology-like, catalytic sub gb:Human retinoic acid receptor gamma 2 ESTs ESTs ESTs Ig superfamily protein ESTs	2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2
25 30	404170 406902 437902 401012 446502 442554 443021 421141 443070 446566 427695 426503 431468 416185 437319	M32074 AA770599 AI302654 AW467376 AA368546 AW117261 BE388662 H95741 R88483 AA380153	Hs.144055 Hs.208024 Hs.129640 Hs.8904 Hs.125914 Hs.8984 Hs.17914	gb:Human retinoic acid receptor gamma 2 ESTs ESTs ESTs ESTs ESTs ESTs ESTs	2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2
30	406902 437902 401012 446502 442554 443021 421141 443070 446566 427695 426503 431468 416185 437319	AA770599 AI302654 AW467376 AA368546 AW117261 BE388662 H95741 R88483 AA380153	Hs.208024 Hs.129640 Hs.8904 Hs.125914 Hs.8984 Hs.17914	ESTs ESTs ESTs Ig superfamily protein ESTs	2.2 2.2 2.2 2.2 2.2 2.2 2.2
30	401012 446502 442524 443021 421141 443070 446566 427695 426503 431468 416185 437319	AI302654 AW467376 AA368546 AW117261 BE388662 H95741 R88483 AA380153	Hs.208024 Hs.129640 Hs.8904 Hs.125914 Hs.8984 Hs.17914	ESTs ESTs ESTs Ig superfamily protein ESTs	22 22 22 22 22 22 22
30	446502 442554 443021 421141 443070 446566 427695 426503 431468 416185 437319	AW467376 AA368546 AW117261 BE388662 H95741 R88483 AA380153	Hs.129640 Hs.8904 Hs.125914 Hs.8984 Hs.17914	ESTs Ig superfamily protein ESTs	2.2 2.2 2.2 2.2
30	442554 443021 421141 443070 446566 427695 426503 431468 416185 437319	AW467376 AA368546 AW117261 BE388662 H95741 R88483 AA380153	Hs.129640 Hs.8904 Hs.125914 Hs.8984 Hs.17914	ESTs Ig superfamily protein ESTs	2.2 2.2 2.2
	443021 421141 443070 446566 427695 426503 431468 416185 437319	AA368546 AW117261 BE388662 H95741 R88483 AA380153	Hs.8904 Hs.125914 Hs.8984 Hs.17914	lg superfamily protein ESTs	2.2 2.2
	443070 446566 427695 426503 431468 416185 437319	8E388562 H95741 R88483 AA380153	Hs.8984 Hs.17914	ESTs	2.2
	446566 427695 426503 431468 416185 437319	H95741 R88483 AA380153	Hs.17914	Homo sapiens chromosome 14 BAC 98L12	
	427695 426503 431468 416185 437319	R88483 AA380153			2.2 2.2
35	426503 431468 416185 437319	AA380153	Hs.172862	membrane-spanning 4-domains, subfamily A ESTs	22
35	416185 437319			gb:EST93093 Skin tumor I Homo sapiens cD	2.2
35	437319	AW248431	Hs.256526	nuclear prelamin A recognition factor	2.2
J J		AW975861 BE410958	Hs.47367 Hs.56406	KIAA1785 protein	2.2 2.2
	4UZU04	BC410330	15.50400	Homo saplens cDNA FLJ13549 fts, clone PL	2.2
	413335	AI613318	Hs.48442	ESTs	2.2
	408212	AA297567	Hs.43728	hypothetical protein	2.2
40	408169 451099	R52795	Hs.25954	interteukin 13 receptor, alpha 2	2.2 2.2
••	407335	AA631047	Hs.158761	Homo sapiens cDNA FLJ13054 fis, clone NT	22
	409715	W42591	Hs.23892	ESTs	2.2
	431921	N48466	Hs.58879	ESTs	2.2
45	443823 432458	8E089782 AI968598	Hs.9877 Hs.78768	hypothetical protein malignant cell expression-enhanced gene/	2.2 2.2
	419726	U50330	Hs.1274	bone morphogenetic protein 1	2.2
	423178	AI033140	Hs.124983	Homo sapiens mRNA; cDNA OKFZp564C142 (fr	2.2
	451089	AA903705	Hs.4190	Homo sapiens cDNA: FLJ23269 fs, clone C	2.2
50	415216 442242	A1825905 AV647908	Hs.193211 Hs.90424	Homo sapiens cDNA FLJ11421 fis, clone HE Homo sapiens cDNA: FLJ23285 fis, clone H	2.2 2.2
	441830	AA383104	Hs.42954	hypothetical protein DKFZp564D0372	2.2
	406660	X65371	Hs.172550		2.2
	443378 432558	AW392550 R97268	Hs.9280 Hs.177269	proteasome (prosome, macropain) subunit, ESTs	2.2 2.2
55	408146	R45621	Hs.81057	hypothetical protein MGC2718	22
	419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	2.2
	439444 438407	AJ277652 AJ457122	Hs.54578	ESTs, Weakly similar to 138022 hypotheti	2.2
	450184	AJ457122 W31096	Hs.129673 Hs.237617	eukaryotic translation initiation factor Homo sapiens, clone IMAGE:3447394, mRNA.	2.2 2.2
60	409130	BE076601	Hs.75658	phosphorylase, glycogen; brain	2.2
	428844	AW972635	Hs.301904		2.2
	429489 433042	AF008203 AW193534	Hs.204039 Hs.281895		2.2 2.2
	440658	H29142	Hs.143032		2.2
65	408204	AA454501	Hs.43666	protein tyrosine phosphatase type IVA, m	2.2
	427498 408006	NM_003926 H57654			2.7
	445703	AV654845	Hs.303345 Hs.27	ESTs, Wealdy similar to 138022 hypotheli glyche dehydrogenase (decarboxylating;	2.2 2.2
5 6	431446	AW294929	Hs.255369		22
70	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	2.2
	433099	NM_002504	Hs.3187 Hs.127797	nuclear transcription factor, X-box bind	2.2
	415857 415245	AA866115 N59650	Hs.27252	Homo sapiens cDNA FLJ11381 ffs, clone HE ESTs	2.7
	443657	R14973		gb:yf42f10.s1 Soares fetal liver spleen	2.2
75	402521	AW501218	Hs.108945	KIAA0515 protein	2.2
	414819	BE177320	Hs.156148		2.2
	446530 415797	AV658909 Al291896	Hs.282642 Hs.72800	PESTS ESTS	2:
	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.3
80	453028	AB006532	Hs.31442	RecQ protein-like 4	2.3
	412133 407881	U83460 AW072003	Hs.73614 Hs.40968	solute carrier family 31 (copper transpo	2:
	437033	AW248364	Hs.5409	heparan suffate (glucosamine) 3-O-suttot RNA polymerase I subunit	2.
				345	4-0

	422732	AA577455	Hs.24937	Proce former 2 states (Line 2 states)	••
	416388	AJ417358	Hs.73677	transformer-2 sipha (htra-2 sipha) ESTs	2.2 2.2
	452849	AF044924	Hs.30792	hook2 protein	2.2
5	446615	BE513202	Hs.15589	PPAR binding protein	2.2
3	428361 446279	NM_015905 AA490770	Hs.183858 Hs.182382	transcriptional intermediary factor 1 ESTs	2.2
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	2.2 2.2
	403969	-			2.2
10	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-recept	2.2
10	429738 447091	AF125304 AW089648	Hs.212680	tumor nacrosis factor receptor superfami	22
	422017	NM_003877	Hs.157779 Hs.110776	ESTs, Weakly similar to CA17_HUMAN COLLA STAT induced STAT inhibitor-2	2.2 2.2
	426728	NM_007118	Hs.171957	triple functional domain (PTPRF interact	2.2
1.5	438726	AB033103	Hs.6385	KIAA1277 protein	22
15	453315	BE544203	Hs.24831	ESTs	2.2
	423244 433610	AL039379 AA806822	Hs.209602 Hs.112547	ESTs, Wealdy similar to ubiquitous TPR m	2.2
	429451	BE409861	Hs.202833	ESTs heme oxygenase (decycling) 1	2.2 2.2
••	417980	R32235		gb:yh67f08.r1 Soares placenta Nb2HP Homo	2.2
20	406347				2.2
	414406 401827	BE297904		gb:601177814F1 NIH_MGC_17 Homo sapiens c	22
	446913	AA430650	Hs.16529	fransmembrane 4 superfamily member (tetr	2.2 2.2
	452294	AI871925	Hs.117895	ESTs, Moderately similar to A47582 B-cel	2.2
25	404084			•	22
	456786	AK002084	Hs.132851	hypothetical protein FLJ11222	2.2
	435031 442609	AI632091 AL020996	Hs.115877 Hs.8518	ESTs selenoprotein N	2.2
	439732	AW629604	Hs.167641	hypothetical protein from EUROIMAGE 1703	21 21
30	421506	BE302796	Hs. 105097	thymidine kinase 1, soluble	21
	439253	AF086064	Hs.332252	ESTs	21
	409669 429574	AW177551 BE268321	Hs.220255 Hs.208912	hypothetical protein MGC13098 hypothetical protein MGC861	2.1
	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	2.1 2.1
35	408945	AW015089	Hs.4964	DKFZP586J1624 protein	21
	447687	A1627947	Hs.150186	hypothetical protein DKFZp566K1946	. 2.1
	459584 439130	AI910884 AA306090	Hs.207898 Hs.124707	ESTs ESTs	2.1
	428180	Al129767	Hs.182874	guanine nucleotide binding protein (G pr	21 21
40	442028	AI239437	Hs.48945	ESTs	2.1
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Horno	2.1
	443609 417164	AV650231 AA338283	Hs.282941 Hs.81361	ESTs, Highly similar to A Chain A, Human	2.1
	444534	AW271626	Hs.42294	heterogeneous nuclear ribonucleoprotein ESTs	2.1 2.1
45	438391	AI262248	Hs.25027	ESTs	21
	442003	AW297497	Hs.201891	ESTs	2.1
	456278 416976	BE300369 BE243985	Hs.289038 Hs.80680	hypothetical protein MGC4126 major vault protein	21 21
	417810	D28419	Hs.82609	hydroxymethylbilana synthase	21
50	445242	BE156478	Hs.21108	ESTs, Wealty similar to ALU1_HUMAN ALU S	2.1
	452712	AW838616		9b:RC5-LT0054-140200-013-D01 LT0064 Homo	2.1
	434926 421564	BE543269 AB007864	Hs.50252 Hs.105850	mitochondrial ribosomal protein L32 KIAA0404 protein	2.1
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	2.1 2.1
55	432742	AA564453	Hs.162339	ESTB	21
	435958	H98180	Hs.117975	ESTs	21
	421531 410431	AA713505 BE261320	Hs.291769 Hs.158196	ESTs transcriptional adaptor 3 (ADA3, yeast h	2.1
	420503	AI570943	Hs.337546	ESTs	2.1 2.1
60	448127	A1478416	Hs.282883	ESTs, Weakly similar to ALU1_HUMAN ALU S	21
	452897	BE066058	Hs.269233	ESTs, Moderately similar to 178885 serin	2.1
	447112 406577	H17800	Hs.7154	ESTs	2.1 2.1
	437162	AW005505	Hs.5484	thyroid hormone receptor coactivating pr	2.1
65	451460	AJ797550	Hs.209652	ESTs	2,1
	447402	H54520	Hs.18490	hypothetical protein FLJ20452	2.1
	435828 436396	AA700705 AI683487	Hs.13852	ESTs	2.1
	420582	BE047878	Hs.152213 Hs.99093	wingless-type MMTV integration site fami Horno sapiens chromosome 19, cosmid R2837	21 21
70	452020	AA722012	Hs.255757	ESTs, Weakly similar to AT2A_HUMAN POTEN	21
	415585	Z45481		gb:HSC2QE041 normatized infant brain cDN	2.1
	452620 457066	AA436504 BE 244613	Hs.119286	ESTS	2.1
	435472	BE244613 AW972330	Hs.158272 Hs.283022	ESTs, Wealty similar to CA13 MOUSE COLLA triggering receptor expressed on myeloid	2.1
75	431741	AA514783	Hs.191701	ESTs	2.1 2.1
	446840	AW294828	Hs.209203	ESTs	21
	440818	A1147060	Hs.146726	ESTs	2.1
	410174 400822	AA306007	Hs. 59 461	DKFZP434C245 protein	2.1
80	412760	AW379030	Hs.41324	EST8	2.1 2.1
	410653	BE383768	Hs.65238	95 kDa retinoblastoma protein binding pr	2.1
	426925	NM_001196	Hs.315689	Homo sapiens eDNA: FLJ22373 fis, clone H	21
	424242	AA337476	Hs.293984	hypothetical protein MGC13102	2.1

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	452560	BE077084	Hs.335432	EST ₅	21
	456437	AJ924228	Hs.115185	ESTs. Moderately similar to PC4259 femi	2.1
	458922	BE501831	Hs. 282053	EST8	21
5	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	21
,	419488	AA316241	Hs.90691	nucleophosmin/hucleoplasmin 3	21
	411829	AW865749	N= 22452	gb:QV3-SN0021-100500-185-c03 SN0021 Homo	21
	457192 422128	AL135682 AW881145	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	2.1
	452571	W31518	Hs.34665	gb:QV0-QT0033-010400-182-a07 QT0033 Homo ESTs	2.1 2.1
10	423699	H41850	Hs.131846	PCAF essociated factor 65 alpha	21
	405610	1141000	112.101010	To associate factor of april	21
	453638	AW814996		gb:MR1-ST0206-170400-024-h09 ST0206 Homo	2.1
	418856	AA362858		gb:EST72900 Ovary II Homo saplens cDNA 5	2.1
	437523	D63880	Hs.5719	chromosome condensation-related SMC-asso	21
15	410908	AA121686	Hs.10592	ESTs	2.1
	420221	N25991	Hs.43725	ESTs	2.1
	424739	AA346108	Hs.221610	ESTS	2.1
	425398	AL049689	Hs.156369	hypothetical protein similar to tenascin	2.1
20	424901	Z11933	Hs.182505	POU domain, class 3, transcription facto	2.1
20	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	21
	415635	F13168	Ha 02727	gb:HSC3JF101 normalized infant brain cDN	21
	418181 407103	U37012 AA424881	Hs.83727	cleavage and polyadenylation specific fa	21
	454389	AW752571	Hs.256301	hypothetical protein MGC13170	21
25	400021	A4132311		gb:IL3-CT0213-170100-055-F02 CT0213 Homo	2.1 2.1
	439228	N51700		gb:yy72d01.s1 Soares_multiple_sclerosis_	21
	456505	AA504595	Hs.111418	ESTs	2.1
	405258			==:=	21
	444645	A1184564	Hs.101654	ESTs	2.1
30	430246	AI269069	Hs.109268	hypothetical protein FLJ12552	2.1
	458687	AW024815	Hs.170088	GLUT4 enhancer factor	21
	403857				2.1
	400258				2.1
35	422221	AA306649	Hs. 169370	FYN oncogene related to SRC, FGR, YES	2.1
33	441054	AA913591	Hs. 126480	ESTs	2.1
	452700	A1859390	Hs.288940	five-span transmembrane protein M83	2.1
	454606	AW809752	N= 00010	gb:MR4-ST0124-181299-020-b06 ST0124 Homo	2.1
	448954 443148	AB014564 Al034357	Hs.22616 Hs.211194	KIAA0664 prolein	2.1
40	453486	AL039201	Hs.173554	ESTs, Wealdy similar to ALUS_HUMAN ALU S	2.1
	437695	AA769202	Hs.192142	ubiquinol-cytochrome c reductase core pr ESTs	21 21
	425449	X52056	Hs.157441	spicen focus forming virus (SFFV) provir	2.1
	447270	AC002551	Hs.331	general transcription factor IIIC, polyp	21
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	2.1
45	436382	AW977063	Hs.250181	ESTs	2.1
	435837	Al689210	Hs.187276	Homo sapiens cONA FLJ11431 fs. clone HE	2.1
	458287	AA987556	Hs.12867	ESTs	21
	423794	BE551781	Hs.231895	ESTs	21
50	408049	AW076098	Hs.74316	desmoplakin (OPI, OPII)	2.1
50	402721 451999	AW176401	Hs.27424	DEADRE (Ass. Ch. Ale AssAffet have selvere	2.1
	417541	AI992191	Hs.180040	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep hypothetical protein FLJ22439	21
	414857	AW402389	Hs.920	modulator recognition factor i	2.1 2.1
	435760	AF231922	Hs.213004	chromosome 21 open reading trame 62	21
55	428086	AL110193	Hs.224137	hypothetical protein	21
	447853	AI434204	Hs.164285	ESTs, Wealthy similar to AFG1_YEAST AFG1	21
	419034	NM_002110	Hs.89555	hemopoietic cell kinase	2.1
	431019	NM_005249	HS.2714	forkhead box G1B	21
60	421084	AI245432	Hs.101382	turnor necrosis factor, alpha-induced pro	2.1
60	416435	AI431301	Hs.179703	KIAA0129 gene product	2.1
	437014	AA808757	Hs.222531	ESTs. Weakly similar to S59501 interfero	21
	459369	T83080		gb:yd40e03.r1 Soares fetal liver spleen	21
	402239 412280	AW205116	Us 770044	handthalland and all Chief To an are a man	2.1
65	426012	AA367507	Hs.272814 Hs.75874	hypothetical protein DKFZp434E1723	2.1
05	438885	AI886558	Hs.184987	pregnancy-associated plasma protein A	21
	426076	AW962714	113.10-307	gb:EST374787 MAGE resequences, MAGG Homo	2.1 2.1
	404561			Borco. or an anochood on contract	21
	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	21
70	408175	W29089	Hs.19066	hypothetical protein DKFZp667O2416	2.1
	423867	AA331886		gb:EST35757 Embryo, 8 week I Homo seplen	21
	458604	W37944	Hs.4007	Sarcolemmal-associated protein	21
	409650	T08490	Hs.288969	HSCARG protein	2.1
75	401729				2.1
75	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	21
	456741	W37608	Hs. 184492		21
	417037	BE083936	Hs.80976	antigen identified by monoclonal antibod	2.1
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	2.1
80	439262 403108	AA832333	Hs.333045	ESTs	21
-0	436718	AW015227	Hs.289053	hypothetical protein FLJ14733	21
	440696	AI762757	Hs.187660		2.1 2.1
	409745	AA077391	,	gb:7B14E12 Chromosome 7 Fetal Brain cONA	2.1
				Promise and an annual section of the control of the	2.1

	450405				
	453485 418177	BE620712	Hs.33026	hypothetical protein PP2447	21
	457292	N44967 AI921270	Hs.5663 Hs.334882	ESTS	2.1
	454434	AA083558	Hs.261286	hypothetical protein FLJ14251 ESTs	21
5	406085	74 100000	19201200	E318	2.1 2.1
	424441	X14850	Hs.147097	H2A histone family, member X	2.1
	422726	U11690	Hs.1572	faciogenital dysplasia (Aarskog-Scott sy	21
	424576	BE154142	Hs.96833	ESTS	2.1
10	423660	AL045228	Hs.130831	Homo sapiens mRNA; cDNA DKFZp434L137 (tr	2.1
10	403509 441940	AF231919 AW298115	Hs.18759	KIAA0539 gene product	2.1
	439190	AW978693	Hs.128152 Hs.293811	ESTs ESTs	21
	417791	AW965339	Hs.111471	ESTS	21 21
	423701	AA329856	Hs.143022	ESTs	21
15	427239	BE270447	Hs.174070	ubiquitin carrier protein	21
	459642	BE243103		gb:TCAAP2E0949 Pediatric acute myelogeno	21
	450385	AI631024	Hs.24948	synuclein, alpha interacting protein (sy	21
	425159 425591	NM_004341 AW294734	Hs.154868	carbamoyi-phosphate synthetase 2, aspart	21
20	445101	175202	Hs.279727 Hs.12314	Homo sapiens cDNA FLJ14035 fis, clone HE Homo sapiens mRNA; cDNA DKFZp586C1019 (f	21
	412811	H06382	Hs.21400	ESTs	21 21
	426359	AF134157	Hs.169487	Kreisler (mouse) mal-related leucine zip	21
	435924	AW029203	Hs.191952	ESTs	2.1
25	418388	R72332	Hs.29258	Homo sepiens cDNA FLJ11384 fis, clone HE	2.1
23	452235 452313	AL039743	Hs.28514	testes development-related NYD-SP21	2.1
	450704	Y00486 H85157	Hs.28914 Hs.40696	adenine phosphoribosyltransferase ESTs	2.1
	427539	AA405205	Hs.97960	ESTs, Weakly similar to T51146 ring-box	2.1
	402028			Edia, Freday analo to 101140 mg oox	2.1 2.1
30	405362				2.1
	414718	H95348	Hs.107987	ESTs	2.1
	433424 444875	R68252 Al200759	Hs.163566 Hs.44737	ESTs ESTs	21
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	2.0
35	456072	H54381		gb:yq89a03.s1 Soares fetal liver spleen	2.0 2.0
	436331	A1239495	Hs.120169	EST ₈	2.0
	448418	243704	Hs.21192	Homo sapiens clone 25155 mRNA sequence	2.0
	447250	AI878909	Hs.17883	protein phosphatase 1G (formerly 2C), ma	2.0
40	448192 448966	R43915 AW372914	Hs.4958 Hs.86149	ESTs phosphoinositol 3-phosphate-binding prot	2.0
. •	408605	AF025374	Hs.46465	T-cell, immune regulator 1	2.0 2.0
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	2.0
	436872	X15624		gb:Human H1 RNA	20
45	432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKFZp434K1815 (I	2.0
73	446307 436588	T50083 AA759233	Hs.9094 Hs.126506	ESTs ESTs	2.0
	452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13329 fs, clone OV	20 20
	430420	AW140027	Hs.26373	Homo sapiens cDNA: FLJ23449 fs, clone H	2.0
50	432036	AF224266	Hs.272373	interleukin 20	2.0
50	414460	L00727	Hs.898	dystrophia myotonica-protein kinase	20
	433507 427964	Al817336 AA418082	Hs.191791 Hs.98286	ESTs	2.0
	443108	W86975	Hs.203707	ESTs, Wealthy similar to T20655 hypotheti ESTs	2.0
	434504	AI887341	Hs.121590	hypothetical protein FLJ 12827	2.0 2.0
55	454310	AW818390	Hs.175613	homolog of Xenopus Claspin	2.0
	443566	AI290284	Hs.159872	EST ₈	2.0
	449722 452682	BE280074 AA456193	Hs.23960	cyclin B1	2.0
	412362	AW945484	Hs.9071 Hs.184252	progesterone membrane binding protein ESTs, Weakly similar to ALUB_HUMAN ALU S	2.0
60	429341	X73874	Hs.2393	phosphorylase kinase, alpha 1 (muscle)	2.0 2.0
	435863	AF255346	Hs.62919	Jun dimerization protein p21SNFT	2.0
	400774	R58624	Hs.2186	eukaryotic translation elongation factor	2.0
	453944 419227	AW975369	Hs.292570	Homo sapiens, clone IMAGE:3502107, mRNA,	2.0
65	448529	BE537383 T26460	Hs.89739 Hs.22550	cholinergic receptor, nicotinic, beta po ESTs	2.0
	443206	AB011420	Hs.9075	serine/threonine kinase 17a (apoptosis-i	2.0 2.0
	439360	AA448488	Hs.336629	ribosomal protein L44	2.0
	436660	AI658870	Hs.184513	ESTs .	20
70	449030	AI365582	Hs.57100	Homo sapiens mRNA for FLJ00016 protein,	2.0
, 0	411048 406624	AK001742 AF052762	Hs.67991	hypothetical protein DKFZp434G0522	2.0
	450666	T99968	Hs.18799	gb:Homo saplens clone csneg8-1 immunoglo ESTs, Wealdy similar to I38022 hypotheti	2.0
	446143	BE245342	Hs.305079	sec61 homolog	2.0 2.0
76	437698	R61837	Hs.7990	ESTs, Moderately similar to 184505 celci	2.0
75	426607	AA382330	Hs.124223	ESTs	2.0
	449246 422564	AW411209	Hs.23363	hypothetical protein FLJ10983	2.0
	432682	AJ148008 AJ376400	Hs.222120 Hs.159588	ESTs ESTs	2.0
00	422140	8E295918	Hs.112193	mutS (E. coli) homolog 5	2.0 2.0
80	408215	BE614290	Hs.43812	syntaxin 10	2.0
	417129	AI381800	Hs.300684	catcitonin gene-related peptide-receptor	2.0
	442772	AW503680 AW015595	Hs.5957	Homo sapiens clone 24416 mRNA sequence	2.0
	434928	V1101000	Hs.4267	Home sepiens clones 24714 and 24715 mRNA	2.0

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	411380	AW841619	15- 043000	gb:RC1-CN0017-120200-012-b09 CN0017 Homo	2.0
	430603 425905	AA148164 AB032959	Hs.247280 Hs.318584	HBV associated factor novel C3HC4 type Zinc finger (ring finge	20 20
	401125	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	15.510001	notes conton type think makes (in a major	20
5	412939	AW411491	Hs.2186	eukaryotic translation elongation factor	20
	448740 454390	BE250632 AB020713	Hs.8026 Hs.56966	sestrin 2 KIAA0906 protein	20 20
	415012	NM_004383	Hs.77793	c-src tyrosine kinase	20
	410407	X56839	Hs.63287	carbonic anhydrase IX	20
10	403478				20
	456485 430294	AI393037 AI538226	Hs.97871 Hs.32976	Homo sapiens, clone IMAGE:3845253, mRNA, guanine nucleotide binding protein 4	20 20
	411669	BE612676	Hs.303116	stromal cell-derived factor 2-like 1	20
	451944	AW445218	Hs.210876	ESTS	2.0
15	436395	AJ227900		gb:Homo sapiens partial mRNA; ID EE2-168	2.0
	456457	AA252905 060920	Hs.194477	E3 ubiquitin ligase SMURF2 KIAA0130 gene product	20
	449123 409214	AW405967	Hs.23106 Hs.333388	Homo sapiens, clone IMAGE:3957135, mRNA,	2.0 2.0
••	437619	AW351491	Hs.334853	hypothetical protein FLJ23544	20
20	453348	BE272318	Hs.8595	hypothetical protein FLJ12438	2.0
	424382 447079	AA351898	Hs.23539	ESTs Worlds similar to 4 (002)/22 2 (U.s.)	20
	449501	AA280057 AJ552924	Hs.105280 Hs.231942	ESTs, Wealtry similar to dJ963K23.2 [H.sa ESTs	20 20
~~	422893	X98411	Hs.121555	myosin IF	20
25	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	20
	434845 410422	BE267057 AL042014	Hs.325321 Hs.334698	hypothetical protein R32184_1 Homo sapiens, clone MGC:15203, mRNA, com	20 20
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	451656	BE327088	Hs.212752	EST ₆	2.0
30	442068	BE312873	Hs.314932		2.0
	446846	AW197626	Hs.271901	ESTs, Moderately similar to S08686 finge	20
	442690 454277	AI014727 AW295069	Hs.160047 Hs.31743	ESTs, Weakly similar to 828096 line-1 pr ESTs, Weakly similar to Z157_HUMAN ZINC	2.0 2.0
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35	402798				2.0
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	TABLE 25	KQ.			
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40	CAT num		e cluster numb		
	Accession	n: Gen	bank accessio	n numbers	
	Pkey	CAT Number	Arrossina		
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	409745 410447	115237_1 1203929_1		AI347618 AI361453 AI088754 AW207491 AW960912 AA9218 BE063456 AW748795 BE150839	1/4 AA286833 AA150/22 BE152353 AW168822 BE152450
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	411380	1242343_1		AW851958 AW851851 AW851985	
	411832 411658	1252361_1 1252987_1		AW854805 AW854841 AW854825 AW854822 AW854830 AV AW855608 BE148763 BE148764 AW855645 AW855615 AW	
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55	412225	1284108_1	AW902042	N77591	
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	414550	14609901	BE379808		
	415346	1534581_1		6295 R13085	
	415406 415586	1536026_1 1540116_1		7926 R53367 2393 T74437	
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70	410000	175_2			W268271 AA055366 AW629027 AA677404 AA831618 AU124782 AA889402
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	420352	192979_1		AW968316 AA258918 AW843305 R14744 AI580388 BE0719	723 R36280
	422128	211994_1	AW88114	5 AA490718 M85637 AA304575 T06067 AA331991	
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80	422176	212714_1		W32951 H62656 H53902 R88904 AW835732 E147695 AA305496 AW962366 AA436754	
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AA381071 AA381084 AA380862
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AL120811 BE006189 BE006189
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BE142075 BE142148 BE142189 AW816249 BE142147 BE142002 BE142406 BE142094 BE142020 BE142074 BE142347 BE142000 BE142375
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                TABLE 25C:
                Pkey:
Ref.
                                         Unique number corresponding to an Eos probeset
Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
                                         sequence of human chromosome 22' Dunham, et al. (1999) Nature 402:489-495. Indicates DNA strand from which exons were predicted.
                Strand:
  60
                Nt_position:
                                          Indicates nucleotide positions of predicted exons.
                Pkey
400822
                                                                   Nt_position
186223-186402,186878-187275
                                                  Strand
                               7465000
                                                 Plus
                400859
400917
                               9757499
                                                  Minus
                                                                   91888-92018,98131-98294,99474-99570
  65
                               7283186
                                                  Minus
                                                                   173259-173631
                 400992
                                                                   140390-140822
                               8096828
                                                  Plus
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401048
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7232177
                                                                   736-1137
132430-132761
                                                  Minus
                                                 Plus
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234057-234174
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                                                 Plus
Minus
                401384
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7139678
                                                                   58360-58545
103510-104090
                                                  Plus
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                               8575943
                                                                   238100-238432
                                                  Minus
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                               9965536
                                                  Plus
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96484-96681
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2262095
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                                                  Minus
                401827
                                                  Plus
                401876
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7139781
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                                                  Plus
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38175-38304,42133-42266
                               8117294
                                                  Plus
                               7690131
                                                  Plus
                402408
                               9796239
                                                                   110326-110491
                402424
                               9796344
                                                  Minus
                                                                   64925-65073
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	402516	9798099	Minus	195342-195511
	402604	9909420	Plus	20393-20767
	402627	9931216	Plus	12138-12272,16487-16628,17654-17798,18494-18621,18933-19089,20669-20790,21134-21298,22866-22973,23688-23820,26626-
_				26895, 29279-29469
5	402721	8969253	Minus	144428-144715
	402798	3355547	Plus	23596-23867
	402856	9801288	Minus	90119-90411
	403048	4210991	Plus	44275-44592,49656-49 955
10	403108	8980955	Plus	93253-93667
10	403142	9444521	Plus	89286-90131
	403166	9838127	Minus	67762-67940,68695-68856,70394-70507
	403478	9958258	Plus	116458-116564
	403680	7331517	Minus	157184-157415
	403751	7229815	Minus	158794-160929
15	403790	8084957	Minus	87826-87947,89835-90002
	403797	8099896	Minus	123065-125008
	403857	7708910	Minus	2524-3408
	403881	7710245	Minus	107250-107685,108924-109213
~~	403961	7596976	Minus	110393-110603
20	403959	8569909	Plus	31237-31375,32405-32506
	404020	8655966	Minus	174449-174563
	404054	35 48785	Plus	66713-69175
	404084	9944055	Plus	2795-2969
	404108	8247074	Mirrus	63603-64942
25	404170	9930793	Plus	168836-169248
	404185	4572584	Minus	129171-129327
	404240	5002624	Minus	116132-116407,116653-116922
	404295	9856663	Minus	75747-75947
20	404299	5738652	Minus	3826-4025
30	404366	9964977	Plus	96589-96801
	404554	7243881	Plus	42637-42839
	404561	9795980	Minus	69039-70100
	404584	9857511	Plus	138651-139153
25	404589	9931665	Minus	32824-32985
35	404642	9796810	Plus	102999-103145
	404652	9796969	Minus	108172-108296
	404721	9856648	Minus	173763-174294
	404756	7706327	Ptus	82849-83627
40	404802	4581357	Minus	3093-30600
40	404984	6939882	Plus	87221-87505
	405159	9966252	Plus	79659-79804
	405258	7329310	Plus	129930-130076
	405288	6139075	Minus	126268-126436
45	405353	2811095	Plus	118525-118892
43	405362	2337862	Minus	105008-105142,105980-106091,140445-140556,142519-142641
	405558	1621110	Plus	4502-4644,5983-6083
	405588	5002511	Plus	46180-46366
	405605	5836195	Minus	117070-117270
50	405701	4263751	Plus	93243-93364
30	405741	9966947	Minus	158747-156875,156936-157208
	405747	8469069	Minus	153933-154060
	405771	7018349	Plus	91191-91254,91510-91589
	405808	9929207	Plus	109758-111166
55	405884	6758747	Plus	62383-62583
55	405915	7712162	Minus	43717-43859
	406028 406085	8312303	Minus	177469-177829
	406169	9123888 6684220	Plus	18665-18843 12620-14251
	406267		Minus	
60	406326	7528342 9212385	Minus	2570-2731
O	406347	9212385	Plus Plus	84508-84655
	406474	9795567	Plus	90900-91091
	406577	7711730	Plus	52758-53211 11377-11600
	406610	8312226	Plus	11377-11509 13096-13334
65	-20010	₩.ZZZ	F-143	TORAC HOUSE
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TABLE 26A: ABOUT 582 GENES SIGNIFICANTLY DOWN-REGULATED IN GUIDBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES
Table 26A fists about 582 genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on the
Affymetrix/Eco Hxt3 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 3. The "average" normal CNS level was set to the 65° percentile amongst various normal CNS level was set to the 65° percentile amongst various timor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10° percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey:
Unique Eos probeset identifier number
Exemptiar Accession number, Genbank accession number
UnigenelD:
Unigene Title:
Unique agene title
Ratio of 75° percentile normal central nervous system tissue to 85° percentile tumor 70

75

00	Pkey	ExAcon	UnigenelD	Unigene Title	R1
80	453655	AW960427	Hs.79059	transforming growth factor, beta recepto	136.7
	417275	X63578	Hs.295449	parvalbumin	29.0
	430829	AW451999	Hs.194024	ESTs	25.7
	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype	22.6

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	419954	D14720	Hs.93883	myelin protein zero (Charcot-Marie-Tooth	21.2
	459247	N46243	Hs.110373	ESTs, Highly similar to 142626 secreted	18.5
	416133	NM_001683 AW138239	Hs.89512	ATPase, Ce++ transporting, plasma membra	15.5
5	416018 417167	AW206437	Hs.78977 Hs.4290	proprotein convertase subtilisin/kexin t	15.2
9	433940	H05129	Hs.7459	ESTS	14.8
	413324	V00571	Hs.75294	cyclic AMP-regulated phosphoprotein, 21 conticotropin releasing hormone	13.4 13.1
	439830	AA846666	Hs.151489	ESTs, Weakly similar to XE7_HUMAN PROTEI	12.6
	408068	AW148652	Hs.167398	ESTs -	12.6
10	412636	NM_004415	Hs.74316	desmoplakin (OPI, OPII)	12.5
	429096	AB011106	Hs.196012	KIAA0534 protein	12.2
	412638	AA910199	Hs.203838	ESTs	12.2
	423690	AA329648	Hs.23804	ESTs, Wealdy similar to PN0099 son3 prot	12.1
15	456844	Al264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	11.9
13	418318 442593	U47732 R39804	Hs.84072 Hs.31961	transmembrane 4 superfamily member 3	10.9
	446353	A1290919	Hs. 153661	ESTs ESTs	10.8
	420290	AW977318	Hs.194480	ESTs	10.4
	414220	BE298094	14.154100	gb:601118231F1 NIH_MGC_17 Homo sapiens c	10.3 10.3
20	414290	AJ568801	Hs.71721	ESTs	10.2
	426365	AA376667	Hs.10283	RNA binding motif protein 8B	10.0
	414937	R38698	Hs.12382	ESTs	10.0
	419643	F06066	Hs.91791	chromosome 11 open reading frame 25	9.5
25	407173	T64349		gb:yc10d08.s1 Stratagene lung (937210) H	9.5
23	412454	RS5745	Hs.167330	EST8	9.5
	439368 415315	AF100143 F12240	Hs.6540	fibroblasi growth factor 13	9.4
	441790	AW294909	Hs.250655 Hs.132208	prothymosin, atpha (gene sequence 28) ESTs	9.3
	448117	H49129	Hs.172982	ESTs	9.2
30	400661	1140120	15.172302	Cors	9.1 9.0
	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	9.0
	412453	R20205	Hs.167330	ESTs	9.0
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	8.9
25	409031	AA376836	Hs.76728	ESTs	8.7
35	428106	BE620016	Hs. 182470	PTD010 protein	8.3
	446544	AI631932	Hs.7047	ESTs, Wealthy similar to Unknown (H.sapie	8.2
	423479 439480	NM_014326 AL038511	Hs.129208	death-associated protein kinase 2	8.2
	418036	Z37976	Hs.125316 Hs.83337	ESTs, Weakly similar to \$33990 finger pr	8.2
40	456490	U83171	Hs.97203	latent transforming growth factor beta b small inducible cytokine subfamily A (Cy	8.0
. •	410200	AA082557	Hs.101915	Stargardt disease 3 (autosomal dominant)	8.Q 8.O
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (I	8.0
	408428	NM_014787	Hs.44896	Dna.1 (Hsp40) homolog, subfamily 8, membe	7.9
4.5	437073	AI885608	Hs.94122	ESTs	7.9
45	408434	AW195317	Hs.107716	hypothetical protein FLJ22344	7.9
	438150	AA037534	Hs.79059	transforming growth factor, beta recepto	7.9
	440209	H05049	Hs.22269	neurexin 3	7.8
	408119 417421	W26213	Hs.101672	ESTs, Wealdy similar to T00331 hypotheti	7.8
50	410587	AL138201 AA370706	Hs.82120 Hs.86412	nuclear receptor subfamily 4, group A, m	7.8
	429611	AI889077	Hs.211388	chromosome 9 open reading frame 5	7.8
	405800	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	113.211.300	Homo sapiens BAC clone CT8-60N22 from 7q	7.7 7.7
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	7.7
	426356	BE536838	Hs.98682	hypothetical protein FKSG32	7.7
55	423440	R25234	Hs.143434	contactin 1	7.7
	445148	AI214510	Hs.146304	ESTs	7.6
	416294	D86980	Hs.79170	KIAA0227 protein	7.6
	424087 437479	N89333	Hs.143434	contactin 1	7.6
60	405071	R61866	Hs.101277	ESTs	7.5
	421224	AW402154	Hs.125812	ESTs .	7.5
	442025	AW887434	Hs.11810	CDA11 protein	7.4 7.4
	459476	BE185844		gb:fL5-HT0731-110500-087-c08 HT0731 Homo	7.2
	430573	AA744550	Hs.136345	ESTs	7.1
65	401836				7.1
	448958	AB020651	Hs.22653	KIAA0844 protein	7.1
	430152	AB001325	Hs.234642	equaporin 3	7.1
	419474	AW968619	Hs.155849	ESTa	7.1
70	401780	AA358760			7.1
	446052 423605	AF047826	He 120007	gb:EST67699 Fetal tung II Homo sapiens c	7.0
	433098	AW190593	Hs.129887 Hs.151143	cadherin 19, type 2 ESTs	7.0
	449511	AI436187	Hs.296261	guanine nucleotide binding protein (G pr	7.0
	451285	AW137912	Hs.227583	Homo sapiens chromosome X map Xp11,23 L-	6.9 6.8
75	428414	AL049980	Hs.184216	DKF2P564C152 protein	6.8
	419273	BE271180	Hs.293490	ESTs, Weakly similar to 138022 hypotheti	6.8
	443155	R\$4485	Hs.23772	ESTs	6.8
	450561	R49674	Hs.25909	ESTs	6.8
80	433068	NM_006456			6.8
50	440729 448426	AA904739	Hs.128204		6.8
	423589	BE018315 AA328082	Hs.280776 Hs.209569		6.7
	415681	AI379882	Hs.72630	ESTs	6.6
					6.5

	417510	F13044		± 110000001101	
	413510 427992	Y15014	Hs.181353	gb:HSC3HH101 normalized infant brain cDN	6.4
	453344	BE349075	Hs.44571	UDP-Gat:belaGicNAc beta 1,3-galactosyttr ESTs	6.4
_	450642	R39773	Hs.7130	copine IV	6.4
5	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	6.4 6.4
	429322	D86984	Hs.199243	KIAA0231 protein	6.4
	444927	AW016637	Hs.199425	ESTs	6.4
	447482	AB033059	Hs.18705	KIAA1233 protein	6.4
10	400332	S56407	Hs.248032	FLT4	6.3
10	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	6.3
	446129 454076	AW244073 AW204712	Hs.145946	ESTs	6.3
	425526	AA359933	Hs.61957	ESTs gb:EST69040 Fetal lung II Homo sapiens c	6.3
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	6.3
15	434273	AA913143	Hs.26303	ESTs	6.3 6.2
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	6.2
	451301	AI769514	Hs.209890	EST	6.2
	430754	AW862610	Hs.157068	ESTs	6.2
20	438356	AA805530	Hs.48527	ESTs	6.2
20	422743 453355	BE304678	Hs.119598	ribosomal protein L3	6.2
	426388	AW295374 AW081394	Hs.31412 Hs.97103	Homo sapiens cDNA FLJ11422 fis, clone HE	6.2
	452502	AI904296	113.57 103	ESTs gb:PM-87046-220199-286_1 87046 Homo sapi	6.2
	402546	14004230		80% mo (040-550 (32-500) 8 (040 Little 250	6.1 6.1
25	457534	AI781307	Hs.232226	ESTs	6.1
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	6.1
	404958				6.1
	432501	BE546532	Hs.25682	Homo sepiens mRNA for KIAA1863 protein,	6.1
30	442979	AW440782	Hs.174743	ESTs .	6.1
50	422262 408713	AL022315 NM_001248	Hs.113987 Hs.47042	lectin, galactoside-binding, sotuble, 2	6.0
	454065	BE394588	ns.47042	ectoriucleoside triphosphate diphosphohyd gb:601311808F1 NIH_MGC_44 Homo sapiens c	6.0
	430004	U27768	Hs.227571	regulator of G-protein signatting 4	6.0 5.9
	401521			regulate of protein eight = 1g 4	5.9
35	425087	R62424	Hs.126059	ESTs	5.9
	446298	AF187813	Hs.14637	kidney- and liver-specific gene	5.9
	417761	R13727	Hs.21435	ESTs	5.9
	424806 441695	AA382523	Hs.105689	MSTP031 protein	5.9
40	457483	T12411 AB034694	Hs.183745 Hs.272558	hypothetical protein FLJ13456 endomucin-1	5.9
. •	417175	R44558	Hs.94002	ESTs	5.9
	437483	AL390174	10.51002	gb:Homo sapiens mRNA; cDNA DKFZp547J184	5.8 5.8
	436427	A1344378	Hs.143399	ESTs	5.8
40	411939	AI365585	Hs. 146246	ESTs	5.8
45	459053	A1807052	Hs.210361	ESTs	5.7
	411052	AW814950		gb:MR1-ST0208-130400-023-d06 ST0206 Homo	5.7
	431063	Z98949	Hs.326843	hypothetical protein bk125H2.1	5.7
	450382 408478	AA397658 NM_000806	Hs.60257 Hs.45740	Homo sapiens cDNA FLJ13598 fis, clone PL	5.7
50	442676	AI733585	Hs.130897	gamma-aminobutyric acid (GABA) A recepto ESTs	5.7
	446443	AV659082	Hs.134228	ESTs	5.7 5.7
	400865				5.7
	459080	AW192083	Hs.290855	ESTs	5.6
55	407952	AI215902	Hs.88845	ESTs, Highly similar to T50835 hypotheti	5.6
JJ	431984 425705	AL080239	Hs.272284	Human DNA sequence from clone GS1-256O22	5.6
	442238	AF007833 AW135374	Hs.159265 Hs.270949	kruppel-related zinc finger protein hcKr	5.6
	422994	AW891802	Hs.296276	ESTs, Moderately similar to F41925 hypot ESTs	5.6
	457148	AF091035	Hs.184827	KIAA0118 protein	5.6 5.6
60	428356	AL046991	Hs.10338	ESTs	5.6
	415927	AL120168	Hs.78919	Kell blood group precursor (McLeod pheno	5.5
	402092	4.0000			5.5
	440526	A1832243	Hs.211471	ESTs	5.5
65	444409 417877	A1792140 A1025829	Hs.49265	ESTs .	5.5
05	458238	AW071521	Hs.86320 Hs.333541	ESTs	5.4
	430702	U56979	Hs.250651	beta-amyloid binding protein precursor H factor 1 (complement)	5.4 5.4
	456189	H91010	Hs.44940	ESTs	5.4
70	427424	AA402453	Hs.113011	ESTs	5.4
70	437354	AA749215	Hs.291886	ESTs	5.4
	455617	BE078070		gb:CM1-BT0614-160300-149-f02 BT0614 Horno	5.4
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	5.3
	427861 408556	AA813185 U49516	Hs.98183	ESTS	5.3
75	444209	AJ753134	Hs.46362 Hs.146494	5-hydroxytryptamine (serotonin) receptor ESTs	5.3
-	422831	R02504	Hs.332943	ESTs	5.3 5.3
	403180				5.3 5.3
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	5.3
80	430339	W28608	Hs.239625	integral membrane protein 28	5.2
OU	431596	T34708	Hs.272927	Sec23 (S. cerevisiae) homolog A	5.2
	431930	AB035301	Hs.272211	cadherin 7, type 2	5.2
	437403 438285	Al208149 AA782845	Hs.121196	ESTs	5.2
		141135043	Hs.22790	ESTs	5.2

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	439901	N73885	Hs.124169	ESTs	
	438507	AA809052	Hs.211275		5.2
	449222	AW293984	Hs.197621	ESTs	5.2
				ESTs	5.2
5	402834	AK001507	Hs.306084	Homo sapiens clone FLB6914 PRO1821 mRNA	5.2
,	419042	T81429	Hs.221065	ESTs	5.2
	438777	AA731199	Hs.293130	ESTs	5.2
	445071	AJ280246	Hs.149504	ESTs	5.1
	408016	AW136827	Hs.256096	ESTs	5.1
10	412047	AA934589	Hs.49696	ESTs	5.1
10	436953	AW959074	Hs.23648	Homo sepiens cDNA FLJ 13097 ffs, clone NT	5.1
	436773	AW078629	Hs.82110	PC4 and SFRS1 interacting protein 1	5.1
	409263	AA069573	Hs.50319	ESTs	5.1
	453830	AA534296	Hs.20953	ESTs	5.1
1.5	459580	AA022888	Hs.176065	ESTs	5.1
15	417616	R07728	Hs.268668	ESTs	5.1
	423457	F08208	Hs.283844	similar to rat tricarboxylate carrier-fi	5.1
	441535	AL135735	Hs.7885	phosphatidylinositol binding clathrin as	5.0
	416490	AF090116	Hs.79348	regulator of G-protein signalling 7	5.0
20	417284	N62889	Hs.107242	Homo sapiens cDNA FLJ12965 fis, clone NT	5.0
20	447135	T58148		gb:yb98g06.s1 Stratagene lung (937210) H	5.0
	448605	AL109678	Hs.21597	Homo sapiens mRNA full length insert cON	5.0
	442240	A1791883	Hs.292719	ESTs	4.9
	459399	BE407712	Hs.153998	creatine kinase, mitochondrial 1 (ubiqui	4.9
25	427972	AA854870	Hs.181304	putative gene product	4.9
23	432944	AA570687	Hs.38512	ESTs	4.9
	440198	BE560093	14. 40	gb:601345159F1 NIH_MGC_8 Homo sapiens cD	4.9
	444047	AI097452	Hs.135095	ESTs	4.9
	416040	AW819158	Hs.289044	Homo sapiens cDNA FLJ12048 fis, clone HE	4.9
30	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.8
3U	436670	AI690021	Hs.201536	ESTs	4.8
	448072	A1459306	Hs.24908	ESTs	4.8
	408936	AL138043	Hs.293549	ESTs	4.8
	412622	AW664708	Hs.171959	ESTs	4.8
35	414943	D80647	Hs.124193	ESTs	4.8
22	429254	H10133	Hs.91846	hypothetical protein DKFZp761C121	4.8
	453567	A1742835	Hs.33368	hypothetical protein FLJ11175	4.8
	407906 441028	AA369665	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	4.8
		A1333660	Hs.17558	Homo sapiens cDNA FLJ14446 fis, clone HE	4.7
40	405130	******			4.7
70	455225	AW996689		gb:QV3-BN0046-150400-151-g09 BN0046 Homo	4.7
	446218 443347	AV657159	14. 422244	gb:AV657159 GLC Homo saplens cDNA clone	4.7
	402176	A1052543	Hs.133244	metanoma-derived teucine zipper, extra-n	4.7
		0500000			4.7
45	416577 436221	BE063207	Hs.79381	grancalcin	4.7
7,7	420480	AK001781	Hs.296543	Homo sapiens cONA FLJ 10919 fis, clone OV	4.7
	400800	AL137361	Hs.98173	hypothetical protein	4.7
	435161	Y10262	Hs.46925	eyes absent (Orosophila) homotog 3	4.6
	404793	AF124150	Hs.272091	ESTS	4.6
50	430895	U66581	Hs.248121	Complete accorded accordes 00	4.6
50	438571	AW020775	Hs.56022	G protein-coupled receptor 22 ESTs	4.6
	445924	AJ264671	Hs.164166	ESTs	4.6
	444585	AW170015	Hs.6594	ESTS	4.6
	421044	AF061871	Hs.311736	Human DNA sequence from clone RP1-238D15	4.6
55	418274	AI458587	Hs.128677		4.6
	425475	W56339	Hs.107057	Human DNA sequence from clone RP1-50O24 ESTs	4.6
	434311	BE543469	Hs.266263		4.6
	414272	At651603	Hs.46988	Homo sapiens cDNA FLJ14115 fts, clone MA ESTs	4.5
	445235	AJ564022	Hs.138207	ESTs	4.5
60	414327	BE408145	Hs.185254	ESTs, Wealdy similar to T24435 hypotheti	4.5 4.5
	414630	BE410857		gb:601301177F1 NIH_MGC_21 Home sepiens c	4.5
	414456	H74314		gb:yu56e10.r1 Soares fetal liver spieen	4.5
	401024			garyana ian i adalah telah ater apicen	4.5
	414699	Al815523	Hs.76930	synuclein, alpha (non A4 component of am	4.5
65	423449	AJ497900	Hs.33067	ESTs	4.5
	405138				4.5
	413544	BE147225		gb:PM2-HT0225-031299-003-111 HT0225 Homo	4.5
	453880	AI803166	Hs.28462	ESTs, Wealdy similar to 138022 hypotheti	4.5
	433521	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	4.4
70	441184	AA922009	Hs.150269	ESTs	4,4
	429876	AB028977	Hs.225974	KIAA1054 protein	4.4
	445481	AW661846	Hs.148836	ESTs	4.4
	452340	NM_002202		ISL1 transcription factor, LIM/homeodoma	4.4
70	404769				4.4
75	444331	AW193342	Hs.24144	ESTs	4.4
	429726	AW628326	Hs.27151	ESTs	4.4
	449093	AB035356	Hs.22998	neuraxin 1	4.4
	451959	AA056203	Hs.27337	hypothetical protein FLJ20623	4.4
00	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	4.4
80	417888	R23053		gb:yh31a05.r1 Soares placenta Nb2HP Homo	4.4
	419656	AB002314	Hs.92025	KIAA0316 gene product	4.4
	425884	U56420	Hs.159903		4.4
	435078	AW518888	Hs.40937	ESTS	4.4
					•

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	413493	BE144444		gb:MR0-HT0168-141199-002-09 HT0168 Homo	4.3
	432712	AB015247	Hs.288031	sterol-C5-des aturase (fungal ERG3, delta	4.3
	459650	R25754	Hs.301185	ESTs (Manager Change Change Changer Ch	4.3
	404828				4.3
5	423782	AJ472209	Hs.323117	ESTs	4.3
	426867	AA460967	Hs.22668	ESTs	4.3
	426802	AA385182	Hs.46699	ESTs	4.3
	457353	X65633	Hs.248144	melanocortin 2 receptor (adrenocorticotr	
	412112	BE180342	14.240144	gb:RC3-HT0622-130400-012-a07 HT0622 Homo	4.3 4.3
10	401522	N47812	Hs.306198	CGI-35 protein	
	419055	Al365384			4.3
		H07892	Hs.11571	Horno seplens cDNA FLJ11570 fis, clone HE	4.3
	410171		Hs.12431	ESTs	4.3
	419564	U08989	Hs.91139	solute carrier family 1 (neuronal/epithe	4.3
15	458789	AL157468	Hs.325825	Homo sapiens cDNA FLJ20848 fis, clone AD	4.3
IJ	455040	AW852286		gb:QV0-CT0225-100400-187-608 CT0225 Homo	4.3
	438533	AJ440266	Hs.170673	ESTs, Wealdy similar to T24832 hypotheti	4.3
	459005	AA447679	Hs.144558	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.2
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	4.2
20	433389	AF038171		gb:Homo saplens clone 23671 mRNA sequenc	4.2
20	454356	AW390363	Hs.11522	hypothetical protein from Xq28	4.2
	442339	BE299668	Hs.227591	ESTs, Weakly similar to 1901303A Leu zip	4.2
	421249	AA285362		gb:HTH277 HTCDL1 Homo sapiens cDNA 5/3	4.2
	443998	AI520561	Hs.296276	ESTs	4.2
~ -	452197	AW023595	Hs.232048	ESTs .	4.2
25	451117	AA015752	Hs.205173	ESTs	4.2
	404501	AW247252	Hs.75514	nucleoside phosphorytase	4.2
	410378	R23324	Hs.41693	DnaJ (Hsp40) homolog, subfamily 8, membe	4.2
	422528	AB011182	Hs.118087	KIAA0610 protein	4.2
	440323	AA970614	Hs.127992	ESTs	4.1
30	425767	AF054176	Hs.159483	chromosome 1 open reading frame 7	4.1
••	434460	AA478486	Hs.3852	KIAA0368 protein	
	410362	H04811	Hs.93164	proprotein convertase subtilisin/kexin t	4.1
	413121	T96090	Hs.142678		4.1
	409403	AA668224	Hs.6634	ESTs	4.1
35				Homo sapiens cDNA: FLJ22547 ffs, clone H	4.1
55	450235	AA007512	Hs.17538	ESTs	4.1
	449754	H00820	Hs.30977	ESTs, Wealthy similar to 834087 hypotheti	4.1
	421813	BE048255		gb:tz49b05.y1 NCI_CGAP_Bm52 Homo sapien	4.1
	408496	AI683802	Hs.136182	ESTs	4.1
40	430261	AA305127	Hs.237225	hypothetical protein HT023	4.1
40	434101	AA625205	Hs. 259599	KIAA1522 protein	4.1
	451837	T92157	Hs.16970	ESTs .	4.1
	411772	BE170301		gb:QV4-HT0536-040500-193-f05 HT0536 Homo	4.1
	437630	AI252782	Hs.153026	SWAP-70 protein	4.1
4 =	430212	AA469153		gb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	4.0
45	400216			•	4.0
	429830	AI537278	Hs.225841	OKFZP434D193 protein	4.0
	453165	674727	Hs.32042	aspartoacylase (aminoacylase 2, Canavan	4.0
	418047	R37633	Hs.4847	ESTs	4.0
	405354				4.0
50	427931	AW206512	. Hs.186996	ESTs	4.0
	428775	AA434579	Hs.143691	ESTs	4.0
	449422	AA001373	Hs.59821	ESTa	4.0
	453864	AW021407	Hs.21068	hypothetical protein	4.0
	456407	AW968614		gb:EST380690 MAGE resequences, MAGJ Homo	
55	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	4.0 4.0
	420784	T65158	Hs.102399	ESTs. Moderately similar to S65657 alpha	
	425195	AA352026	Hs.94319	VPS10 domain receptor protein	4.0
	429628	H09604	Hs.13268		4.0
	410087	F12079	Hs.332579	ESTs ESTs	4.0
60	409840	AW502122	0.3323/3		4.0
- •	452854	AA437061	Hs.14060	gb:UI-HF-BR0p-gir-c-08-0-UI.r1 NIH_MGC_5	4.0
	419910	AA662913	Hs.190173	prokinaticin 1 precursor	4.0
	427443	AA402713			4.0
	414990		Hs.97872	ESTs	4.0
65	412678	C17758	Hs.221652		3.9
UJ		AA115575	Hs.114914	ESTs	3.9
	405629	4/054034		44-	3.9
	420299	AI056871	Hs.15276	ESTs	3.9
	453098	Z25935	Hs.86379	ESTa	3.9
70	435752	AF2308D1		gb:Homo sapiens growth hormone receptor	3.9
70	441005	Z41305	Hs.303172	Homo sapiens mRNA; cDNA DKFZp547G133 (fr	3.9
	414516	A1307802	Hs.135560	ESTs, Wealdy similar to T43458 hypotheti	3.9
	442257	AW503831	Hs.323370	Human EST clone 25267 mariner transposon	3.9
	422563	BE299342	Hs.19348	hypothetical protein FLJ13119	3.9
75	406697	M21388	Hs.123017	Human unproductively rearranged lg mu-ch	3.9
75	443850	AW014723	Hs.334612	ESTs	3.9
	412677	AW029608	Hs.17384	ESTs	3.9
	422788	AL117352	Hs.120828		3.9
	405377				3.9
00	414376	BE393856	Hs.66915	ESTs, Wealdy similar to 16.7Kd protein	3.9
80	453341	AI758912	Hs.296341	adenytyl cyclase-associated protein 2	3.9
	431960	AW241821	Hs.301927		3.9
	416854	H40164	Hs.80298	Purkinje cell protein 4	3.9
	427264	AA400117	Hs.125747	ESTs	3.9
					4.3

	477746	NIN 004494	Un 110061	alustro- A	
	422746 452345	NM_004484 BE243534	Hs.119651	glypican 3	3.9
	414666		Hs.76828	gb:TCBAP 100885 Pediatric pre-B cell acut	3.9
	418217	NM_004466 AJ910647	Hs.13442	glypican 5 ESTs	3.8
5	419118	AA234223	Hs.139204	ESTS	3.8
	445017	AJ205493	Hs.176860	ESTS	3.8
	405867	74200-34	13.170000	LUI	3.8
	422760	BE409561		gb:601299865F1 NIH_MGC_21 Homo sapiens c	3.8
	453863	XXX2544	Hs.572	orosomucoid 1	3.8
10	457821	H47166	Hs.124322	ESTs, Weakly similar to A47582 B-cell gr	3.8 3.8
	457330	AB013818	Hs.247220	peroxisome biogenesis factor 10	3.8
	435600	AL047034	Hs.119747	ESTs	3.8
	456083	U46922	Hs.77252	fragile histidine triad gene	3.8
	413341	H78472	Hs.191325	ESTs, Weakly similar to T18967 hypotheti	3.8
15	449057	AB037784	Hs.22941	KIAA1363 protein	3.6
	421855	F06504	Hs.27384	ESTs, Moderately similar to ALU4_HUMAN A	3.8
	414764	AW013887	Hs.72047	ESTS	3.8
	404391				3.7
	433629	R13140	Hs.13359	ESTs	3.7
20	424738	AI963740	Hs.46826	ESTs	3.7
	401315				3.7
	407706	AA191085	Hs.26612	ESTs, Moderately similar to S23650 retro	3.7
	440530	AA888646	Hs.174187	ESTs .	3.7
25	433930	AA620338	Hs.273781	ESTs	3.7
25	409662	AW452320	Hs.279726	ESTa	3.7
	437268	AJ754847	Hs.227571	regulator of G-protein signalling 4	3.7
	445688	A1248205	Hs.153244	ESTs	3.7
	408593	R19566	Hs.197617	ESTs .	3.7
20	417091	AA193283	Hs_291990	ESTs	3.7
30	448556	AW885606	Hs.5064	ESTs	3.7
	423135	N67655	Hs.26411	ESTs	3.7
	400135				3.7
	459150	BE155356		gb:PM1-HT0350-160300-009-d06 HT0350 Homo	3.7
35	457221	AW383197	Hs.218260	ESTs	3.7
33	451560	AJ807927	Hs.249601	ESTs	3.7
	401600 446818	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	3.7
	447795	AL342668 AW295151	Hs.279765	ESTS	3.7
	427562	R56424	Hs.163612 Hs.26534	ESTS ESTS	3.7
40	412258	AA376768	Hs.324841	hypothetical protein FLJ22622	3.6
	454339	AW381980	113.324041	gb:QV4-HT0316-091199-028-d05 HT0316 Homo	3.6
	439274	AF086092	Hs.48372	ESTs	3.6
	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
	422897	AA679784	Hs.4290	ESTs	3.6 3.6
45	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	3.6
	421908	AW935200	Hs.285814	sprouty (Orosophila) homolog 4	3.6
	407978	AW385129	Hs.41717	phosphodiesterase 1A, calmodulin-depende	3.6
	426452	AW614271	Hs.121647	ESTs, Highly similar to AC006014 8 simil	3.6
	400685				3.6
50	417154	AI674701	Hs.21388	ESTs	3.6
	447176	Z42549	Hs.160893	ESTs	3.6
	423893	AL031709	Hs.134846	Human DNA sequence from clone 316G12 on	3.6
	449231	BE410360	Hs.298573	KIAA1720 protein	3.6
66	411607	AW853498		gb:RC1-CT0252-170200-025-h02 CT0252 Homo	3.6
55	405977				3.6
	441470 .	BE503874	Hs.301986	ESTa	3.6
	423568	NM_005256	Hs.129818	growth arrest-specific 2	3.6
	441235	AI884586	Hs.135570	Homo sapiens cDNA: FLJ21268 fis, clone C	3.6
60	450236 425364	AW162998	Hs.24684	KIAA1376 protein	3.6
00	426775	AF052150 AA384564	Hs.155959	Homo sapiens clone 24533 mRNA sequence	3.6
	414831	M31158	Hs.108829 Hs.77439	ESTs	3.6
	416876	AW501916		protein kinasa, cAMP-dependent, regulato	3.6
	400878	V4400 1210	Hs.117897	ESTs	3.6
65	425153	AW023193	Hs.27046	ESTs	3.6
•	432222	AI204995	119.27010	gb:sn03c03.x1 Stratagene schizo brain S1	3.6
	415047	F13142		gb:HSC3JD031 normalized Infant brain cDN	3.5
	401532			Any seconds inclined an under the Stit CDM.	3.5
	446495	D60923	Hs.153460	ESTs	3.5 3.5
70	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	3.5
-	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	3.5
	455901	BE155527		gb:PM1-HT0350-190400-013-b08 HT0350 Homo	3.5
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	35
	455697	BE067952		gb:CM0-BT0365-061299-122-g09 BT0365 Homo	3.5
75	405678			and india	3.5
	418207	C14685	Hs.34772	EST ₈	3.5
	425383	D83407	Hs.156007		3.5
	417027	AA192306	Hs.23926	triadin	3.5
0Δ	408367	AK001178	Hs.44424	homolog of rat orphan transporter v7-3	3.5
80	417702	R09935	Hs.191148	ESTs	3.5
	445687	W80382	Hs.149297		3.5
	408776	AA057365	Hs.63356	ESTs, Weakly similar to 138022 hypotheti	3.5
	413164	8E068494		gb:MR1-BT0371-050500-009-a12 BT0371 Homo	3.5

	414593	BE386764		gb:601273249F1 NIH_MGC_20 Horno sapiens c	3.5
•	453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein.	3.5
	415621	AJ648602	Hs.55468	ESTs	3.5
5	454437	AI248173	Hs.191460	hypothetical protein MGC12936	3.5
3	446066	AI343931	Hs.149383	ESTs	3.5
	423374	AB037770	Hs.127656	KIAA1349 protein	3.5
	419347 418516	C15944 NM_006218	Hs.90005	superiorozavical ganglia, neural specifi	3.5
	451776	W45679	Hs.85701 Hs.169854	phosphotnositide-3-kinase, catalytic, al hypothetical protein SP192	3.5
10	432305	M62402	Hs.274313	insulin-like growth factor binding prote	3.5
• •	456995	T89832	Hs.170278	ESTs	3.5
	403323			2010	3.5 3.5
	425022	M95724	Hs.154207	centromere protein C 1	3.5
	439394	AA149250	Hs.56105	ESTa	3.4
15	433803	AI823593	Hs.27688	ESTs	3.4
	450715	AI266484	Hs.31570	ESTs, Wealthy similar to KIAA1324 protein	3.4
	411474	AW848427		gb:IL3-CT0214-150200-075-H10 CT0214 Homo	3.4
•	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	3.4
20	423826	U20325	Hs.1707	cocaine- and amphetamine-regulated trans	3.4
20	459495	BE544158		gb:601076707F1 NtH_MGC_12 Homo sapiens c	3.4
	427173	BE255017	Hs.97540	ESTS	3.4
	408112	AW451982	Hs.248613	ESTs	3.4
	446092	N33522	Hs.145894	ESTs	3.4
25	416858 458234	AI656856	Hs.292597	ESTs	3.4
LJ	419555	BE551408 AA244416	Hs.127196	ESTS	3.4
	414314	BE312991		gb:nc07d11.s1 NCI_OGAP_Pr1 Homo sapiens	3.4
	400425	AY004252	Hs.287385	gb:601150275F1 NIH_MGC_19 Homo sapiens c PR domain containing 12	3.4
	414366	BE549143	. 10.207.303	gb:601076456F1 NIH_MGC_12 Homo sapiens c	3.4 3.4
30	434053	AW445136	Hs.134946	ESTs	3.4
-	449997	AI683052	Hs.201577	KIAA1829 protein	3.4
	433461	AI636047	Hs.197623	ESTs	3.4
	428006	AA418743	Hs.98306	KIAA1862 protein	3.4
26	424695	U58331	Hs.151899	sarcoglycan, delta (35kD dystrophin-asso	3.4
35	443294	A1733625	Hs.133053	ESTs	3.4
	428212	AW444451	Hs.134812	ESTs	3.4
	457673	AA551569	Hs.272034	hypothetical protein PRO2822	3.4
	446390	AA233393	Hs.14992	hypothetical protein FLJ11151	3.3
40	428536	AI143139	Hs.2288	visinin-like 1	3,3
40	426597	AA382250	Hs.145601	EST8	3.3
	410366	AI267589	Hs.302689	hypothetical protein	3.3
	458258 401738	AW406546	Hs.127971	ESTs	3.3
	409038	T97490	Hs.50002	ameli ladualitia autobias autobia-1. A 10.	3.3
45	425785	T27017	Hs.159528	small inducible cytoldrie subfamily A (Cy Homo sapiens clone 24400 mRNA sequence	3.3
	433328	AW298159	Hs.23644	ESTs, Weakly similar to S65824 reverse t	3.3
	414541	BE 293116	Hs.76392	aldehyde dehydrogenase 1 family, member	3.3 3.3
	434998	AW975157	Hs.26037	ESTs	3.3
	456359	AI967991	Hs.93574	homeo box D3	3.3
50	426527	NM_001037	Hs.170238	sodium channel, voltage-gated, type I, b	3.3
	454267	AA437199	Hs.656	cell division cycle 25C	3.3
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	3.3
	434077	AF116659	Hs.321151	Homo sapiens PRO1412 mRNA, complete cds	3.3
55	436602	AJ793222	Hs.166817	ESTs	3.3
55	449204	AB000099	Hs.23251	Down syndrome critical region gene 4	3.3
	417935 423310	R53697 AA325225	Hs.170044	ESTS	3.3
	436624	T64297	Hs.124023 Hs.5241	Homo sapiens cDNA FLJ14218 fts, clone NT	3.3
	453406	Al192987	Hs.61784	fatty acid binding protein 1, liver hypothetical protein FLJ14451	3.3
60	420164	AW339037	Hs.24908	ESTs	3.3
	447826	AW779317	Hs.258556	ESTs ESTs	3.3 3.3
	419875	AA853410	Hs.93557	proenkephalin	3.3
	444612	AW138111	Hs.22902	ESTs	3.3
	418504	BE159718	Hs.85335	Homo sapiens mRNA; cDNA DKFZp564D1462 (f	3.2
65	415242	R45988	Hs.295014	ESTs	3.2
	418188	AW139413	Hs.151880	ESTs	3.2
	430355	NM_006219	Hs.239818	phosphoinositide-3-kinase, catalytic, be	3.2
	421640	AW966652	*=	gb:EST378726 MAGE resequences, MAGI Homo	3.2
70	432359	AA076049	Hs.274415		3.2
, 0	408806 400409	AW847814 AF153341	Hs.289005		3.2
	446015	T30968	Hs.283954		3.2
	425495	AA358454	Hs.13531 Hs.78026	hypothetical protein FLI10971	3.2
	403092	W-000434	rts./0020	ESTs. Weakly similar to similar to ankyr	3.2
75	452971	AI873878	Hs.91789	ESTs	3.2
-	454186	BE141030	19.31703	gb:MR0-HT0067-201099-002-h11 HT0067 Homo	3.2
	401485			Same a contract of the same and	3.2 3.2
	401949				3.2
00	457452	AW972875		gb:EST384766 MAGE resequences, MAGL Homo	3.2
80	454100	A1693231	Hs.126043	chromosome 21 open reading frame 51	3.2
	448440	AA173457	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	3.2
	421200	AA284811	Hs.264433	ESTs	3.2
	430142	NM_000437	Hs.234392	platelet-activating factor acetythydrota	3.2

	433197 443509	AB040889			
		AV645470	Hs.281022	KIAA1456 protein gb:AV645470 GLC Homo sapiens cDNA clone	3.2 3.2
	440827	AI733110	Hs.128128	ESTs .	3.2
_	432799	NM_016161	Hs.278960	alpha-1,4-N-acetylglucosaminyttransferas	3.2
5	409257	AW370362		gb:RC1-BT0255-181099-012-607 BT0255 Homo	3.2
	459235	BE246010	Hs.271468	Homo sapiens mRNA for FLI00038 protein,	3.2
	416789	AA223439	Hs.79933	cyclin I	3.2
	429809	AL162010 AW449258	Hs.223603	Homo sapiens mRNA; cDNA DKFZp761D09121 (3.2
10	420156 455577	BE006341	Hs.6187	ESTS	3.2
	400617	AF151084	Hs.36069	gb:RC2-BN0127-240300-011-b05 BN0127 Homo hypothetical protein	3.2
	437129	AL049327	Hs.302057	Homo sapiens mRNA; cDNA DKFZp564E016 (fr	3.2
	451820	AW058357	Hs.337353	ESTs	3.2 3.2
	457535	AA609685	Hs.278672	membrane component, chromosome 11, surfa	3.2
15	419956	AL137939	Hs.40096	ESTs	3.1
	456235	AA203637		gb:zx58b12.r1 Soares_fetal_liver_spleen_	3.1
	423930	AA332697	Hs.42721	ESTs	3.1
	403796				3.1
20	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	3.1
20	445886	AI793176	Hs.145596	EST ₅	3.1
	414401 441573	AI760159 · BE563966	Hs.124833	ESTs	3.1
	450725	R71389	Hs.6529 Hs.175951	ESTs, Weakly similar to 178885 serine/th ESTs	3.1
	458805	AI282933	Hs.23294	hypothetical protein FLJ14393	3.1
25	417868	AI078534	Hs.122592	ESTs	3.1 3.1
	458391	AJ792628	Hs.133273	ESTs	3.1
	423346	AI267677	Hs.127416	synaptojanin 1	3.1
	454486	AW857077		gb:RC1-CT0302-140300-016-f04 CT0302 Homo	3.1
20	408341	AW182952	Hs.249957	ESTs	3.1
30	410669	AW805749	Hs.318885	superoxide dismutase 2, milochondrial	3.1
	404907	*******			3.1
	434910	AJ333863	Hs.215474	ESTs, Moderately similar to alternativel	3.1
	436990 441921	AI149729	Hs.120557	ESTs	3.1
35	454673	A1733376 AW812807	Hs.164478	hypothetical protein FLJ21939 similar to	3.1
	429470	AJ878901	Hs.203862	gb:RC3-ST0166-070100-016-c04 ST0186 Homo guanine nucleotide binding protein (G pr	3.1
	404345	AA730407	Hs.159156	protocadherin 11	3.1 3.1
	408217	AI433201	Hs.279860	tumor protein, translationally-controlle	3.1
	417313	AA195602		gb:zr32f09.r1 Soares_NhHMPu_S1 Homo sepi	3.1
40	427322	AK002017	Hs.176227	hypothetical protein FLJ11155	3.1
	411003	AA181018	Hs.13056	hypothetical protein FLJ13920	3.1
	425339	AA935330	Hs.198113	ESTs	3.1
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (lg),	3.:
45	449078	AK001258	Hs.22975	KIAA1576 protein	3.1
73	429608	U49250	Hs.210862	T-box, brain, 1	3.1
	442308 428465	AA989402	Hs.111	fibroblast growth factor 9 (glia-activat	3.1
	411666	AW970976 AF106564	Hs.293653 Hs.71346	ESTs	3.
	447965	AW292577	Hs.94445	neurofilament 3 (150kD medium) ESTs	3.
50	413918	AW015898	Hs.71245	ESTs	3. 3.
	419682	H13139	Hs.92282	paired-like homeodomain transcription (a	3. 3.
	425810	AI923627	Hs.31903	ESTs	3.
	427855	AA416931	Hs.126065	ESTs	3.
<i>C E</i>	429060	AW139155	Hs.194995	hypothetical protein DKFZp43400320	3.
55	430708	U78308	Hs.278485	olfactory receptor, family 1, subfamily	3.
	448084	AI467800	Hs.271000	ESTs, Wealdy similar to I38022 hypotheti	3.
	454506	AW847346		gb:RC0-CT0205-240999-021-e01 CT0205 Homo	3.
	414629 422963	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	3.
60	417696	M79141 BE241524	Hs.13234 Hs.82401	ESTS CD69 antigen (n60 arety T coll auticati	3.
55	448175	BE296174	Hs.225160	CD69 antigen (p60, early T-cell activati hypothetical protein FLJ13102	3.
	414686	BE409757	Hs.23189	ESTs, Moderately similar to T882_HUMAN T	3.
	458360	AI027207	Hs.132253	ESTs	3. 3.
	451829	AW964081	Hs.247377	ESTs	3.
65	445179	AI949743	Hs.224768	ESTs	3.
	433090	A1720050	Hs.145362	Immortatization-upregulated protein	3.
	432018	AA524447	Hs.152377	ESTs	3.
	407988	N47760	Hs.285107	hypothetical protein FLJ13397	ä
70	405911	4100-044		COT	3
, 0	418808	AI821836	Hs.10359	ESTs	3.
	431900	AW972048	Hs.192534		3.
	452893 423952	H18017 AW877787	Hs.22869 Hs.136102	ESTs, Moderately similar to KIAA1395 pro	3.
	412000	AW576555	Hs.15780	KIAA0853 protein ATP-binding cassette, sub-family A (ABC1	3.
75	405793	***************************************	119.13/00	CIT	3.
	410711	AB002316	Hs.65746	KIAA0318 protein	3.
	411279	AW884776		gb:QV4-OT0067-010300-121-d01 OT0067 Homo	3. 3.
	423957	AW978309	Hs.135235		3
00	427071	AA397958	Hs.192719		3.
80	434961	AW974956		gb:EST387061 MAGE resequences, MAGN Homo	3.
					•
	TABLE 2				



	CAT numb		e cluster number bank accession (
_	Pkey	CAT Number		
5	409257	1112994_1	AW370362 A	
	409840 411052	1156071_1 1230374_1		W502125 AW501663 AW501720 98513 H69459 BE176242 H54583
	411279	1237516_1		W935737 AW835261 AW835247 AW835246 AW835263 AW835240 AW835258
• •	411474	1247047_2		W848890 AW848159 AW848118 AW848634 AW848285 AW848086 AW848485 AW848283 AW848162
10	411607	1251251_1		W853442 AW853590 AW853433 AW853592
	411772 412112	1257386_1 1277883_1		NS81539 AW904851 BE154338 BE154090 BE154275 E180347 AW901900 BE180222 BE180218 BE180226 BE180413 BE180416 AW901899 BE180228 AW901897 BE180224 AW901898
	412112	1277003_1		E180219 BE180346 BE180343 BE180418 BE180225 BE180221 BE180341 AW901899 BE180217 BE180227 AW901891 BE180345
				W893815 H85799 H83501 BE180220
15	413164	1351422_1		E668414 BE068332 BE068347 BE068706 BE068623 BE068450 BE068480 BE068350 BE068295 BE068498 BE068765 BE068328
				E068871 BE068526 BE068493 BE068433 BE068740 BE068306 BE068631 BE068580 BE068445 BE068567 BE068521 BE068549 E068307 BE068692 BE068473 BE068754 BE068476 BE068685 BE068626 BE068591 BE068745 BE068434 BE068759 BE068628
				E068529 BE068689 BE068383 BE068422 BE068470 BE068522 BE068518 BE068354 BE068748 BE068683 BE068303 BE068602
20			BE068739 BI	E068374 BE068302 BE068625 BE068596 BE068663 BE068429 BE068605 BE068693 BE068872 BE068401 BE068579 BE068329
20				E058419 BE058393 BE058447 BE058675 BE058311 BE058540 BE058301 BE058543 BE058719 BE058369 BE058324 BE058588
				E068317 BE068384 BE068547 BE068574 BE068436 BE068321 BE068361 BE068676 BE068499 BE068299 BE068352 BE068410 E068418 BE068552 BE068598 BE068327 BE068550 BE068712 BE068661 BE068733 BE068525 BE068752 BE068357 BE068330
				E068538 BE068340 BE068537 BE068761 BE068632 BE068758
25	413493	1373555_1	BE14444 BI	
23	413510 413544	1374377_1 1375671_1		009 BE145525 BE145493 E147205 BE147234
	414220	1426940_1	BE298094 B	
	414314	1435028_1	BE312991 B	EZ72945
30	414366	1438636_1		E390613 BE277344
50	414456 414593	1447655_1 1464909_1	H74314 BE2 BE386764 B	
	414630	1468083_1	8E410857 B	
	415047	1517450_1		926 F06135 F06147 H08517 D51360 T75341
35	417313 417888	166644_1 1706092_1	R23053 R79	/01148 N40632
55	419555	185884_1	AA244416 A	
	421249	200649_1		W752386 AW847156 AA285373 AW879575 AW879558
	421640	204833_1		NY966653 AA294989 AA385977
40	421813 422760	207654_1 221034_1		A313083 AA298419 E162756 AW732798
	425526	252776_1		A358889 AW955306 AW962995 AW837746 AW837755 AW837697
	430212	314437_1	AA469153 A	J718503 AA469225
	432222 433389	343347_1 36497_1		N827539 AW969908 AW440776 AA528756
45	434961	396357_1		43209 F07347 NA781075 AA654944
-	435752	41050_1		F230800 AA401795 AA398260
	437483 440198	43756_1	AL390174 A	W898817
	443509	488242 57199_1	BE560093 AV645470 T	84636 T82805
50	446052	65988_1		VA158850 AW062737 AW062738 AV656291
	446218	66688_1		E145509 BE145512 BE145505 BE145507
	447135 452346	70963_1 912206_1		\$16579 AW059603 BE243752 AI880229 L44326
	452502	919733_1		E007223 R30687
55	454065	998401_1		W024754 BE183166 BE183167
	454186	1049791_1	BE141030 E	3E141474 BE141467 BE141753 BE141024 BE141761 AW177583 AW177579 AW177582 AW177585 AW177587 AW807582 AW177581 3E141520 BE141456 BE141492 BE141028 BE141775 BE141489 BE141751 AW177599 BE141750 AW177597 BE141512 BE141460
			BE141749	AW177598
60	454339	1122972_1		BE152244 BE152235 BE152238 BE152232
UU	454486 454506	1215703_1 1219857_1		AW661268 AW847383 AW795787 AW847395 AW847408 AW847385 AW847342 AW847396 AW847339 AW801718 AW801787
	454673	1228669_1		AW812815 AW812802
	455040	1250028_1		AW851934 AW852096 AW852274
65	455225 455577	1262318_1 1333898_1		AW996380 AW996453 BE085650 AW868687 BE085595 BE006307 BE006311
05	455617	1348117_1		BE061030 BE077927
	455697	1351148_1	BE067952 (BE067945 BE067942 BE067943 BE067949 BE067954 BE067944 BE067953 BE067956 BE067945
	455901	1381569_1		BE155503 BE155188 BE155126
70	456235 456407	168686_1 184986_1		AA832266 H67452 AA243209 AA281411
	457452	339381_1		AAS41366 AAS23039
	459150	919196_1	BE 155356	BE153488 BE153481 BE155059 BE155210 BE155413 BE153577 BE153688 BE155063 BE155347 Al903640 BE155492
	TABLE 2	κ r ·		
75	Pkey:		nique number co	vresponding to an Eos probeset
	Ref:	S	equence source.	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et at," refers to the publication entitled "The DNA
	Strand:	56	quence of huma	in chromosome 22" Dunham, et at. (1999) <u>Natura</u> 402:489-495.
•	Nt_posit			and from which exons were predicted. Se positions of predicted exons.
80	_			· · · · · · · · · · · · · · · · · · ·
	Pkey 400661	Ref 8118474	Strand	NL position
	400685	8118768	Ptus Minus	84912-85107 72969-73050,73713-73800

WO 03/025138 PCT/US02/29560

	400865	1945037	Minus	44482-45526
	400878	9864757	Ptus	31493-32842
	401024	8117489	Plus	60551-60802
_	401315	9212515	Minus	198960-199619
5	401485	7341723	Plus	68009-68209,68841-69077
	401521	7705251	Plus	9127-9234
	401532	7798785	Plus	124414-124950,125050-125418
	401738	2982169	Minus	41547-41757
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
10	401836	7534063	Plus	71981-72084
	401949	3492889	Plus	160728-161660
	402092	7249154	Minus	107533-108094
	402178	7543687	Minus	10-750
	402548	7637348	Ptus	24873-25170
15	403092	8954241	Plus	174720-175016.175104-175406.175508-175813
	403180	7523976	Minus	63603-63759
	403323	8348082	Minus	120366-120845
	403796	8099896	Minus	75073-77664
~~	404391	3135305	Minus	26030-26173,27852-27997
20	404769	6099713	Minus	175801-176823
	404793	7232206	Minus	61087-61590
	404828	6580415	Minus	26291-27253
	404907	7331453	Minus	102880-103828
0.5	404958	7407941	Minus	2731-4531
25	405071	7708797	Minus	11115-11552
	405130	8516045	Plus	150235-150449
	405138	8576241	Plus	90303-90516
	405354	2642452	Plus	52213-53089
20	405377	5649375	Plus	216656-216848
30	405629	4508116	Minus	101678-101866
	405678	4079670	Plus	151821-152027
	405793	1405887	Minus	89197-89453
	405800	2791346	Plus	19271-19813
25	405867	6758731	Minus	74553-75173
35	405911	6758795	Plus	101008-101643
	405977	8247789	Minus	135548-136177

40 45

Pkey: ExAcon: Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number

UnigenetD: Unigene Title: 50

Examplar Accessor number. Centralis accessor in the Cultiple of Lindber Unigene gene title. Ratio of 75° percentile normal central nervous system tissue to 85° percentile turnor Ratio of 85° percentile central nervous system tissue to 85° percentile normal body tissue. R1: R2:

55	Pkey	ExAcon	UnigenelD	Unigene Title	RI	R2
23	417275	X63578	Hs.295449	parvalbumin	29.0	30.0
	430829	AW451999	Hs.194024	ESTs .	25.7	6.2
	410657	AF063228	Hs.65248	dyneln, cytoplasmic, intermediate potype	22.6	25.8
	419954	D14720	Hs.93883	myelin protein zero (Charcot-Maria-Tooth	21.2	30.3
60	416133	NM_001683	Hs.89512	ATPase, Ca++ transporting, plasma membra	15.5	16.8
60	416018	AW138239	Hs.78977	proprotein convertase subfilisin/kexin t	15.2	18.0
	417167	AW206437	Hs.4290	ESTs	14.8	17.7
	433940	HQ5129	Hs.7459	cyclic AMP-regulated phosphoprotein, 21	13.4	18,1
	413324	V00571	Hs.75294	corticotropin releasing hormone	13.1	18.0
	439830	AA846666	Hs. 151489	ESTs, Wealty similar to XE7_HUMAN PROTEI	12.6	16.5
65	408068	AW148652	Hs.167398	ESTs	12.6	16.9
	429096	AB011106	Hs.196012	KIAA0534 protein	12.2	21.1
	412638	AA910199	Hs.203838	ESTs	12.2	16.0
	442593	R39804	Hs.31961	ESTs	10.8	15.0
	446353	Al290919	Hs.153661	ESTs	10.4	13.2
70	426365	AA376667	Hs.10283	RNA binding motif protein 8B	10.0	5.9
	414937	R38698	Hs.12382	ESTs	10.0	10.8
	419643	F06066	Hs.91791	chromosome 11 open reading frame 25	9.5	10.9
	412454	RS5745	Hs.167330	ESTs	9.5	14.1
	439366	AF100143	Hs.6540	fibroblast growth factor 13	9.4	12.3
75	441790	AW294909	Hs.132208	ESTs	9.2	3.2
	448117	H49129	Hs.172982	ESTs	9.1	12.8
	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	9.0	14.7
	412453	R20205	Hs.167330	ESTs	9.0	13.7
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	8.9	17.3
80	409031	AA376836	Hs.76728	ESTs	8.7	
	446544	AI631932	Hs.7047	ESTs, Weakly similar to Unknown (H.sapig		8.6
	439480	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger or	8.2	20.0
	410200	AA082557	Hs.101915	Starpardt disease 3 (autosomal dominant)	8.2	8.3
	710200	1002001	ns. (U1915	PisiBaror orsesse a ferrezoura dougravi)	8.0	8.9

	408428	NM_014787	Hs.44896	OnaJ (Hsp40) homolog, subfamily B, membe	7.9	9.6
	437073	AI885608	Hs.94122	ESTs	7.9	11.3
	408434	AW195317	Hs.107716	hypothetical protein FLJ22344	7.9	16.4
5	440209	H05049	Hs.22269	neurexin 3	7.8	34.3
,	408119 429611	W26213 AJ889077	Hs.101672 Hs.211388	ESTs, Wealdy similar to T00331 hypotheti Homo sapiens BAC clone CTB-60N22 from 7g	7.8	9.0
	423440	R25234	Hs.143434	contactin 1	7.7 7.7	5.0 9.9
	445148	AI214510	Hs.146304	ESTs	7.6	9.1
10	415294	D86980	Hs.79170	KIAA0227 protein	7.6	7.6
10	424087 437479	N69333 R61866	Hs.143434 Hs.101277	contactin 1 ESTs	7.6	10.3
	430573	AA744550	Hs.138345	ESTs	7.5 7.1	9.3 2.8
	448958	AB020651	Hs. 22653	KIAA0844 protein	7.1	10.4
15	419474	AW968619	Hs.155849	ESTs	7.1	3.0
13	423605 433098	AF047826	Hs.129887	cadherin 19, type 2	7.0	6.9
	449511	AW190593 AJ436187	Hs.151143 Hs.296261	ESTs guanine nucleotide binding protein (G pr	7.0 6.9	9.2
	428414	AL049980	Hs.184216	OKFZP564C152 protein	6.8	3.1 5.0
20	443155	R54485	Hs.23772	ESTs	6.8	3.5
20	450561	R49674	Hs.25909	ESTs	6.8	8.1
	433068 423589	NM_006456 AA328082	Hs.288215 Hs.209569	tialytransferase ESTs	6.8	2.0
	415681	AI379882	Hs.72630	ESTs	6.6 6.5	10.5 9.0
25	413510	F13044		gb:HSC3HH101 normalized infant brain cDN	6.4	7.1
25	427992	Y15014	Hs.181353	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	6.4	9.5
	450642 429322	R39773 D86984	Hs.7130	copine IV	6.4	5.7
	447482	AB033059	Hs.199243 Hs.18705	KIAA0231 protein KIAA1233 protein	6.4 6.4	8.2
• •	446129	AW244073	Hs.145946	ESTs	6.3	2.3 8.3
30	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	6.3	2.1
	434273	AA913143	Hs.26303	ESTs .	6.2	10.3
	408480 451301	AI350337 AI769514	Hs.164568 Hs.209890	fibroblast growth factor 7 (keratinocyte	6.2	3.5
	438356	AA805530	Hs.48527	EST ESTs	6.2 6.2	12.4
35	426388	AW081394	Hs.97103	ESTs	6.2	8.1 8.6
	452502	A1904296		gb:PM-BT046-220199-286_1 BT046 Homo sapi	6.1	2.8
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	6.1	6.3
	442979 408713	AW440782 NM_001248	Hs.174743 Hs.47042	ESTs	6.1	6.3
40	430004	U27768	Hs.227571	ectonucleoside triphosphate diphosphohyd regulator of G-protein signalling 4	6.0 5.9	3.8
	425087	R62424	Hs.126059	ESTs	5.9	21.4 8.1
	441695	T12411	Hs.183745	hypothetical protein FLJ 13456	5.9	3.1
	417175	R44558	Hs.94002	EST ₈	5.8	12.5
45	437483 436427	AL390174 Al344378	Hs.143399	gb:Homo sapiens mRNA; cDNA OKFZp547J184 ESTs	5.8	2.2
	450382	AA397658	Hs.60257	Homo seplens cDNA FLJ13598 fis, clone PL	5.8 5.7	13.8 4.4
	408478	NM_000806	Hs.45740	gamma-aminobutyric acid (GABA) A recepto	5.7	12.5
	442676	A1733585	Hs.130897	ESTs	5.7	6.8
50	446443 459080	AV659082 AW192083	Hs.134228	EST _{\$}	5.7	6.4
30	431984	AL080239	Hs.290855 Hs.272284	ESTs Human DNA sequence from cione GS1-256022	5.6 5.6	15.6
	428356	AL046991	Hs.10338	ESTs	5.6	8.2 6.2
	417877	AI025829	Hs.86320	ESTs	5.4	4.9
55	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	5.3	13.1
55	408556 431930	U49516 AB035301	Hs.46362 Hs.272211	5-hydroxytryptamine (serotonin) receptor	5.3	6.6
	438285	AA782845	Hs.22790	cadherin 7, type 2 ESTs	5.2 5.2	6.0 7.3
	439901	N73885	Hs.124169	ESTs	5.2	2.7
60	449222	AW293984	Hs.197621	ESTs	5.2	8.1
55	408016 436953	AW136827 AW959074	Hs.256096	ESTs	5.1	2.5
	438773	AW078629	Hs.23648 Hs.82110	Homo sapiens cDNA FLJ13097 fis, clone NT PC4 and SFRS1 interacting protein 1	5.1 5.1	3.0
	409263	AA069573	Hs.50319	ESTs	5.1	7.3 12.9
65	453830	AA534296	Hs.20953	ESTS	5.1	3.4
Ų.	441535 416490	AL135735	Hs.7885	phosphatidylinositol binding clathrin as	5.0	4.8
	417284	AF090116 N62889	Hs.79348 Hs.107242	regulator of G-protein signalling 7	5.0	20.1
	448505	AL109678	Hs.21597	Homo sapiens cDNA FLJ12965 fis, clone NT Homo sapiens mRNA full length insert cDN	5.0 5.0	3.9 6.1
70	442240	AI791883	Hs.292719	ESTs	4.9	6.7
70	427972	AA864870	Hs.181304	putative gene product	4.9	5.2
	416040 444922	AW819158	Hs.289044	Homo sapiens cDNA FLJ12048 fis, clone HE	4.9	2.8
	408936	Al921750 Al.138043	Hs.144871 Hs.293549	Homo sepiens cDNA FLJ13752 fis, clone PL ESTs	4.8	3.7
	414943	D80647	Hs.124193	ESTs	4.8 4.8	6.6 3.1
75	429254	H10133	Hs.91846	hypothetical protein DKFZp761C121	4.8	23
	407906	AA369665	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (1	4.8	9.1
	416577 420480	BE063207	Hs.79381	grancation and and and and and and and and and an	4.7	2.2
	404793	AL137361	Hs.98173	hypothetical protein	4.7	2.8
80	430895	U66581	Hs.248121	G protein-coupled receptor 22	4.6 4.6	2.2 7.4
	438571	AW020775	Hs.56022	ESTs	4.6	5.4
	444585	AW170015	Hs.6594	EST8	4.6	6.0
	414272	AI651603	Hs.46988	ESTs	4.5	2.2



	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	4.5	30.9
	423449	A1497900	Hs.33067	ESTs	4.5	20.8
	433521	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	4.4	2.0.
5	429876	AB028977	Hs.225974	KIAA1054 protein	4.4	19.2
,	429726 449093	AW628326	Hs.27151 Hs.22998	ESTs	4.4	10.2
	415716	AB035356 N59294	Hs.179662	neurexin 1 mucleosome assembly protein 1-like 1	4.4 4.4	9.4 15.1
	419656	AB002314	Hs.92025	KIAA0315 gene product	4.4	8.2
	425864	U56420	Hs.159903	offactory receptor, family 5, subfamily	4.4	2.4
10	435078	AW518888	Hs.40937	ESTs	4.4	5.7
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	4.3	5.9
	426887	AA460967	Hs.22668	ESTs	4.3	6.0
	412112	BE180342		gb:RC3-HT0622-130400-012-807 HT0622 Homo	4.3	3.2
1.5	410171	H07892	Hs.12431	ESTs	4.3	5.3
15	442339	BE299668	Hs.227591	ESTs, Wealdy similar to 1901303A Lau zip	4.2	5.0
	421249 422528	AA285362	Hs.118087	gb:HTH277 HTCDL1 Homo sepiens cDNA 5/3	4.2	3.5
	434460	AB011182 AA478486	Hs.3852	KIAA0610 protein KIAA0368 protein	4.2 4.1	3.9
	410362	H04811	Hs.93164	proprotein convertase subtilisin/kexin t	4,1	8.3 7.0
20	449754	H00820	Hs.30977	ESTs, Weakly similar to B34087 hypotheti	4.1	3.9
	408496	AI683802	Hs.136182	ESTs	4.1	4.7
	434101	AA625205	Hs.259599	KIAA1622 protein	4,1	6.3
	430212	AA469153		gb:nc57f04.s1 NOI_CGAP_Pr1 Homo sapiens	4.0	2.5
0.5	453165	S74727	Hs.32042	aspartoacytase (aminoacytase 2, Canavan	4.0	7.4
25	456407	AW968614		gb:EST380690 MAGE resequences, MAGJ Homo	4.0	5.1
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	4.0	32.3
	429628	H09604	Hs.13268	ESTs	4.0	4.5
	410087 419910	F12079	Hs.332579	ESTs	4.0	6.9
30	441005	AA662913 Z41305	Hs.190173 Hs.303172	ESTs, Wealdy similar to A46010 X-linked	4.0	26
50	412677	AW029608	Hs.17384	Homo sapiens mRNA; cDNA DKFZp547G133 (tr ESTs	3.9 3.9	21.7 2.2
	453341	AI758912	Hs.296341	adenylyl cyclase-associated protein 2	3.9	7.2
	416854	H40164	Hs.80296	Purkinje cell protein 4	3.9	2.2
	414666	NM_004466	Hs.76828	glypican 5	3.8	6.2
35	418217	AI910647	Hs_13442	ESTs	3.8	3.2
	421855	F06504	Hs.27384	ESTs, Moderately similar to ALU4_HUMAN A	3.8	2.2
	414764	AW013887	Hs.72047	ESTs	3.8	10.7
	433629	R13140	Hs.13359	ESTs	3.7	2.7
40	424738	AI963740	Hs.46826	ESTs	3.7	2.1
40	407706 437268	AA191085	Hs.26612	ESTs, Moderately similar to \$23650 retro	3.7	5.3
	423135	AI754847 NS7655	Hs.227571 Hs.26411	regulator of G-protein signalling 4	3.7 3.7	53.7
	446818	AI342668	Hs.279765	ESTs ESTs	3.7	21.7 2.6
	427562	R56424	Hs.26534	ESTs	3.6	3.6
45	439274	AF086092	Hs.48372	ESTs	3.6	34.5
	452381	H23329	Hs.290880	ESTs, Wesldy similar to ALU1_HUMAN ALU S	3.6	6.0
	422897	AA679784	Hs.4290	ESTs	3.6	5.1
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	3.6	24.6
50	417154	A1674701	Hs.21388	ESTs	3.6	5.8
20	447176	Z42549	Hs. 160893	ESTs	3.6	6.4
	405977 423568	MINA ODESES	Un 120010	armuth amost assocife 2	3.6	3.9
	441235	NM_005256 AI884586	Hs.129818 Hs.135570	growth arrest-specific 2 Homo sapiens cDNA: FLJ21268 fis, clone C	3.6 3.6	2.5 5.4
	426775	AA384564	Hs.108829	ESTs	3.6	3.4
55	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	3.6	2.8
	425153	AW023193	Hs.27046	ESTs	3.6	4.9
	446495	D60923	Hs.153460	ESTs	3.5	9.8
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	3.5	16.6
-60	418421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.5	5.0
60	418207	C14685	Hs.34772	ESTs	3.5	16.0
	425383	D83407	Hs.156007		3.5	6.2
	417027 408367	AA192306 AK001178	Hs.23926	triadin	3.5	2.5
	408776	AA057365	Hs.44424 Hs.63356	homolog of rat orphan transporter v7-3 ESTs, Wealdy similar to I38022 hypotheti	3.5 3.5	5.3 5.5
65	453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	3.5	23.6
	419347	C15944	Hs.90005		3.5	42.3
	433803	AI823593	Hs.27688	supenorcervical gangilla, neural specifi ESTs	3,4	3.6
	450715	AJ266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.4	4.1
~~	415076	NM_000857		guanylate cyclase 1, soluble, bela 3	3.4	9.8
70	423826	U20325	Hs.1707	cocaine- and amphetamine-regulated trans	3.4	4.7
	427173	BE255017	Hs.97540	ESTs .	3.4	2.4
	446092	N33522	Hs.145894		3.4	3.5
	416868	A)656856	Hs.292597		3.4	4.5
75	458234	BE551408	Hs.127196		3.4	4.5
13	434053 428536	AW445136 AI143139	Hs.134946		3.4	3.9
	410356	A1143139 A1267589	Hs.2288 Hs.302689	visinin-like 1 hypothetical protein	3.3	42.3
	425785	T27017	Hs.159528		3.3 3.3	14.4 4.6
	434998	AW975157	Hs.26037	ESTs Come 2-00 moder sequence	3.3	4.7
80	456359	AI967991	Hs.93574	homeo box D3	3.3	4.4
	426527	NM_001037			3.3	5.2
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	3.3	9.0
	419875	AA853410	Hs.93557	proenkephalin	3.3	3.6



	444612	AW138111	Hs.22902	ESTs	3.3	3.0
	415242	R45986	Hs.295014	ESTs	3.2	2.2
	421640 408806	AW966652 AW847814	Hs.289005	gb:EST378726 MAGE resequences, MAGI Homo Homo sagiens cDNA: FLJ21532 fis, clone C	3.2 3.2	3.8 2.4
5	446015	T30968	Hs.13531	hypothetical protein FLJ10971	3.2	3.2
_	425495	AA358454	Hs.78026	ESTs, Weakly similar to similar to ankyr	3.2	2.2
	403092				3.2	2.9
	452971	AJ873878	Hs.91789	ESTs	3.2	4.5
10	454100 448440	AI593231	Hs.125043	chromosome 21 open reading frame 51	3.2	2.7
10	421200	AA173467 AA284811	Hs.62402 Hs.264433	p21/Cdc42/Rac1-activated kinase 1 (yeast ESTs	3.2 3.2	2.8 2.7
	440827	AI733110	Hs.128128	ESTs	3.2	21
	429809	AL162010	Hs.223603	Homo sapiens mRNA; dDNA DKFZp761D09121 (3.2	4.3
	420156	AW449258	Hs.6187	ESTs	3.2	19.0
15	457535	AA509685	Hs.278672	membrane component, ctvomosome 11, surfa	3.2	2.0
	419956	AL137939	Hs.40096	ESTs	3.1	8.7
	423930 417868	AA332697 A1078534	Hs.42721 Hs.122592	ESTs	3.1 3.1	2.7
	423346	A1267677	Hs.127416	ESTs synaptojanin 1	3.1	12.6 12.0
20	441921	AJ733376	Hs.164478	hypothetical protein FLJ21939 similar to	3.1	4.3
	429470	AI878901	Hs.203862	guanine nucleotide binding protein (G pr	3.1	5.3
	408217	AI433201	Hs.279860	tumor protein, translationally-controlle	3.1	7.1
	427322	AK002017	Hs.176227	hypothetical protein FLJ11155	3.1	6.3
25	449078	AK001256	Hs.22975	KIAA1576 protein	3.1	30.1
25	429608 442308	U49250 AA989402	Hs.210862 Hs.111	T-box, brain, 1 fibroblast growth factor 9 (glia-activat	3.1 3.1	2.2 3.0
	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	3.1	10.9
	427865	AA416931	Hs.126065	ESTs	3.1	7.5
20	430708	U78308	Hs.278485	offactory receptor, family 1, subfamily	3.1	3.4
30	451829	AW964081	Hs.247377	ESTs	3.0	6.2
	405911	41004000	11- 40050	507.	3.0	24
	418808 452893	AI821836 H18017	Hs.10359 Hs.22869	ESTs Abdocatoby similar to KIAA1395 and	3.0 3.0	6.2
	423952	AW877787	Hs.136102	ESTs, Moderately similar to KIAA1395 pro KIAA0853 protein	3.0	5.1 2.1
35	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC)	3.0	2.1
	405793				3.0	2.7
	410711	AB002316	Hs.65746	KIAA0318 protein	3.0	14.3
	427071	AA397958	Hs.192719	ESTs	3.0	2.1
40	453534 413903	NM_014796 AA496493	Hs.33187 Hs.23136	KIAAI748 gene product	3.0	14.5
40	426866	U02330	Hs.172816	ESTs neuregulin 1	3.0 3.0	2.2 11.3
	434945	AB033065	Hs.4280	KIAA1239 protein	3.0	3.5
	412639	AW961284	Hs.296235	ESTs	2.9	4.9
45	453590	AF150278	Hs.33578	KIAA0820 protein	2.9	33.1
45	414502	AL133721	Hs.224680	ESTs	2.9	2.3
	434367 425121	AB020700 AJ797511	Hs.3830	KIAA0893 protein	2.9	23.1
	412494	AL133900	Hs.154879 Hs.792	synaptotagmin I ADP-ribosylation factor domain protein 1	2.9 2.9	8.1 20.8
	401213	74.100300	110.102	Act amonates outlier protest i	2.9	3.2
50	401028	AW673312	Hs.50848	hypothetical protein FLJ20331	2.9	3.4
	415191	AA190381	Hs.120810	ESTa	2.9	3.0
	449275	AW450848	Hs.205457	perlaxin	2.9	5.6
	419863	AW952691	Hs.93485	Homo sapiens mRNA; cDNA DKFZp761D191 (fr	2.9	35.0
55	411421 430865	BE272110 AI073424	Hs.21177 Hs.5232	ESTs HSPC125 protein	2.9 2.9	2.0 11,4
-	437486	AW952089	Hs.5636	RAB6A, member RAS oncogene family	29	2.2
	442357	AJ458585	Hs.135706	ESTs	2.9	6.0
	408274	R17315		gb:yg12g11.r1 Soares Infant brain 1NIB H	2.9	2.2
60	444185	AW298350	Hs.66020	ESTs	2.8	5.0
00	420173 428358	AA256151	Hs.22999	ESTs	2.8	5.1
	447252	AA993222 R90916	Hs.101915 Hs.12449	Stargardt disease 3 (autosomal dominant) Homo sapiens transmembrane protein HTMP1	2.8 2.8	7.0 4.4
	440260	AI972867	Hs.7130	copine IV	2.8	10.6
	417084	H08370	Hs.33067	ESTs	2.8	8.4
65	438257	AW474419	Hs.224794	ESTs	28	2.8
	441934	T23939	Hs.7344	ESTs .	2.8	6.2
	447885	F11528	Hs.303172		2.8	3.5
	423552 450940	AF107028 AI744943	Hs.129783 Hs.143209		2.8	3.4
70	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	28 28	14.4 21.7
	445887	Al263105	Hs.145597		2.8	5.1
	425494	N55540	Hs.78026	ESTs, Weakly similar to similar to anklyr	2.8	2.4
	438202	AW169287	Hs.22588	ESTs	2.8	11.9
75	436199	R38946	Hs.127951		2.8	6.0
13	434826	AF155661 RS2692	Hs.22265	pyruvate dehydrogenase phosphalase	2.8	2.4
	415462 418070		Hs.12698 Hs.83407	ESTs glutamate receptor, metabotropic 7	28	3.4
	432149		Hs.157022		2.8 2.8	4, 5 9.5
~~	430371	D87466	Hs.240112		2.8	7.0
80	437357	AL359559	Hs.331666		2.7	2.5
	415838		Hs.7093	ESTs	2.7	3.6
	438875		Hs.213568		2.7	2.5
	419558	AW953679		gb:EST365749 MAGE resequences, MAGC Homo	2.7	3.1

	446318 445183	A1949389 AB007877	Hs.18067 Hs.12385	ESTs	2.7	4.1
	457012	R41480	Hs.127630	KIAA0417 gene product ESTs	2.7 2.7	5.3 19.0
-	431988	AC002302	Hs.77202	protein kinase C, beta 1	2.7	7.2
5	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	27	2.8
	447932 450214	AA837474 BE439763	Hs.20021 Hs.227571	vesicle-associated membrane protein 1 (s regulator of G-protein signatting 4	2.7	3.8
	434731	AA648049	Hs. 121518	ESTs	2.7 2.7	6.9 5.0
10	428839	A1767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	2.7	5.2
10	407709	AA456135	Hs. 23023	ESTs	2.7	2.5
	422420 443305	U03398 AK050693	Hs.1524 Hs.133318	tumor necrosis factor (figand) superfami ESTs	2.7 2.7	3.3
	435648	H24347	Hs.27524	ESTs	27 27	5.9 15.0
16	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	2.7	2.7
15	436771	AW975687	Hs.292979	ESTs	2.7	6.0
	428689 440503	NM_014351 NM_006539	Hs.189810 Hs.7235	sulfortranferase family 4A, member 1	27	4.B
	441006	AW605267	Hs.7627	calcium channel, voltage-dependent, gamm CGI-60 protein	2.7 2.7	4.4 3.1
20	410330	AW023630	Hs.46786	ESTs	26	29.5
20	434398	AA121098	Hs.3838	serum-inducible kinase	2.6	2.6
	438831 419066	BE263273 298492	Hs.6439 Hs.6975	synapsin () PRO1073 protein	26	7.8
	412643	AW971239	Hs.293982	ESTs	2.6 2.6	3.4 2.2
25	430456	AA314998	Hs.241503	hypothetical protein	26	17.9
25	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	26	29
	401421 419530	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	26	2.0
	441817	AW969706	Hs.293332	ESTs	2.6 2.6	4.2 3.8
20	439203	AA448930	Hs.8453	KIAA1587 protein	2.6	4.2
30	426054	U12431	Hs.168109	ELAV (embryonic lethal, abnormal vision,	2.6	5.1
	444583 417919	AW994403 A1928203	Hs.100861 Hs.86379	hypothetical protein FLJ 14600 ESTs	2.6	3.7
	434293	NM_004445	Hs.3796	Eph86	2.6 2.6	3.0 3.2
25	431716	D89053	Hs.268012	fatty-acid-Coenzyme A figase, long-chain	2.6	6.4
35	443037 440736	AW500305 D56919	Hs.299166	syntaxin 7	2.6	2.2
	404648	100919	Hs.265848	myomegalin	2.6 2.6	7.1
	429995	AA463571		gb:zx72e09.r1 Soares_total_fetus_Nb2HF8_	2.6	3.0 3.5
40	436508	AW504381	Hs.121121	ESTs, Wealty similar to S00755 pleckstri	2.6	3.9
40	441190 432278	H09073 AL137506	Hs.25046	ESTS	2.6	3.1
	442731	A1868167	Hs.274256 Hs.131044	hypothetical protein FLJ23563 ESTs	2.6 2.6	2.9
	416836	D54745	Hs.80247	cholecystokinin	2.6	4.1 14.9
45	449071	NM_005872	Hs.22960	breast carcinoma amplified sequence 2	2.5	2.4
45	438321 439693	AA709133	Hs.180144	ESTs	2.5	2.8
	443212	AI741816 AW269515	Hs.125897 Hs.102500	ESTs hypothetical protein FLJ20481	2.5 2.5	3.6
	423981	AL122104	Hs.136664	Homo sapiens mRNA; cDNA DKFZp434A1627 (f	2.5	2.8 3.8
50	407868	NM_000950	Hs.40637	proline-rich Gla (G-carboxyglutamic acid	2.5	3.1
30	443992 444124	AW022228 R43097	Hs.322922 Hs.6818	ESTs	2.5	27.9
	411379	AI816344	Hs.12554	ESTs, Wealty similar to NPL4_HUMAN NUCLE	2.5 2.5	5.3 38.0
	440474	AI207936	Hs.7195	gamma-aminobutyric acid (GABA) A recepto	2.5	3.8
55	446277	A1284218	Hs.159204	ESTs	2.5	2.2
JJ	410111 445162	Al620206 AB011131	Hs.189647 Hs.12376	ESTs piccolo (presynaptic cytomatrix protein)	2.5	3.5
	410718	AI920783	Hs.191435	ESTs	2.5 2.5	4.8 4.5
	417201	T60432	Hs.269084	ESTs, Moderately similar to AF097994 1 L	2.5	2.9
60	420274	AW968000	Hs.143389	ESTs, Weakly similar to T14318 ubiquitin	2.5	2.8
00	433496 437331	AF064254 AL353933	Hs.49765 Hs.21710	VLCS-H1 protein hypothetical protein DKFZp761G0313	2.5	4.7
	437368	AJ471969	Hs.182606	ESTs	2.5 2.5	3.3 3.0
	441985	BE047625	Hs.169815	ESTS	2.5	3.6
65	410025	BE220489	Hs.113592	ESTs, Moderately similar to 154374 gene	2.5	9.2
03	414680 429956	AA743331 Al374651	Hs.272572 Hs.22542	hemoglobin, alpha 2 ESTs	2.5	3.6
	429028	AA443439	Hs.48797	ESTs	2.5 2.5	23.9
	438109	AJ076621	Hs.71367	ESTs, Moderately similar to ALU7_HUMAN A	2.5	3.1
70	439780	AL109688	the garage	gb:Homo sapiens mRNA full length insert	2.5	2.3
. 0	440888 445246	N45600 Al217713	Hs.326880 Hs.147586	ESTs ESTs	2.5	3.9
	440152	AB002376	Hs.7006	KIAA0378 protein	2.5 2.4	2.6 23.6
	432740	AF061034	Hs.278898	tumor necrosis factor alpha-inducible ce	2.4	21.0
75	415122	D60708	Hs.22245	ESTs	2.4	3.9
, 5	432298 437948	AL118812 AA772920	Hs.274293	Homo sepiens mRNA; cDNA DKF2p761G1111 (f	2.4	9.8
	421360	AA297012	Hs.303527 Hs.103839	ESTs erythrocyte membrane protein band 4.1-8	2.4	9.8
	427115	AW972853	Hs.112237	ESTs	2.4 2.4	2.8 2.2
80	452074	8E299035	Hs.27747	G protein-coupled receptor 37 (endotheli	2.4	10.0
ΦV	436639 434520	D14838	Hs.111	fibroblast growth factor 9 (gila-activat	24	3.5
	411529	AA205273 AA430348	Hs.177011 Hs.317596	hypothetical protein Homo sapiens cDNA FLJ12927 fis, clone NT	2.4	3.1
	442272	AA988302	Hs.129172		24 24	3.0 2.1
				~ ~ ~		-

	400003	*******	11- 004 400			
	422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	24	2.7
	444647 415827	H14718 H17462	Hs.11506 Hs.23079	Human clone 23589 mRNA sequence ESTs	2.4	2.8
	451397	AA017432	Hs.84529	ESTs, Weakly similar to 2202_HUMAN ZINC	2.4 2.4	15.0
5	445200	AA084460	Hs.12409	somatostatin	24	3.9 3.7
•	451062	AL110125	Hs.25910	Homo sapiens mRNA; cDNA DKFZp564C1416 (f	2.4	24
	420328	Y19062	Hs.96870	stauten (Drosophila, RNA-binding protein	2.4	4.3
	432122	AA526514		gb:ni60f02.s1 NCI_CGAP_Ov2 Homo sapiens	2.4	4.3
• •	444125	AI124882	Hs.118121	ESTs	24	3.5
10	430538	AB032435	Hs.242821	differentiation-associated Na-dependent	24	10.8
	457519	X69438	Hs.3052	early growth response 4	2.4	2.4
	409371	R51736	Hs.12381	ESTs	24	2.1
	456303	AA224872	Hs.115088	ESTs	2.4	3.2
15	440105 400979	AA594010	Hs.6932	Homo sapiens clone 23809 mRNA sequence .	2.4	23.4
13	435296	R49685	Hs.24980	ESTs	24	4.1
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	2.4 2.4	6.5
	452032	BE244005	Hs.27610	retinoic acid- and interferon-inducible	2.4	18.5 2.2
	432098	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	24	2.7
20	408974	AW015458	Hs.297017	ESTs	2.4	2.5
	412177	ZZ3091	Hs.73734	glycoprotein V (platelet)	2.4	2.8
	413153	N94205		gb:za27a08.r1 Soares fetal liver spleen	24	2.5
	417583	AA668782	Hs.191284	ESTs, Weakly similar to ALU1_HUMAN ALU S	24	2.6
25	452034	F12234	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	23	3.0
25	424940	AA985308	Hs.194327	ESTa	2.3	6.3
	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	2.3	4.1
	419125 423641	AA842452 AL137256	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	23	2.9
	436407	T88803	Hs.130489 Hs.271507	ATPase, aminophospholipid transporter-li	23	8.7
30	448681	AL109781	Hs.21754	ESTs, Weakly similar to TIM_HUMAN PROBAB Homo sapiens mRNA full length insert cDN	23 23	3.2
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	23	5.2 54.7
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	23	9.1
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	2.3	5.0
	414828	AA156651		gb:zl05h05.r1 Soares_pregnant_uterus_NbH	23	2.4
35	445556	AJ910241	Hs.12887	actin-related protein 3-beta	23	8.5
	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	23	26.3
	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	23	2.5
	423420	AI571364	Hs.128382	Homo saplens mRNA; cDNA DKFZp76111224 (f	2.3	7.6
40	439450	R51613	Hs. 125304	EST8	2.3	26.3
40	427127	AW802282	Hs.22265	pyruvate dehydrogenase phosphatase	23	2.2
	447179	AW015633	Hs.157299	EST ₈	2.3	3.8
	414711 433449	AJ310440 AW772282	Hs.288735	Homo sapiens cDNA FLJ13522 fis, clone PL	2.3	2.3
	414320	U13616	Hs.75893	gb:hn71b05.x1 NCI_CGAP_Kid11 Homo sapien	2.3	3.8
45	416778	M16505	Hs.79876	ankyrin 3, node of Ranvier (ankyrin G) sterold sutfatase (microsomaf), arytsutf	2.3 2.3	2.5
	425130	AA448208	Hs.99163	ESTs	2.3 2.3	7.8 4.1
	456664	AW963354	Hs.334409	metallothionein 1G	2.3	2.5
	438283	AI458931	Hs.37282	ESTs	23	4.2
	417455	AW007066	Hs.18949	ESTs. Weakly similar to CA2B_HUMAN COLLA	2.3	3.0
50	412100	AW892731		gb:CM0-NN0005-100300-279-c02 NN0005 Homo	2.3	3.7
	448981	AI968719	Hs.195387	ESTs	2.3	3.2
	416101	R24854	Hs.268806	EST ₈	2.3	6.5
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	2.3	17.8
55	415734	NM_014747	Hs.78748	KIAA0237 gene product	2.3	40.1
33	424598 420230	AB020639	Hs.151017	estrogen-related receptor gamma	2.3	2.9
	451559	AL034344 AL119980	Hs.284188	forkhead box C1	23	2.4
	404835	AL113300	Hs.20935	hypothetical protein DKFZp761D221	2.3 2.3	5.7
	456765	AI497900	Hs.33067	ESTs	23	2.1 4.1
60	455517	AW984068		gb:RC0-HN0006-160300-011-e06 HN0006 Homo	2.3	2.4
	408206	AF041853	Hs.43670	kinesin family member 3A	2.2	18.5
	411770	NM_01427B	Hs.71992	heat shock protein (hsp110 family)	2.2	3.9
	430105	X70297	Hs.2540	cholinergic receptor, nicotinic, alpha p	2.2	2.6
66	458694	F12832	Hs.13298	ESTs	2.2	4.9
65	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	2.2	4.4
	439642	W81441	Hs.153967		2.2	2.4
	450138	AW152104	Hs.200879	ESTs	2.2	4.9
	454222 405328	BE144344	Hs.7589	ESTs, Wealthy similar to A46010 X-linked	22	3.7
70	431342	A1A/071010	Un 21660	ECT-	2.2	2.7
. •	453101	AW971018 AW952776	Hs.21659 Hs.94943	ESTs ESTs	2.2	5.2
	408897	N50204	Hs.283709		2.2 2.2	3.3
	451398	AI793124	Hs.144479		2.2	2.8 4.6
	438208	AL041224	Hs.65379	ESTs	2.2	4.6 10.4
75	408449	NM_004408			2.2	6.1
	414130	AJ670831	Hs.71592	Homo sapiens cDNA: FLJ21893 fis, clone H	2.2	3.1
	445016	U79716	Hs.12246	reelin	2.2	3.9
	424375	AF070547	Hs.146312	Homo sapiens clone 24820 mRNA sequence	2.2	2.3
90	424645	NM_014682		KIAA0535 gene product	2.2	11.7
80	409729	D51315	Hs.106289		2.2	4.9
	432809	AA565509	Hs.131703		2.2	19.9
	422890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.2	10.4
	428532	AF157326	Hs.184786	TBP-Interacting protein	2.2	6.5



	412074	AI871368	Hs.8417	handhallad and in DVT-2761180422		
	413074 414442	AA156238	Hs.32501	hypothetical protein DKFZp761M0423 ESTs	2.2 2.2	3.4 3.2
	452768	AW069459	Hs.61539	ESTs	2.2	2.0
5	450440	AB024334	Hs.25001	tyrosine 3-monoprygenase/typtophan 5-mo	2.2	3.2
5	426281 428411	AK000987 AW291464	Hs.169111 Hs.10338	oxidation resistance 1	2.2	2.3
	413787	AI352558	Hs.75544	ESTs tyrosine 3-monooxygenase/tryptophan 5-mo	2.2 2.2	2.3 3.1
	451734	NM_006176	Hs.26944	neurogranin (protein kinase C substrate,	2.2	8.5
10	439108	AW163034	Hs.6467	synaptogyrin 3	2.2	7.9
10	405385 447285	AI371849	Hs.200696	ATPena Claus III Ama IIIC	22	2.4
	452667	T87219	Hs.13219	ATPase, Class VI, type 11C ESTs	2.2 2.2	2.2 3.1
	422234	AF119818	Hs.113287	discs, large (Drosophila) homolog-essoci	21	6.3
16	410339	Al916499	Hs.298258	ESTa	21	3.2
15	413231 447104	D87461 R19085	Hs.75244 Hs.210706	BCL2-Eke 2	21	4.5
	451952	AL120173	Hs.301663	Homo sepiens cDNA FLJ13182 fls, clone NT ESTs	21 21	2.2 36.5
	415841	Z45637	Hs.7093	ESTs	21	24
20	441086	A1928489	Hs.213490	ESTs, Weakly similar to N33_HUMAN N33 PR	2.1	2.2
20	450407 427627	NM_000810 R87582	Hs.24969	gamma-aminobutyric acid (GABA) A recepto	21	6.6
	449712	R56545	Hs.179915 Hs.6100	guanine nucleofide binding protein (G pr ESTs	21 21	5.3 4.5
	409660	AW452065	Hs.258905	ESTs	21	21
25	430434	AL049548	Hs.241420	Homo sapiens mRNA for KIAA1756 protein,	21	5.4
25	434138	AA625804	Lin 24602	gb:zu86h01.s1 Soares_testis_NHT Horno sap	2.1	3.0
	448610 418948	NM_006157 AI217097	Hs.21602	nel (chicken)-fike 1 gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	21 21	4.8 2.9
	414876	AW950925	Hs.924	crystallin, mu	21	3.4
20	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	2.1	3.7
30	451249	AA016227	Hs.27280	ESTs	21	4.1
	451475 448743	T19093 AB032962	Hs.26450 Hs.21896	KIAA0725 protein KIAA1136 protein	2.1 2.1	2.1 29.7
	430814	U89336	Hs.247993	NG5 protein	21	2,7
25	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	2.1	23
35	426642 427335	AW068223	Hs.171581	ubiquitin C-terminal hydrotase UCH37	2.1	4.5
	459089	AA448542 F13036	Hs.251677 Hs.27373	G antigen 7B Homo sapiens mRNA; cDNA DKFZp56401763 (f	2.1 2.1	. 2.2
	435832	AA425688	Hs.41641	Bruno (Drosophila) -like 4, RNA binding	2.1	5.9
40	446383	T05816	Hs.92511	ESTs	2.1	2.9
40	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-438B2	21	2.1
	453976 415111	BE463830 R39039	Hs.163714 Hs.328455	ESTs EST	21 21	4.2 3.3
	452238	F01811	Hs.187931	ESTs	2.1	3.3 4.9
AE	445279	R41900	Hs.22245	ESTs	2.1	9.8
45	448799	A1937094	Hs.179080	ESTs .	2.1	3.1
	418338 445725	NM_002522 AK000956	Hs.84154 Hs.13209	neuronal pentraxin I hypothetical protein FLJ10094	2.1 2.1	8.3
	443537	D13305	Hs.203	cholecystokinin B receptor	2.1	5.4 4.1
50	454066	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	2.1	6.4
50	429954	AI918130	Hs.21374	ESTs	2.1	7.2
	415292 423563	H29016 R34734	Hs.200576 Hs.75209	ESTs protein kinase (cAMP-dependent, catalyti	21 21	3.9 3.1
	424906	A1565086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	21	4.7
66	459309	AA040620	Hs.5672	hypothetical protein AF 140225	2.1	2.2
55	439340 402598	AB032436	Hs.6535	brain-specific Na-dependent inorganic ph	2.1	4.7
	435406	8E314624 F26698	Hs.3128 Hs.4884	polymerase (RNA) II (DNA directed) polyp calclum/calmodulin-dependent protein kin	2.1 2.1	5.4 6.6
	448792	R42550	Hs.12826	ESTs	21	4.1
60	449500	AW956345	Hs.12926	ESTs	2.1	2.4
UU	441134 433361	W29092 AW469373	Hs.7678 Hs.300141	cellular retinoic acid-binding protein 1 ribosomal protein L39	21	5.0
	452946	X95425	Hs.31092	EphA5	2.1 2.1	2.7 5.0
	426167	AF039023	Hs.167496	RAN binding protein 6	2.0	2.2
65	453666	AW015681	Hs.135229		2.0	3.1
03	424632	AB014523	Hs.151406	171111111111111111111111111111111111111	2.0	3.5
	430416	AF017090 AC005531	Hs.21554 Hs.57806	Homo sapiens PAC clone RP4-701016 from 7	2.0 2.0	4.1 2.3
	445627	AW818475	Hs.7363	ESTs	2.0	21
70	417092	H97508	Hs.181165		2.0	2.5
70	453653 435850	AW505554 AF250847	Hs.144559		2.0	4.7
	435086	AF 250647 AW975243	Hs.283514 Hs.122596		2.0 2.0	3.7 2.1
	423191	D61506	Hs.8417	hypothetical protein DKFZp761M0423	20	2.1
75	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.0	2.8
75	431645	AF078849	Hs.266483		2.0	2.5
	429834 439607	A1929645 BE540565	Hs.225938 Hs.159460		2.0 2.0	3.6
	408033	AW138045	Hs.242256		2.0	17.5 4.0
00	430317	AB020645	Hs.239189	glutaminase	2.0	2.7
80	419631	AW188117	Hs.303154		2.0	2.6
	432660 454048	AJ288430 H05626	Hs.64004 Hs.6921	ESTs ESTs	20	2.3
	426917	AA913814	Hs.172854		2.0 2.0	15.9 3.1
				•		



	423246	AL119114	Hs.77196	spectrin, alpha, non-erythrocytic 1 (alp	2.0	2.9			
	415989 420276	AI267700 AA290938	Hs.317584 Hs.190561	ESTs. Highly similar to SORL_HUMAN SORTI	2.0 2.0	4.8 5.1			
_	424983	AJ742434	Hs.169911	ESTs	2.0	15.9			
5	446296	AA985662	Hs.63131	Homo sapiens cDNA FLJ13155 fis, clone NT	20	2.7			
	450006	AJ241555	Hs.60171	ESTS	2.0	3.5			
	TABLE 278	ł:							
	Pkey:		ue Eos probese	t identifier number					
10	CAT numb	er. Gen	e chuster numbe						
	Accession:	Gen	bank accession	numbers					
	Pkey	CAT Number	Accession						
	408274	104999_1		964 AA053547					
15	412100	1277224_1		108502 Z45826					
	412112	1277883_1		E180347 AW901900 BE180222 BE180218 BE18					
				E180219 BE180346 BE180343 BE180418 BE18 \W893615 H85799 H83501 BE180220	KUZ 25 BE 1604	221 BE 180341 AW901894 B	E180217 BE180227 AW901891 BE180345		
	413153	1350849_1		67565 BE067556					
20	413510	1374377_1		009 BE145525 BE145493					
	414828	149563_1		A156622 R14472	_				
	418948 419558	180808_1 185904_1		N886090 W38035 W38792 AA232835 AW93604 NW953680 AA244436 H82527 AA361046 AA244					
	421249	200649_1		W752388 AW847156 AA285373 AW879575 AW					
25	421640	204833_1		W966653 AA294989 AA385977					
	429995	311738_1		J277645 AL118763					
	430212 432122	314437_1 341756_1		1718503 AA469225					
	433449	366532_1	AW772282	.W973343 AA554293 AA592974					
30	434138	380572_1		W418787 AW074833 AI675642 AI393368					
	437483	43756_1	AL390174 A						
	439780 452502	47673_1 919733_1		123665 R26578 E007223 R30687			,		
	455517	1321782_1		AW984072 AW984077					
35	456407	184986_1		AA243209 AA281411					
	T. D. C 07								
	TABLE 27C: Pkey: Unique number corresponding to an Eos probeset								
	Ref:			The 7 digit numbers in this column are Genbank	Identifier (GI) numbers. "Dunham, et al."	refers to the publication entitled "The DNA		
40				n chromosome 22" Dunham, et al. (1999) Nature	402:489-495				
	Strand:			nd from which exons were predicted.					
	Nt_positio	ar. Ing	ACALES HUCTEOUG	e positions of predicted exons.					
	Pkey	Ref	Strand	Nt_position					
45	400979	8072554	Plus	160842-161028					
	401213 401421	9858408 7452889	Plus Minus	98243-98380,98489-98619 142291-142461					
	403092	8954241	Plus	174720-175016,175104-175406,175508-1758	313				
	404648	9796894	Minus	115334-116020					
50	404793	7232206	Minus	61087-61590	07.01000				
	404835 405326	6970743 4375975	Plus Plus	85462-85684,68139-88287,90338-91018,948 10633-10709,30805-30893,38078-38253,551		718-57818 66606-66841			
	405385	6552772	Plus	48332-48454	12-33321,311	110-31 0 10,000 50-000+1			
	405793	1405887	Minus	89197-89453					
55	405911	6758795	Plus	101008-101643					
	405977	8247789	Minus	135548-136177					
	TABLE 2	8A: About 139	genes up-regu	lated in glioma compared to normal adult tissues					
60							associated with glioma, a non-redundant set of 6614		
				ied were removed from the starting collection of the			iO3 GeneChip® array. Genes associated with s was greater than or equal to 2.5, and the "average"		
				to 50 units (this selects for the most abundant of					
	amongst	variou glioblas	toma, astrocyto	ma, and oligodendroglioma specimens; the "aver	rage" normal:	adult tissue level was set to t	he 85th percentile value amongst various non-		
65				r non-malignant brain tissues. In order to remove					
	amongst Pkey:			was subtracted from both the numerator and the set identifier number	e denominator	r before the ratio was evaluat	ted. Predicted protein domains are noted.		
	ExAcon;			ion number. Genbank accession number					
~~	Unigene	ID: U	nigene number						
70	Unigene		nigene gene titl						
	Prot. Oa R1;		redicted Protein ioma vs normal						
	KI.	9	mus a2 nouns	aduk ussues					
7.0	Pkey	ExAcon	UniGene I	O Unigene Title	P	rotein Domains	R1		
75	443902		Hs.12600				4.0		
	441476		Hs.17313				4.0		
	446048 407061		Hs.18208	1 KIAA1811 protein gb:H.sapiens PTX3 gene promotor reg		4_	3.6 3.7		
	414323			B KIAA0273 gene product	tr	n3;TM;	3.6		
80	439769	AA448828	Hs.30596	Homo sapiens mRNA full length inser	ti	actamase_8,Rhombold,TPR	3.6		
	429319		Hs.19906 Hs.9305	8 simitar to catcium/catmodufin depen angiotensin receptor-fika 1	P	kinase;TM;SS	3.6		
	443412 425533		Hs.9305	angiotensin receptor-like 1			3.5 3.5		
				- garage varyer and v	262		2.0		



	408610	AW026692	Hs.285050	ESTs	ion_trans.K_tetra.Kv2chan	3,4
	450678	AL109703	Hs.25314	Homo sapiens mRNA full length inser	KOUTASER'VTGAR'VASCHSU	3.4
	419171	NM_002846	Hs.89655	protein tyrosine phosphatase, recep	Y_phosphatase,ART;TM;SS	3.4
_	445875	AF070524	Hs.13410	Homo sapiens clone 24453 mRNA seque		3.4
5	412581	AA224244	Hs.182704	ESTs, Moderately similar to alterna		3.3
	424911 452753	AA984354 AA028049	Hs.7913 Hs.277728	ESTs SEC14 (S. cerevisiae)-like 2	CRAL_TRIO	3.3 3.3
	436648	R18656	Hs.352385	ESTs	pkinase_bkinase_C,PMP22_C	3.3 3.2
	452130	AW248349	Hs.28088	SGC32445 protein	TB2_DP1_HVA22;TM;SS	3.2
10	448848	AF131851	Hs.22241	hypothetical protein		3.2
	426470	AA528794	Hs.128644	ESTs		3.2
	419344 439783	U94905 A1125760	Hs.277445 Hs.24835	diacylglycerol kinase, zeta (104kD)	ank,DAGKa,DAGKc,DAG_PE-bi	3.2 3.2
	411358	R47479	Hs.94761	hypothetical protein FLJ14594 KIAA1691 protein	ig.LRR.LRRNT,LRRCT;TM;S TM;SS	3.2
15	409433	AA074382	Hs.135255	ADAMTS14	***************************************	3.2
	456940	H46986	Hs.31861	ESTs		3.1
	423744	D26158	Hs.1701	ELAV (embryonic lethal, abnormal vi	rm,Gene66;	3.1
	432227 449181	U28389 X96783	Hs.274122 Hs.23179	erythrocyte membrane protein band 4 synaptotagmin V	VHP;TM; C2TM:SS	3.1 3.1
20	422274	NM_015564	Hs.114169	KIAA0416 protein	LRR,LRRNT,LRRCT;TM;SS	3.1
	424607	NM_016848	Hs.151123	neuronal Shc	PID.SH2:	31
	416898	BE219510	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02	EGF,Rhabd_glycop;TM;SS=	3.1
	438162	NM_014618	Hs.6090	deleted in bladder cancer chromosom	TMLSS	3.1
25	439892 445330	AL043463 R52656	Hs.6755 Hs.21691	RaP2 interacting protein 8 ESTs	RUNSS	3.1 3.0
20	451768	NM_001406	Hs.26988	ephrin-83	7tm_1 Ephrin;TM;SS	3.0
	444457	- AI204146	Hs.92556	ESTS	Forlunead .	3.0
	458247	R14439	Hs.209194	ESTs		3.0
30	424616	U72671	Hs.151250	Intercellular adhesion molecula 5,	ig,ICAM_N;TM;SS	3.0
30	408971 423940	R38990 NM_012429	Hs.13485 Hs.277728	ESTs SEC14 (S. cerevisiae)-like 2	CRAL_TRIO;TM;	3.0 3.0
	458124	AW005548	Hs.124590	ESTs	CIVIL_INIO,IM	3.0
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA seque		3.0
26	444808	H20019	Hs.286084	ESTs	ank,ras,PH,ArfGap,HCO3_co	3.0
35	437696	Z83844	Hs.5790	hypothetical protein dJ37E16.5	Hydrolase;TM;	2.9
•	424016 421680	AW163729 AL031186	Hs.6140 Hs.289106	hypothetical protein MGC15730 Human DNA sequence from clone CTA-9	ig;SS Collagen;TM;SS	29 29
	418055	R18516	Hs.351299	ESTs, Weakly similar to 138022 hypo	ZZ,ZZ	2.9
40	444819	AI697836	Hs.148433	ESTs		2.9
40	420524	AB010575	Hs.98547	amiloride-sensitive cation channel	ASC;TM;	2.9
	416237	H30684	Hs.159863	ESTs		2.9
	432270 405569	AK001008	Hs.274233	Homo sapiens cDNA FLJ10146 ffs, clo NM_031481*:Homo sapiens solute carr	mito_carr,TM;SS	2.9 2.9
	428950	BE311879	Hs.194673	phosphoprolein enriched in astrocyt	DED:TM:	2.9
45	426128	NM_001471		gamma-aminobutyric acid (GABA) 8 re	7tm_3,sushi,ANF_receptor;	2.9
	447758	H17302	Hs.93967	ESTs, Wealthy similar to NBHUC8 deco	LRR, LRRNT, LRRCT; TM; SS	2.9
	445331 431010	H04489 BE251246	Hs.12520	Homo sapiens clone 23568, 23621, 23	PC_rep	2.9
	433065	N62902	Hs.248214 Hs.343660	complexin 1 Homo sapiens PAC clone RP4-651K2 fr	TM; ;SS	2.9 2.9
50	426845	AB025186	Hs.172740	microtubule-associated protein, RP/	EB1,CH;TM;	2.9
	454360	L78207	Hs.54470	ATP-binding cassette, sub-family C	ABC_tran,ABC_membrane,PRK	2.9
	438859	AI559626	Hs.93522	Homo sapiens mRNA for KIAA1647 prot	bZIP,K-box,7tm_2,EGF,cadh	2.9
	410515 434022	F12086 R18374	Hs.4257 Hs.117956	ESTs ESTs	PID,SH2,PID,SH2 hormone_rec,zf-C4	2.8 2.8
55	428960	AF052224	Hs.194684		Carta_C4,RPH3A_effector;T	2.8
	426290	A8007918	Hs.169182		WD40,TM;	2.8
	417287	AJ831678	Hs.285714		C2:TM;	2.8
	422575 417941	AK000546 A1056049	Hs.118552		PTR2;TM;SS	2.8
60	452707	A1093823	Hs.96297 Hs.45070	ESTs ESTs	Band_41,ERM	2.8 2.8
• •	424873	AB018294	Hs.153610		C2.PDZ;TM;	28
	408209	NM_004454	Hs.43697	ets variant gene 5 (ets-related mol	Ets;TM;	2.8
	415935	H09663	Hs.106490		PID	2.8
65	437999 428248	AW905038 AJ126772	Hs.90242 Hs.40479	ESTs ESTs	ion_trans	2.8 2.8
Ų,	414001	AJ610347	Hs. 103812		Gelsolin,VHP,p450	2.8
	406634	AA386235	Hs.74576	GDP dissociation inhibitor 1	GDI;TM;	2.8
	453439	AI572438	Hs.32976	guanine nucleotide binding protein	G-gamma;TM;	2.8
70	433320	D60647	Hs.250879		rm	2.8
70	420888 440001	AB006713 AI740721	Hs.100058 Hs.128292		Dihydroorotase;TM;	2.7 2.7
	417622	AW298163			WH2;TM;	2.7
	438626	AI198059	Hs.26370	ESTs	***************************************	2.7
7.0	404439			ENSP0000067222*:Mitochondrial 28S	OLF;\$S	2.7
75	448375	NM_004644		adaptor-related protein complex 3,	Adaptin_N;TM;	2.7
	420989 419651	AB002372 NM 007023	Hs.323833 Hs.91971		TM;	27
	414562				cNMP_binding,DEP,RasGEF,R	2.7 2.7
	410865		Hs.66727		IRK	2.7
80	421146		Hs.97993	ESTs, Moderately similar to SERP1 [2.7
	419087	AI871245	Hs.24835		IB, LRR, LRRNT, LRRCT; TM; S	2.7
	421499 425014		Hs.236131 Hs.171935		pkinase,Peptidase_M1;TM PID,PDZ	2.7 2.7
	- 20017		11 130		FIUFUL	2.1

	448655	AL035289	Hs.21708	hypothetical protein from clone 248	TM;SS	2.7
	424410	W79027	Hs.271762	ESTs		27
	447117	Al352798	Hs.40183	ESTs		27
5	447478	BE618843	Hs.28144	fibronectin type 3 and SPRY domain-	fn3,SPRY;TM;	2.7
,	437645 433698	R20728 H24201	Hs.21164 Hs.247423	ESTs adducin 2 (beta)	Abdeless M.T.A	2.7 2.7
	419701	AA248999	Hs.7913	ESTs	Aldolase_t1;TM;	27
	410510	AW294625	Hs.64064	potassium voltage-gated channel, su	cNMP_binding.ion_trans,PA	27
	452869	AB014534	Hs.30898	KIAA0634 protein	fn3;SS	27
10	428045	T15465	Hs.182231	thyrotropin-releasing hormone	:SS	27
	425218	NM_014909	Hs.155182	KIAA1038 protein	TM:	2.7
	425558	AF040723	Hs.158300	huntingtin-associated protein 1 (ne	TM:	2.6
	440789	AB007857	Hs.7416	KIAA0397 gene product	TBC,RUN:TM:	26
	418423	NM_014732	Hs.301658	KIAA0513 gene product	TM;	2.6
15	450400	AI594722	Hs.279744	ESTs	lectin_c	2.6
	413566	AW604451	Hs.285814	sprouty (Drosophila) homolog 4	SH2,SH3;TM;SS	2.6
	443759	BE390832	Hs.134729	FXYD domain-containing ion transpor	ATP1G1_PLM_MAT8;TM;\$\$	2.6
	425069	AA687465	Hs.298184	potassium voltage-gated channel, sh	aldo_ket_red	2.6
20	429291	A1933057	Hs.349189	mannosyl (alpha-1,3-)-glycoprotein		2.6
20	424798	AW016523	Hs.182850	ESTs		2.6
	447455	H38335	Hs.6750	Homo sepiens mRNA for FLJ00058 prot	TM;\$S	2.6
	417212	AW952823	Hs.351547	NS1-binding protein	E2_N,E2_C,DNA_mis_repair.	2.6
	432265	BE382679	Hs.285753	SCG10-like-protein	Stathmin;TM;SS	2.6
25	417005	C21115	Hs.26612	ESTs, Moderately similar to \$23650		2.6
23	421091	W22821	Hs.351612	ribosomal protein L26	TM;	26
	445472	AB005631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene	homeobox,CUT;TM;	2.6
	431967	AJ243653	Hs.373498	organic cation transporter	sugar_trTM;SS	26
	439151 424134	AW135066	Hs.283110 Hs.140950	carbonic anhydrase X	carb_anhydrase;TM;SS	26
30	430213	AF070637 AW993446	Hs.235445	hypothetical protein hypothetical protein FLJ21313	DUF176;SS -	2.6 2.6
50	445954	AA148926	Hs.27836	hypothetical protein FLJ22362	GRAM:TM; fn3;TM;	2.6
	445084	H38914	Hs.250848	hypothetical protein FLJ14761	TM;SS	2.6
	446236	NM_006293		TYRO3 protein tyrosine kinase	fn3,ig,pkinase;TM;	2.6
	433706	AW947250	Hs. 283645	ESTs	PH.RhoGAP	2.6
35	423606	AB011094	Hs.129892	KIAA0522 protein	PH,bZIP,IQ,Sec7;TM;	2.5
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome	· · · · · · · · · · · · · · · · · · ·	2.5
	448923	AL034562	Hs.22584	prodynorphin	Opiods_neuropep;S\$	2.5
	408115	AB033107	Hs.42796	KIAA1281 protein		2.5
	446772	AW294404	Hs.144515	Homo sapiens cDNA FLJ11672 fis, clo		2.5
40	427989	H85525	Hs.40479	gb:yv88h06.r1 Soares melanocyte 2Nb	TM;SS	2.5
	435833	8E259178	Hs.41641	Bruno (Orosophila) -like 4, RNA bin	rrm;TM;	2.5
	423797	8E259364	Hs.132898	fatty acid desaturase 1	heme_1,FA_desaturase;TM	2.5
	448277	BE622827	Hs.99486	hypothetical protein FLJ13044	mito_carr;TM;SS	2.5
4.5	417298	AW665639	Hs.37958	ESTs		2.5
45	415577	AF257770	Hs.20930	poly(rC)-binding protein 4	KH-domain;TM;	2.5
	420742	U79251	Hs.99902	opioid-binding protein/cell adhesio	ig;TM;SS	2.5
	419109	BE169157	Hs.172717	ESTs	pkinase,LRRCT,ig,LRR,LRRN	2.5
		••				
50	TABLE 2					
30	Pkey:			rresponding to an Eos probeset		
	Ref:	360	Dence source.	The 7 digit numbers in this column are Genban	k Identifier (GI) numbers. "Dunham, et al." refers to	the publication entitled The UNA
	Strand:			in chromosome 22" Ounham, et al. (1999) Natural and from which exons were predicted.	g 40Z403-435.	
	Nt_positi			le positions of predicted exons.		
55	породо	UII. 1110		to preside to predicted exerts.		
	Pkey	Ref	Strand	Nt_position		
	405569	6006906	Plus	99719-99873		
	404439	7139680	Plus	55316-55585		
60	TABLE 2	9A: ABOUT 362	GENES UP-F	REGULATED IN GLIOMA COMPARED TO NON	HALIGNANT ADULT BRAIN TISSUE	
					It brain tissue. These were selected as for Table 2	BA, except that the ratio of "average" of
					as set to the 99th percentile value amongst various	
					dult brain specimens, the "average" glioma value wa	
		d protein domair				-
65	Pkey:	Uni	ique Eos probe	set identifier number		•
	ExAccn:			ion number, Genbank accession number		
	Unigene		igene number			
	Unigene		igene gene title			
70			edicted Protein			
70	R1:	Çik	ma vs non-ma	fignant adult brain tissue		
	6 4	F=4		3. Heinen V.He	Busin Burni	D+
	Pkey	ExAccr	Unigene II		Protein Domains	RI
	414477 407241	U41635	Hs.76228	amplified in osteosarcoma	pkinase,LRR,TM;SS	11.2
75	408972	M34516 AL050100	He 40270	gb:Human ornega light chain protein	TM;	10.9
, ,	417512		Hs.49378 Hs.82226	OKF2P585D0919 protein glycoprotein (transmembrane) nmb	TM; PKD:TM:SS	7.0 6.9
	414001	A/6534 AI610347	Hs.10381	grycoprotein (transmembrane) nmo 2 ESTs, Moderately similar to ALU1_HU	Getsofin, VHP.p450	6.3
	428847	AI954833	Hs.98881		Octobra (Aut., bago	6.2
	407061	X97748		gb:H.sapiens PTX3 gene promotor reg		5.4
80	440020		Hs.17713			5.4 5.4
	408832					5.3
	406837		Hs.15611			5.2
	407607				crystalt,TM;	5.1
	-					

	435013	H91923	Hs.110024	NM_020142:Homo sapiens NADH:ubiquin		5.1
	424916	AW867440	Hs.23096	ESTs	em	5.1
	409659	AW970843	Hs.55682	eukaryotic translation initiation f	;SS	5.1
_	432576	AW157424	Hs.165954	ESTs. Wealtly similar to 138022 hypo	am	5.1
5	406621	X57809	Hs.181125	Immunoglobulin lambda locus	ig.HSP70,Ppx-GppA;TM;SS	5.1
	430418	R98852	Hs.36029	heart and neural crest derivatives	HLH	5.1
	441633 429707	AW958544 W76631	Hs.112242 Hs.211819	normal mucosa of esophagus specific matrix metafloproteinase 238	TM:SS	5.0
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome	ig,Peptidase_M10;TM;SS=	5.0 5.0
10	441321	H17182	Hs.7771	B-cell associated protein	Band_7;TM;	5.0
-	406848	AI264844	Hs.275865	ribosomal protein S18	Ribosomal_S13;	4.9
	423505	AF064090	Hs.129708	tumor necrosis factor (figand) supe	TNF;TM;SS	4.8
	433848	AF095719	Hs.93764	carboxypeptidase A4	Zn_carbOpept.Propep_M14;T	4.8
15	431882 446295	NM_001426 Al355029	Hs.271977 Hs.101660	engralled homolog 1	homeobox;TM; UM	4.8
13	409170	W91994	Hs.16145	ESTs, Wealdy similar to T14171 atax ESTs	rm	4.8 4.8
	421155	H87879	Hs.102267	lysyl oxidase	Lysyl_oxidase,Aldose_epim	4.7
	409202	AA236881	Hs.51043	hexosaminidase B (beta polypeptide)	Glyco_hydro_20,Glyco_hydr	4.7
~~	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	:88:	4.7
20	450463	AW952018	Hs.201398	G protein coupled receptor interact	C1q.Collagen;TM;SS	4.7
	445960	AI268399	Hs.140489	ESTs, Wealthy similar to LIN1_HUMAN	zl-C2H2,bZIP	4.7
	406807 409190	AA057605 AU076538	Hs.180920 Hs.50984	ribosomal protein S9	- Ribosomal_S4,S4,IRNA_int_	4.6 4.6
	401599	AUU/0536	ns.30304	sarcoma amplified sequence Target Exon	transmembrane4;TM;SS TM;	4.6
25	408901	AK001330	Hs.48855	hypothetical protein FLJ 10468	TNC	4.6
	441669	R78195	Hs.29692	Homo sapiens cDNA FLJ11436 ffs, clo	•	4.6
	405868	AA505445	Hs.300697	immunoglobulin heavy constant gamma	ig:TM;	4.6
	406699	L06505	Hs.182979	ribosomal protein L12	Ribosomal_L11;TM;	4.6
30	406663	U24683	Un 2100	immunoglobulin heavy constant mu	;\$\$	4.6
50	427714 407260	AF119850 L09095	Hs.2186	eukaryotic translation etongation f gb:Homo sapiens mRNA fragment.	COX8,SHMT,MIF,GST_C,EF1G_	4.6 4.5
	406803	H42321	Hs.163593	ribosomal protein L18a	Ribosomal_L18ae;TM;	4.5
	430397	AI924533	Hs.105607	bicarbonate transporter related pro	HCO3_cotransp:TM:	4.5
25	414044	BE614194	Hs.75721	profilin 1	profilin;TM;	4.5
35	424238	AA337401	Hs.137635	ESTs	TM;SS	4.5
	421532	AW138207	Hs.146170	hypothetical protein FLJ22969	Armadillo_seg,HEAT;TM;S	4.4
	421241 436398	X91817 H87136	Hs.102866 Hs.5174	transketolase-like 1 ribosomal protein S17	transketolase,transket_py	4.4 4.4
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and	Ribosomal_S17e,PotyA_pot; pkinase,ICE_p10,ICE_p20;T	4.4
40	446921	AB012113	Hs.16530	small inducible cytokine subfamily	ILB;SS	4.3
	433271	BE621697	Hs.14317	nucleolar protein family A, member	:	4.3
	406964	M21305		FGENES predicted novel secreted pro		4.3
	432191	AA043193	Hs.273186	hypothetical protein, clone Teletho	ABC1;TM;	4.3
45	420890 413053	AA434058	Hs.100071	6-phosphogluconolactonase	Glucosamine_iso;TM;	4.3
73	406687	AW963263 M31126	Hs.65377 Hs.352054	ESTs, Moderately similar to KIAA139 matrix metalloproteinase 11 (strome	TM; hemopexin,Peptidase_M10;T	4.3 4.2
	425157	NM_006227	Hs.283007	phospholipid transfer protein	LBP_BPI_CETP.LBP_BPI_CETP	4.2
	426386	AA748850	Hs.125830	bladder cancer overexpressed protei		4.2
	446490	AK000706	Hs.15125	hypothetical protein FLJ20699	TM;	4.2
50	431750	AA514986	Hs.283705		cpn60_TCP1	4.2
	428327	AW206236	Hs.28773	ESTs	cystatin,Coprogen_oxidas,	4.2
	417342 433688	W40277 AA628467	Hs.81994 Hs.112572	glycophorin C (Gerbich blood group) Homo sapiens cDNA FLJ14130 fis, clo	TM;	4.1 4.1
	433170	A8037816	Hs.8982	KIAA1395	TM;	4.1
55	423084	AU076474	Hs.123178	translocase of inner mitochondrial	m	4.1
	407926	AW956382	Hs.59771	ESTs	TYA;SS	4.1
	445636	AW105401	Hs.350068			4.1
	418689	AI360883	Hs.375584		filament,GTP_EFTU,EFG_C,G	4.1
60	450690 419092	AA296696 J05581	Hs.333418 Hs.89603		ATP1G1_PLM_MAT8;TM;SS	4.1
O O	447813	AI394345	Hs.238513	mucin 1, transmembrane hypothetical protein MGC5442	SEA;TM;SS ublauitin;TM:SS	4.0 4.0
	436419	AI948626	Hs.171356		AT_hook,ATHILA	4.0
	458147	AW752597		gb:IL3-CT0214-161299-045-B06 CT0214	PMM	4.0
10	443402	U77846	Hs.356316		PDZ,UM,pkinase	4.0
65	433435	BE545277	Hs.340959		EF_TS,UBA;	4.0
	413595	AW235215	Hs.16145	ESTs	rm :-Theo	4.0
	412607 419913	Z33642 AW270040	Hs.74115 Hs.34455	Immunoglobulin superlamity, member ESTs	ig:TM;SS	4.0
	415209	F00183	Hs.172004		EPH_fbd,fn3,pkinæse,	4.0 4.0
70	439310	AF086120	Hs.102793		casein_kappa,pkinase,ig,n	3.9
	421777	BE562088	Hs.108196		TM:	3.9
	409485	S80990	Hs.252138	fcolin (collagen/librinogen domain	Collagen_fibrinogen_C;TM=	3.9
	402241			Target Exon	p450;TM;SS	3.9
75	432716	A1762964	Hs.205180		LRR.UPAR_LY6;TM;	3.9
15	418140 434214		Hs.83551 Hs.155860	microfibrillar-associated protein 2	TM:SS	3.9
	406855	AF119871 AA902829	ns. 100000	hypothetical protein PRO2268 gb:ok72e06.s1 NCI_CGAP_GC4 Homo sap	;SS	3.9 3.9
	421567		Hs.198265		hemopexin,Peptidase_M10;T	3.9
	403364			Target Exon	SH2,Y_phosphatase	3.9
80	412339		Hs.314466	ESTs.	tubulin	3.8
	423007		Hs.196029		TIMP	3.8
	427600 405201		Hs.179774		PA28_alpha,PA28_beta;	3.8
	⇒ U⊃ZU1			Target Exon	mito_carr,SH2,SH3,Alpha_a	3.8

	436906	H95990	Hs.181244	mains histonome ethilities assessed	SAME LANCE	20
	407319	AI743332	Hs.257729	major histocompatibility comptex, c ESTs, Moderately similar to ALU7_HU	ig.MHC_I;TM;SS	3.8 3.8
	400290	H18836	Hs.31608	hypothetical protein FLI20041	rm,Upoprotein_2 Cys_knot	
	430240	BE303038	Hs.236547	Homo sapiens, clone IMAGE:2905978,		3.8
5	442487	AF191019	Hs.8361	hypothetical protein, estradigl-ind	HEAT_PBS;TM; URR,URRNT;TM;SS	3.8
_	408135	AA317248	Hs.42957	methyltransferase-like 1	Methyltransf_4;TM;	3.8
	419942	U25138	Hs.93841	potassium large conductance calcium	CaKB;TM;SS	3.8
	410584	AB011112	Hs.64742	KIAA0540 protein	OB (0,1 M,30)	3.8
	440676	NM_004987	Hs.112378	UM and senescent cell antigen-like	LIM:SS	3.8 3.8
10	406874	AW151706	Hs.180842	ribosomal protein L13	Ribosomal_L13e;SS	3.6 3.7
	429249	X81479	Hs.2375	egl-like module containing, mucin-l	7tm_2.EGF,GPS,S_locus_gly	3.7
	430799	C19035	Hs.164259	ESTs	FKBP,TPR	3.7
	453099	H62087	Hs.31659	thyroid hormone receptor-essociated	WD40;TM;	3.7
	421794	X85096	Hs.108371	E2F transcription factor 4, p107/p1	E2F_TDP.KOW,Ribosomal_L14	3.7
15	444795	AI193356	Hs.160316	ESTs	Tropornyosin ACOX	3.7
	443834	AI741510	Hs.173548	ESTs	CUB,MAM,F5_F8_type_C	3.7
	429731	AKD01592	Hs.212172	beta-carotene 15,15'-dioxygenase	RPE65;SS	3.7
	426433	L38969	Hs.169875	thrombospondin 3	TSPN,tsp_3,EGF,toxin;TM	3.7
	426395	BE151985	Hs.355669	hypothetical protein FLJ23316	pkinase	3.7
20	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardia	myosin_head,IQ,Myosin_tai	3.7
	447860	AF193807	Hs.131835	Rhesus blood group, B glycogrotein	Ammonium_transp_FecCD;TM=	3.7
	430281	A1878842	Hs.237924	CGI-69 protein	milo_carr,homeobox;TM;S	3.7
	448360	AL117560	Hs.306352	Homo sapiens mRNA; cDNA DKFZp566P23		3.7
0.5	446057	A1420227	Hs.366053	Trp-p8 transient receptor potential		3.7
25	432078	BE314877	Hs.24553	hypothetical protein FLJ12541 simil	TM;SS	3.7
	406854	AA513705	Hs.252259	ribosomal protein S3	KH-domain, Ribosomal_S3_C;	3.7
	422532	AL008726	Hs.118126	protective protein for beta-galacto	serine_carbpept.GalP_UDP_	3.7
	428171	AA489323	Hs.182825	ribosomal protein L3S	Ribosomal_L29;	3.6
20	442285	W28729	Hs.356072	uncharacterized hypothalamus protei	- '	3.6
30	411281	BE392792	Hs.4786	Homo sepiens cDNA: FLJ22849 fis, cl	cadherin	3.6
	457657	AW411509	Hs.352567	hypothetical protein PRO2121	UQ_con;TM;	3.6
	414624	BE389320	Hs.23628	3 beta-hydroxy-delta 5-C27-steroid		3.6
	451564	AU076698	Hs.132760	hypothetical protein MGC15729	sugar_tr,Condensation;TM=	3.6
25	445411	AL137255	Hs.12646	hypothetical protein FLJ22693	hormone_rec,zf-CCCH;TM;	3.6
35	400785			C11000861:gi[9938016 ref[NP_064687.	TM;SS	3.6
	413343	BE392026	Hs.334346	hypothetical protein MGC13045	TM;	3.6
	427380	NM_005534	Hs.177559	Interferon gamma receptor 2 (interf	fn3;TM;SS	3.6
	427818	AW511222	Hs.193765	ESTs	•	3.6
40	449957	031365	Hs.24220	hypothetical protein	TM;	3.6
40	451529	AI917901	Hs.208641	ESTs	actin	3.6
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	NoI1_Nop2_Sun;TM;	3.6
	431659	AA031875	Hs.266940	t-complex-associated-testis-express	Tctex-1;TM;	3.6
	433350	BE583152	Hs.10362	Homo sapiens cDNA: FLJ20944 fis, cl	zI-C3HC4,SPRY	3.6
45	412896	AW804157	Hs.375570	major histocompatibility complex, c	ig,MHC_II_beta;TM;SS	3.6
7)	441748	R14439	Hs.209194	ESTs		3.6
	406853	AAB14553	Hs.252259	hypothelical protein FLJ23059	KH-domain,Ribosomal_S3_C;	3.5
	457464	AW972234	Hs.126680	ESTs .		3.6
	429619 423309	AL120751	Hs.211568	eukaryotic translation initiation f		3.5
50	438682	8E006775	Hs.126782	sushi-repeat protein	sushi,HYR;SS	3.5
50	453022	AA354489 AA031499	Hs.375594 Hs.118489	EBP50-PDZ interactor of 64 kD	4-114	3.5
	434042	AI589941	Hs.8254	ESTs	Amino_oxidase	. 3.5
	424867	AI024860	Hs.153591	Homo sepiens, Similar to tumor diff	71.00	3.5
	417298	AW665639	Hs.37958	Not56 (D. melanogaster)-like protei ESTs	TM;S\$	3.5
55	403943	A11003003	113.37 330	C5000355:gi 4503225treftNP_000765.1		3.5
•	429497	AB028953	Hs.204121	KIAA 1030 protein	m3;TM;	3.5
	426613	U96132	Hs.171280	hydroxyacyl-Coenzyme A dehydrogenas	adh_short;TM;SS	3.5
	428343	AL043021	Hs.12705	ESTs	WD40;SS	3.5 3.5
	458376	AA683904	Hs.89862	TNFRSF1A-associated via death domai	desth;TM;	3.5
60	400348	AJ251708	Hs.352588	Target	0000,110,	3.5
	404854			Target Exon	;SS	3.5
	427930	AA417696	Hs.372121	ESTs	,	3.5
	453143	AA382234	Hs.356289	protein tyrosine phosphatase, recep	serpin;SS	3.5
	406806	AW088535	Hs.350108	ribosomal protein, large, PO	TM;	3.5
65	406793	AW264291	Hs.5662	guarine nucleotide binding protein	WD40;TM;	3.5
	414525	C14904	Hs.45184	Homo sapiens cDNA FLJ 12284 ffs, clo		3.5
	419950	AK001645	Hs.93871	hypothetical protein FLJ10783	Glyco_hydro_47;TM;\$\$	3.5
	404243			NM_006778:Homo sapiens ring finger	zf-C3HC4,zf-B_box;TM;SS	3.4
70	424611	NM_001421	Hs.151139	E74-like factor 4 (ets domain trans	Ets;SS	3.4
70	432831	AI821702	Hs.115959	ESTs, Weakly similar to 138022 hypo		3.4
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clo	TM;	3.4
	418558	AW082266	Hs.85131	Fas (TNFRSF6)-associated via death	death,DED:SS	3.4
	408930	AA146721	Hs.334686	hypothetical protein FLJ21588	CUE;TM;	3.4
75	403246	. 37		Target Exon	HMG_box;SS	3.4
75	416330	AU077101	Hs.79222	galactosidase, beta 1	Glyco_hydro_35;TM;SS	3.4
	404864			NM_025204":Homo sapiens hypothetica		3.4
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, cl	7tm_3	3.4
	430284	AI693534	Hs.293196			3.4
90	433669	AL047879	Hs.194251		RNA_pol_L,RNA_pol_L,RasGA	3.4
80	456050	R79445	Hs.76230	ribosomal protein \$10	S10_plectin;TM;	3.4
	422311	AF073515	Hs.114948		tn3;TM;	3.4
	408909	AW502034	Hs.287379			3.4
	428028	U52112	Hs.182018	interleukin-1 receptor-associated k	death,pkinase;TM;	3.4

	424042	050000					
	424213 416432	BE390125 BE391767	Hs.143187	hypothetical protein		DEAD,helicase_C;TM;	3.4
	400233	DE331101	Hs.79322	glutaminyl-IRNA synthetase		53	3.4
	403252			Eos Control Target Exon		Ribosomat_S9;	3.4
5	409433	AA074382	Hs.135255	ADAMTS14		TM;SS	3.4
	426053	U68105	Hs.172182	poly(A)-binding protein, cytoplasmi		mm,PABP;TM;	3.4
	448222	A1648587	Hs.20725	Mov10 (Moloney leukemia virus 10, m		TM:	3.4
	432982	AA531058	Hs.182248	truncated calcium binding protein		OPR.ZZ:TM:	3.4 3.4
10	453914	NM_000507	Hs.574	fructose-1,6-bisphosphatase 1		FBPase:TM:	3.4
10	444626	AA320893	Hs.117062	hypothetical protein FLJ14497		Pyr_redocTM;SS	3.4
	427751	AF000152	Hs.355816	conserved gene amplified in osteosa		NIF;TM;	3.4
	416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial		mito_cam;TM;	3.4
	428046 456575	AW812795	Hs.337534	ESTs, Moderately similar to 138022		ank	3.4
15	407366	AW063659 AF026942	Hs.191649	ESTS		Myosin_tail	3.4
1.5	414738	L24038	Hs.17518 Hs.77183	gb:Homo sapiens cig33 mRNA, partial		IBR	3.4
	456356	M74715	Hs.89560	v-raf murine sarcoma 3611 viral onc Iduronidase, alpha-L-		pkinase,DAG_PE-bind,RBD,T	3.4
	429668	AA626142	Hs.179991	ESTs, Weakly similar to S28942 prot		Glyco_hydro_39:SS	3.3
	404913			NM_024408*:Homo sapiens Notch (Dros		EGF,ank.notch.metalthio,E	3.3
20	426059	BE292842	Hs.166120	interferon regulatory factor 7		IRF:SS	3.3 3.3
	451619	AA018854	Hs.353196	glutathione peroxidase 3 (plasma)		PHSS	3.3
	410225	AW608964	Hs.12030	ESTs			33
	402534			Target Exon		;	3.3
25	433750	H15448	Hs.31330	Homo sepiens clone HQ0319		GLFV_dehydrog,GLFV_dehydr	3.3
2.7	421712 433333	AK000140	Hs.107139	hypothetical protein		TM;SS	3.3
	424915	AJ016521 R42755	Hs.71816	v-skt murine thymoma viral oncogene		pkinase,PH,pkinase_C	3.3
	408494	AA554714	Hs.23096 Hs.187578	ESTs		άm	3.3
	445084	H38914	Hs.250848	Nomo sapiens cDNA FLJ11639 ffs, clo hypothetical protein FLJ14761		71400	3.3
30	446478	AI950021	Hs.370306	ESTs		TM;SS	3.3
	425274	BE281191	Hs.155462	minichromosome maintenance deficien		TM; MCM;TM;	3.3
	456655	AI376736	Hs.111779	secreted protein, acidic, cysteine-		kazal;SS	3.3
	438912	AF085843		gb:Homo sapiens full length insert		Maca,00	3.3 3.3
25	428396	U70539	Hs.184161	exostoses (multiple) 1		Exostosin;TM;SS	3.3
35	437546	AW074836	Hs.173984	T-box 1		T-box,WD40;TM;	3.3
	410693	BE044206		gb:ho40c08x1 Soares_NFL_T_GBC_S1 H		C1q,Collagen,cystati	3.3
	414961	U27266	Hs.927	myosin-binding protein H		fn3,ig;TM;	3.3
	422766	AA334108	Hs.159572	heparan sulfate (glucosamine) 3-O-s			3.3
40	426120 452383	AA.325243 T70900	Hs. 166887 Hs. 27189	copine I		C2,mm;TM;	3.3
-10	456799	AC004923	Hs.135187	ESTs		zi-C2H2,PRK	3.3
	409227	AA806165	Hs.130323	unc93 (C.elegans) homolog B Homo sepiens, clone IMAGE:3950432,		TM;	3.3
	432659	AA281633	Hs.278586	KIAA1108 protein		NA;NA	3.3
	448997	AA130390	Hs.25549	hypothetical protein FLJ20898		TBC;TM; TM;SS	3.3
45	446990	AI354717	Hs.223908	ESTs		transmembrane4	3.3 3.3
	437259	AI377755	Hs.120695	ESTs		MHC_II_alpha.ig	3.3
	423461	AB020527	Hs. 128827	solute carrier family 17 (sodium ph		sugar_b;TM;	3.3
	421563	NM_006433	Hs.105806	granulysin		;SS	3.3
50	453804	AA300204	Hs.35276	KIAA0852 protein		TM;	3.3
50	428810 453933	AF068236	Hs. 193788	nitric oxide synthase 2A (inducible		NAD_binding,flavodoxin,FA	3.3
	449267	A1452933	Hs.65377	ESTs		EF_TS,UBA,transmembr	3.3
	418165	A1538640 R45959	Hs.220624 Hs.6637	ESTs			3.3
	446673	NM_016361	Hs.15871	ESTs		mito_can	3.3
55	402475	************	113.13071	LPAP for tysophosphatidic acid phos ublquitin specific protease 18		acid_phosphat;TM;SS	3.3
	404233			Target Exon		HIT	3.2
	406655	M21533	Hs.277477	major histocompatibility complex, c		ig,MHC_J;TM;SS	3.2
	414556	AW975063	Hs.343443	ribosomal protein L36		Ribosomal_t36e;	3.2 3.2
60	450191	AW137243	Hs.248074	ESTs .		homeobox;TM;	3.2
60	435906	AI686379	Hs.110796	SAR1 protein		ertres:TM:	3.2
	412540	C18341	Hs.73999	thyroid hormone receptor interactor		SHAFCHISS	3.2
	422562	AI962060	Hs.118397	AE-binding protein 1		Zn_carbOpept.F5_F8_type_C	3.2
	431051 407984	AA491143	Hs.283374	ESTs, Wealty similar to CA15_HUMAN		TM;	3.2
65	441494	AW134708 AW452344	Hs.243569 Hs.129977	ESTs			3.2
Ų,	423114	AU076497	Hs.1614	ESTs			3.2
	419833	AA251131	Hs.220697	cholinergic receptor, nicotinic, al ESTs		Neur_chan_LBD.Neur_chan_m	3.2
	419036	T80967	Hs.372603	gb:yd23f12.s1 Soares fetal liver sp		WHEP-TRS,IRNA-synt_1b,non	3.2
	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (spe		ness ash.sida.ThtCC	3.2
70	453094	AA740928	Hs.27356	ESTs		zona_pellucida;TM;SS	3.2
	426989	AI815206	Hs.367644			BAG,ubiquitin	3.2
	445033	AV652402	Hs.72901	cyclin-dependent kinase inhibitor 2		ank;	3.2 3.2
	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn sub		SH3,HS1_rep;TM;	3.2
75	438930	AW843633	Hs.343261	hypothetical protein AL110115		HLH	3.2
13	438183	8E263252	Hs.6101	hypothetical protein MGC3178		thiored;TM;	3.2
	421310	AW630087	Hs.103315	trinucleotide repeat containing 1		PHD	3.2
	409293	R02673	Hs.110156	ESTs			3.2
	407115 401174	AA084921	Hs.76230	ribosomal protein S10		S10_plectin;TM;	3.2
80	400217			Target Exon		transmembrane4,EF_TS,UBA	3.2
- •	408676	AI815189	Hs.\$7475	Eas Control sex comb on midleg homotog 1		ras;SS	3.2
	418245	AA088767	Hs.83883	transmembrane, prostate androgen in		Thice	3.2
	403694			Target Exon		TM;SS UDPGT	3.2
				-		our GI	3.2
					77		

	44.455	55440444				
	414265	BE410411	Hs.75864	endoplasmic reticulum glycoprotein		3.2
	451118 422624	AI862096 BE616678	Hs.50640	ESTS	EGF, wc, TIL; SS	3.2
	437388	AL359586	Hs.76152 Hs.14478	KOEL (Lys-Asp-Glu-Leu) endoplasmic	ER_lumen_recept	3.2
5	429150	AF120103	Hs.197366	Homo sapiens mRNA; cDNA DKFZp762H18 smoothened (Drosophila) homolog	COVE CULTING OF A CO.	3.2
	430379	AF134149	Hs.240395	potassium channet, subfamily K, mem	COX8,SHMT,MIF,GST_C,EF1G_ lon_trans;TMSS	3.2
	434956	8E266566	Hs.4288	hypothetical protein DKFZp434K046	Cutlin; TNt	3.2
	422166	W72424	Hs.112405	\$100 calcium-binding protein A9 (ca	ethand,S_100,TM;	3.2 3.2
10	452493	Al904031	Hs.106826	KIAA1696 protein	PHD,Myc-LZ,DC1,AT_hook;TM	3.2
10	413100 420764	BE065208		gb:RC1-BT0314-310300-015-b09 BT0314		3.2
	421680	BE250676	Hs.19928	hypothetical protein SP329	F-box;TM;	3.2
	406738	AL031186 AA587983	Hs.289106	Human DNA sequence from clone CTA-9	Collagen; TM; SS	3.2
	434288	AW189075	Hs.116265	gb:nj30b09.s1 NCI_CGAP_AA1 Homo sap fibrillin3	TIM,Ribosomal_S5;TM;SS=	3.1
15	438264	T88773	Hs.6133	calpain 5	EGF.granulin,TB,EB,TIL;TM	3.1
	436819	AA731746	Hs.120232	ESTs	Calpain_III,Peptidase_C2,	31
	459298	R85701		gb:ym86d09.r1 Soares adult brain N2	TM:	3.1 3.1
	452127	BE562126	Hs.28081	eukaryotic translation initiation f	mm,7tm_1,SNF;TMc	3.1
20	422305	AJ928242	Hs.293438	ESTs, Highly similar to AF198488 1		3.1
20	414393 423369	AA146855	th mores	gb:zo41h10.r1 Stratagene endothalia		3.1
	429457	BE219099 BE243065	Hs.279513 Hs.202955	ESTs	_	3.1
	409124	AW292809	Hs.50727	hypothetical protein FLJ20507 N-acetylglucosaminidase, alpha- (Sa	Cys-protease-3C;TM;	3.1
	429615	AF258627	Hs.211562	ATP-binding cassette, sub-family A	TM:SS	3.1
25	445519	AI635202	Hs.170132	hypothetical protein FLJ22494	ABC_tran;TM;SS TM;	3.1
	410007	AW950887	Hs.57813	zinc ribbon domain containing, 1	TFUS;TM:	31 31
	407228	M25079	Hs.155376	hemoglobin, beta	globin;TM;	31
	411573 406654	AB029000	Hs.70823	KIAA1077 protein	Sulfatase;TM;	31
30	435072	M90686	Hs.73885	HLA-G histocompatibility antigen, c	ig,MHC_I;TM;SS	31
50	456642	AW592176 AW451623	Hs.116932 Hs.109752	ESTs	zf-RanBP,MDM2	3.1
	445457	AF168793	Hs.12743	putative c-Myc-responsive camitine O-octanoy/transferase	:88	3.1
	448389	AW188950	Hs.345838	ESTs	Carn_acytransf;TM;	3.1
25	458248	BE407379	Hs.108082	ESTs, Wealdy similar to T31636 hypo	20G-Fell_Oxy,rrm,SH3,ras C1q,Collagen;TM;SS	3.1
35	451310	AW250651	Hs.26213	Human DNA sequence from clone RP3-4	TM:	3.1 3.1
	414688	A1750246	Hs.76901	for protein disutfide isomerase-rei	thiored;SS	3.1
	428797	AA496205	Hs.193700	Homo sapiens mRNA; cDNA DKFZp586103	LIM,Ran_BP1,GRIP,TPR,pro_	3.1
	425067 410639	BE223071	Hs.169142	ESTs		3.1
40	413011	BE269047 AW068115	Hs.65234 Hs.821	hypothetical protein FLJ20596	DEAD, helicase_C, PRK, AIP3;	3.1
. •	421502	AF111856	Hs.105039	biglycan solute carrier family 34 (sodium ph	LRR LRRNT;SS	3,1
	447164	AF026941	Hs.17518	vipirin; similar to inflammatory r	Ribosomal_L20,Na_Pi_cotra	3.1
	414907	X90725	Hs.77597	polo (Drosophia)-like kinase	MoaA_NifB_PqqE;TM; Ribosomal_L37aa,pkinasa,P	3.1
AE	418613	AA744529	Hs.86575	mitogen-activated protein kinase ki	pkinase, CNH; TM;	3.1 3.1
45	406734	AI565616		gb:to16h12.x1 NCI_CGAP_Ut2 Homo sap	provided by talk	3.1
	410188	AL096739	Hs.107260	hypothetical protein DKFZp586H0623	Ricin_6_lectin,Glycos_tra	3.1
	437959 406764	AM72068 AA429825	Hs.375604	KIAA1856 protein	elF5_elF2B,W2;TM;	3.1
	406637	U14966	Hs.343443 Hs.180946	ribosomal protein L38	Ribosomal_L36e;	3.1
50	451080	H41082	Hs.271783	ribosomal protein L5 ESTs	Ribosomal_L18p;	3.1
	414875	H42679	Hs.77522	major histocompatibility complex, c	in MUC II alabarTitano	3.1
	416365	U15131	Hs.79265	suppression of tumorigenicity 5	ig,MHC_II_alpha;TM;SS DENN,dDENN,uDENN;TM;SS=	3.1
	400261			Eas Control	ig.MHC_II_beta;TMtSS	3.1 3.1
55	412270	AC005262	Hs.73797	guarrine nucleotide binding protein	G-alpha.arf;TM;	31
	456843 443071	8E301883	Hs.152707	glioblastoma amplified sequence		3.1
	426196	AL080021 BE272095	Hs.8986	complement component 1, q subcompon	C1q,Collagen;SS	3.1
	424010	AL080188	Hs.167791 Hs.137558	reticulocation 1, EF-hand calcium b	efhand;SS	3.1
	439975	AW328081	Hs.6817	Homo sapiens mRNA; cDNA DKFZp434A13 inosine triphosphatase (nucleoside	cadherin,TM;SS	3.1
60	450761	R75930	Hs.174838	Homo sapiens cDNA FLJ14192 fs, clo	Hamip_like;TM;	3.1
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3	Y_phosphatase,DSPc;TM;S	3.1 3.1
	432395	AW295956	Hs.11900	hypothetical protein FLJ14972	Xink.zi-CCCH,G-patch,non	3.1
	407904	W44735	Hs.107260	Homo sapiens cDNA: FLJ21278 fis, cl		3.1
65	452500 432171	AW373011 AJ202503	Hs.54558	hypothetical protein FLJ22222		3.1
05	416768	AA363733	Hs.343661 Hs.1032	ESTs. Wealty similar to ALUB_HUMAN	WD40	3.1
	442492	AA528489	Hs.234518	regenerating islet-derived 1 atpha ribosomal protein L23	lectin_c;TM;SS	3.1
	421210	U80016	Hs. 102598	mucosal vascular addressin cell adh	Ribosomal_L14;	3.0
20	439429	AF150288		gb:AF150286 Human mRNA from cd34 st	TM;SS RA,Band_7,MBQAT	3.0
70	447463	AW378685	Hs.18625	Mitochondrial Acyl-CoA Thioesterase	Acyl-CoA_hydro;TM;	3.0
	448352	AA337951	Hs.20991	SET domain, bifurcated 1	AhpC-TSA,SET,MBD:TM;SS=	3.0 3.0
	428291	AA534009	Hs.183487	interferon stimulated gene (20kD)	- F	3.0
	445669 452862	AI570830 AW378065	Hs.174870	EST8	_	3.0
75	430069	AW378065 Al219293	Hs.8687 Hs.293660	ADAMTS2 (a disintegrin-like and me	Pep_M12B_propep.tsp_1,Rep	3.0
	451028	AA021258	Hs.123073	Homo sapiens, clone IMAGE:3535476, ESTs	SPRY,zl-B_box,zl-C3HC4;TM	3.0
	446021	BE389213	Hs.286	ribosomal protein L4	Dharand 1 4-714	3.0
	434652	AF148713	Hs.125830	bladder cancer overexpressed protei	Ribosomal_14;TM; WD40,DUF6;	3.0
80	425829	AL133079	Hs.134126	crystallin, gamma S	crystall;TM;	3.0 3.0
οv	424909	S78187	Hs. 153752	cell division cycle 258	Rhodanese:SS	3.0 3.0
	423579 444652	NM_004121	Hs.1675	gamma-glutamyttransferase-like acti	G_glu_transpept;TM:SS	3.0
	441283	BE513813 AA927670	Hs.11538 Hs.131704	actin related protein 2/3 comptex.	WD40;TM;	3.0
		~~~~	ra.131704	ESTs	CUB,MAM,F5_F8_type_C	3.0
				•	70	

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	437415 444542 442426	AL137400 Al161293 Al373062	Hs.306456 Hs.280380 Hs.332938	pre-mRNA processing factor 18 arninopeptidase hypothetical protein MGC\$370	Band_41,hormone2,Prp18;TM NAD_binding,flavodoxin,FA zf-RanBP,MDM2	3.0 3.0 3.0
5	447910 426858 445417 430482 427661	AL137679 NM_004182 AK001058 AF131810 AA410292	Hs.20000 Hs.172791 Hs.12680 Hs.241545 Hs.104761	Homo sepiens mRNA; cDNA DKFZp434D24 ubiquitously-expressed transcript a disintegrin-like and metalloprote hypothetical protein ESTs	Exonuclease;SS DUF232;SS bp_1.Reprolysin,Pep_M128 TM;SS writ	3.0 3.0 3.0 3.0 3.0
10	451876 453862 452965 441455	T63141 AL137493 Al904779 AJ271671	Hs.35945 Hs.247525 Hs.7854	gb:yb99a12s1 Stratagene lung (9372 Homo sapiens mRNA; cONA DKFZp434B12 Human DNA sequence from clone RP11- zinc/fron regulated transporter-lik	SH3 ig:TM; C2,PHD,RPH3A_effector.zf- Zp;TM;SS	3.0 3.0 3.0 3.0
15	452600 450775 417634 415152 410093	AI910842 AA902384 W27202 W22644 AW589558	Hs.103381 Hs.73853 Hs.82327 Hs.278712 Hs.299883	ESTs bone morphogenetic protein 2 glutathione synthetase Homo sapiens cDNA FLJ11074 fis, clo ESTs, Wealdy similar to KIAA0970 pr	Exo_endo_phos TGFb_propeptide,TGF-beta, GSH_synthase;TM;	30 30 30 30 30
20	412404 443466	AW075995 BE243123	Hs.86228 Hs.321045	TRIAD3 protein IKK-related kinase epsilon; inducib	pkinase,RIO1;TM;	10 30
20	TABLE 29	B:				
	Pkey.			et identifier number		
25	CAT numb Accession		e cluster numb bank accession			
23	Pkey 458147 406855	CAT Number 1030220_1 0_0		AW848490 AW849062 AW752597 AW752699		
30	400233	11259_1	BC004324 PBE255792 EBE392943 EBM011511 PBF308210 E	VM_001020 BC007977 M60854 BM050628 BG82 8194159 81668218 B1194376 BG716213 BG7144 BE394033 B1858915 B1668334 BE621019 BG7069 B1227282 BG489212 BG478388 BE727789 B1160 BE384213 BG832271 BG828032 BG481641 BF20	08 BE392513 AV722219 AW328077 BM424171 I 955 BE791985 BF967444 B193635 BE761859 B 9880 BG831707 BG324692 BM470427 B1083889 5675 BE899041 BE271558 B1193807 B1153866 I	BI828267 AW958606 BG831252 M466537 BG747165 BG827488 AI133550 BG831605 BG754114 BG420536 BG473786 BG397178 BI194428 BI117210
35			BI160764 B BG481705 I BG248771 I BI258369 B	8G759507 BF975645 BF343657 BM200598 BG8.1160371 BG754991 BF973348 BF683234 BF0325 BG104314 BM64565 BI261500 BG831857 BG83 BF975542 BM042233 B1161149 BG831302 BG83 GG31982 BM458301 BM019513 B1161350 B1114	337 BE388168 BM009051 B1192794 BG831002 B 187648 BG829852 BG756503 BG756419 BG76029 0033 BG829826 BM050064 B1193014 B1161360 178 BG481969 BG474870 BF974048 BF971122 I	IG830459 BG764737 BG761808 58 BG749762 BG480900 BG419627 BG822729 BG110091 BG105500 BE741405 BE395269 BG832027
40			BF183072 ( BF683451 ( BE909808 ) BI161172 B	BG490895 BM413638 BG943529 BG831012 BG5 BM459542 B1193881 BG832043 BG831323 B1194 BE907161 BM045391 B1194396 B1161269 BG747 B160988 B1160251 BG828764 BG826860 BG758 B116773 BG827153 BG825088 BG335419 BG105	545 B1160968 BG755930 BG706018 BE743855   958 BG546643 BF984863 B1160206 B1226402 B1 950 BF568228 B1818282 B1457127 BG831491 B 9404 A1929068 BE906354 BE408564 BM045000	BM465145 BG831227 BG774290 I226336 AW328236 BG339458 BF972634 IG759864 AI830010 BF568381 BE907238 BG339617 BG282794 BG335767
45			BE395717 BF034756 BM463802 BE901567	BF568921 BC829961 BC4773305 BC260397 AI92 BE391427 B192924 BC829757 BC476379 BE38 BE904077 BC630886 BE909153 BE907998 BE38 BE393375 BE393033 AW170187 BE730961 BE3 BE898833 BE880326 BF726889 BE910504 BE39	1536 Be394727 Be257695 Be905344 A433577 15767 A871751 Be744523 B192663 Beg31669 95410 Be744572 Be392297 Be391448 Be39078 0753 Be390131 AA650542 BE744156 Be394125	BE894416 BE886992 BE409223 A1000225 BE743836 BE272515 AA628078 30 BE388821 BE258477 BE905970 5 BE742207 BE395265 BE392942
50			BE907353 BE394133 BI261969 E BG830290	8E378222 6E906926 BE904650 BE393704 BE62 BE910491 BE909796 BE905331 AW248173 AI68 BE391478 BE910068 BE907165 BE742109 AA99 BE741707 BE392216 BM042783 BF570283 B282 BF569308 BF569156 BI194587 BE390831 BG74	3576 BE908826 BE620180 BF037570 BE908312 15746 BE561195 BE908825 BE906872 BE906570 1119 BE395707 BE378298 AW327827 BE334422 5096 Al681675 BE395674 AA136372 BE279892	2 BE615015 BE256977 BE746875 9 BE906017 BE910442 BE514657 1 BF569178 BE283240 AI700512 AA442822 BE384898 AA313519 AI878866
55	438912 410693 413100	4071_1 1054267_1 1490226_1	AA379888 AF085843 BE044206	F33366 BE394852 F29153 F33618 A1133637 AA F29022 BF089981 F31013 F24305 R70623 R70523 AW797320 BE161676 AW797356 AW797352 BE065168 BE065313 BE065208	300009 F34063 F29455 AU099691 AI905085 AI9	06656 AA343249 BE388691 AW404280
60	406738 459298 414393	0_0 90831_2 15833_3	AL532972 BE895187	BFB02216 R86701 BFB02224 R84600 BF356151 BI092731 AI765546 AA393801 AI129669 AI3935 AA393867 BI052082		470541 AL550388 AA146856 AI074762
65	406734 400261 439429	0_0 23110_1 452694_1	AJ357070	A159144 X X33056 NM_002120 M26040 AW469119 AW469 A1865365 AW014799 A1767973 AW518041 AA90 AV739062 AA835857		N629032 AI358810 AI880433 AI440472
	451876	2328579_1	T63141 AI	821021 BF370092 BF370127 BF370060 T62998		•
70	TABLE 2 Pkey: Ref:	Ur Se se	dieuce eonos	orresponding to an Eos probeset  The 7 digit numbers in this column are Genbank an chromosome 22" Dunham, et al. (1999) <u>Nature</u>		o the publication entitled "The DNA
75	Strand: Nt_posit			rand from which exons were predicted. ide positions of predicted exons.		
80	Pkey 401699 402241 403364	Ref 3175654 7690131 8571785	Strand Minus Minus Plus	Nt_position 33285-34084 125073-125206,130996-131125 120351-120465		
80	405201 400785 403943 404854	7230116 8131682 7711864 7143420	Plus Plus Plus Plus	36934-37314 43113-43967 100742-100904,101322-101503 14260-14537		

	404243	5672609	Plus	74695-75123
	403246	7637831	Minus	143547-143654,143741-143900
_	404864	5263010	Phus	94495-94681,95055-95195,97396-97506,9760
	403252	7677983	Plus	102214-102692
5	404913	7341740	Plus	97717-97976
•	402534	9801061	Plus	58989-59457
	402475	7547191	Plus	65363-65725
	404233	8218045	Minus	84791-85123
	401174	9438414	Minus	132847-133917
10	403694	7107765	Plus	142925-143080,165505-166186,167486-16763

TABLE 30A: ABOUT 282 GENES UP-REGULATED IN GLIOMA COMPARED TO NON-MALIGNANT ADULT BRAIN TISSUES THAT ARE LIKELY TO ENCODE EXTRACELLULAR OR CELL-SURFACE PROTEINS

Table 30A lists about 282 genes up-regulated in glioma compared to non-malignant adult brain tissues that are likely to encode extraceflular or cell-surface proteins. These were selected as for Table 28A, except that the ratio of "everage" glioma to "everage" normal adult to train tissues was greater than or equal to 4.0, the "everage" glioma speciments, the "everage" normal adult brain tissue was set to the 75th percentile value amongst various glioma speciments, the "everage" officer was set to the 75th percentile value amongst various non-malignant brain tissues, the "everage" glioma value was greater than or equal to 50 units (this selects for the most abundant of the up-regulated genes), and the predicted protein contained a structural domain that is indicative of extraceflular localization (e.g. ip, fit), efg., 7tm domains, signal sequences, transmembrane domains). Predicted protein domains are noted.

Phase:

Exercise Accession number, Genbank accession number

Unigene Title:

Unigene number

Unigene en title

Protein Domains:

R1:

glioma vs. non-malignant adult brain tissues likely to encode extraceflular or cell-surface proteins 15

20

25

	Pkey 406868	Accession AA505445	UniGene ID Hs.300697	Unigene Title Immunoglobulin heavy constant gamma	Protein Domains ig:TM;	R1 37.6
	407241	M34516	NS.300037	gb:Human ornega light chain protein	TM:	22.7
30	414477	U41635	Hs.76228	amplified in osteosercoma	pkinase,LRR:TM;SS	22.7
50	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	PKD:TM:SS	15.4
	406803	H42321	Hs.163593	ribosomal protein L18a	Ribosomal_L18ae;TM;	14.2
	429707	W76631	Hs.211819	matrix metalloproteinase 238	ig,Peptidase_M10;TM;SS=	12.8
	419092	J05581	Hs.89603	mucin 1, transmembrane	SEA:TM:SS	12.8
35	414738	L24038	Hs.77183	v-rai murine sarcoma 3511 viral onc	pkinase,DAG_PE-bind,RBD;T	12.4
55	441384	AA447849	Hs.288660	Homo saciens cDNA: FLJ22182 fis, cl	7tm_3.none	11.6
	406621	X57809	Hs.181125	immunoglobulin tambda locus	ig,HSP70,Ppx-GppA;TM;SS	11.0
	410584	AB011112	Hs.64742	KIAAD540 protein	none	11.0
	426395	BE151985	Hs.355669	hypothetical protein FLJ23316	pkinase,none	10.7
40	425184	BE278288	Hs.155048	Lutheran blood group (Auberger b an	in:TMtSS	10.7
70	430379	AF134149	Hs.240395	potassium channel, subfamily K, mem		10.7
	408972	AL050100	Hs.49378	DKFZP586D0919 protein	ion_trans;TM;SS TM:	9.9
	446921	AB012113	Hs.16530		1.8:SS	9.9
	452862	AW378065	Hs.8687	small inducible cytokine subfamily		9.9
45	418101			ADAMTS2 (a disintegrin-like and me	Pep_M12B_propep,tsp_1,Rep	
73	400290	AL047476 H18836	Hs.296310	gap junction protein, alpha 4, 37kD	connexin;TM;SS	8.5
	401699	H 10030	Hs.31608	hypothetical protein FLJ20041	Cys_knot	8.4
	423309	BE006775	14. 400700	Target Exon	TM;	8.1
			Hs.126782	sushi-repeat protein	sushi,HYR;SS	8.1
50	427600	AW630918	Hs.179774	proteasome (prosome, macropain) act	PA28_alpha,PA28_beta;	7.9
20	436906	H95990	Hs.181244	major histocompatibility complex, c	ig.MHC_I:TMt.SS	7.8
•	425335	BE394327	Hs.296267	follistatin-like 1	efhand,kazat,arf,ras,7tm_	7.7
	413011	AW068115	Hs.821	biglycan	LRR.LRRNT;SS	7.7
	446295	Al355029	Hs.101660		UM	7.7
55	436398	H87136	Hs.5174	ribosomal protein S17	Ribosomal_S17e,PolyA_pol;	7.6
22	435013	H91923	Hs.110024	NM_020142:Homo sapiens NAOH;ublquin	none	7.4
	431809	A1623488	Hs.333488		TM;SS	7.4
	424608	X80695	Hs.151134	oxidase (cytochrome c) assembly 14	60KD_IMP;TM;	7.3
	438560	AA481690	Hs.300697		0 505 ANAZO WIL 14-4-4-1-	7.3
60	429297	X82494	Hs.198862	fibulin 2	EGF,ANATO,TIL,spidertoxin	7.3
UU	450463	AW952018	Hs.201398		C1q,Collagen;TM;SS	7.2
	417342	W40277	Hs.81994	glycophorin C (Gerbich blood group)	TM;	7.2
	414588	AJ750246	Hs.76901	for protein disultide isomerase-rel	thiored;SS	7.2
	414044	BE614194	Hs.75721	profilin 1	profilin;TM;	7.1
65	404864	05555		NM_025204*:Homo sapiens hypothetica		7.1
05	452127	BE562126	Hs.28081	eukaryotic translation initiation (	rm,7tm_1,SNF;TM;	7.0
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	;SS	7.0
	409826	AW501112	Hs.353013		none	6.9
	434343	AW956705	Hs.3804	DKFZP564C1940 protein	ld1_recept_a;TM;	6.9
70	427714	AF119850	Hs.2186	eukaryotic translation elongation f	COX8,SHMT,MIF,GST_C,EF1G_	6.9
70	437259	AJ377755	Hs.120695		MHC_fl_alpha.ig,none	6.9
	429212	NM_001504	Hs.198252		7tm_1;TM;	6.8
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A re	Neur_chan_LBD,Neur_chan_m	6.8
	423505	AF064090	Hs.129708		TNF;TM;SS	6.8
75	413053	AW963263	Hs.65377	ESTs, Moderately similar to KIAA139	TM;	6.7
75	430542	AJ557486	Hs.119122		Ribosomal_L13,LACT,arf,ra	6.7
	435906	A1686379	Hs.110796		art,ras;TM;	6.6
	429307	AU076592	Hs.198951		bZIP;TM;	6.4
	437388	AL359586	Hs.14478	Homo sapiens mRNA; cDNA DXFZo762H18	none	6.4
80	415714	NM_002290		teminin, alpha 4	taminin_EGF,taminin_G,Tro	6.3
δU	406733	AA976565	Hs.297753		filament,bZIP.Apolipoprot	6.3
	411295	BE207307	Hs.10114	growth suppressor 1	20G-Fell_Oxy;TMtSS	6.3
	441321	H17182	Hs.7771	B-cell associated protein	Band_7;TM;	6.3
	444637	T19101	Hs.11494	fibulin 5	EGF,TIL;\$\$	6.3

	412721	DC343046	15. 95544			
	413731 422901	BE243845 R81936	Hs.75511 Hs.374568	connective tissue growth factor	Cys_knot,ksp_1,vwc,lGF8P;	6.2
	430397	AI924533	Hs.105607	ribosomal protein £44 bicarbonate transporter related pro	sushi,none	6.2
	429630	M85289	Hs.211573	heparan sulfate proteoglycan 2 (per	HCO3_cotransp;TM;	6.1
5	434867	AF159442	Hs.103382	phospholipid scramblase 3	EGF.ig.laminin_B.laminin_ SAPA.Scramblase;TMtSS	6.1
_	431449	M55994	Hs.256278	tumor necrosis factor receptor supe	TNFR_c6;TM;SS	6.1 6.1
	440676	NM_004987	Hs.112378	LIM and senescent cell antigen-like	LIM:SS	6.0
	424558	NM_002406	Hs.151513	mannosyl (alpha-1,3-)-glycoprotein	GNT-I,Glycos_transf_2;TM=	5.9
10	439310	AF085120	Hs.102793	ESTs	casein_kappa,pkinase,ig,n	5.9
10	410169	AI373741	Hs.59384	hypothetical protein MGC3047	ig:TM;	5.8
	423007	AA320134	Hs. 196029	Homo sapiens mRNA for KIAA1657 prot	TIMP,none	5.8
	414265	BE410411	Hs.75864	endoplasmic reticulum glycoprotein	none	5.8
	427715	BE245274	Hs.180428	KIAA11B1 protein	TM;	5.8
15	409220 450690	BE243323 AA296696	Hs.51233	tumor necrosis factor receptor supe	TNFR_c6.death,Lipoprotein	5.8
13	433848	AFD95719	Hs.333418 Hs.93764	FXYO domain-containing ion transpor	ATP1G1_PLM_MAT8;TM;SS	5.8
	446404	AAD19961	Hs.26216	carboxypepődase A4 LOC50627	Zn_carbOpept,Propep_M14;T	5.7
	441641	A1650417	Hs.247068	ESTs. Moderately similar to ALU8_HU	none Proje 4a Shrinasaa C Ca	5.7
	418875	W19971	Hs.233459	ESTs	Pterin_4a,fibrinogen_C,Co Xlink,none	5.7 5.7
20	424748	AA346257	Hs.134933	ESTs	none	5.7 5.7
	439737	AJ751438	Hs.41271	Homo sapiens collagen, type VIII, a	C1q,Coflagen,none	5.7
	448950	AF288687	Hs.9275	CGI-152 protein	E1-E2_ATPase,Hydrolase;TM	5.6
	406654	M90686	Hs.73885	HLA-G histocompatibility antigen, c	Ig.MHC_I:TM;SS	5.6
25	423084	AU076474	Hs.123178	translocase of inner mitochondrial	mm	5.6
23	402241			Target Exon	p450;TM;SS	5.6
	425157	NM_006227	Hs.283007	phospholipid transfer protein	LBP_BPI_CETP,LBP_BPI_CETP	5.6
	428343 447990	AL043021 BE048821	Hs.12705	ESTs	WD40;SS	5.6
	412607	Z33642	Hs.20144 Hs.74115	small inducible cytokine subfamily	ILB;SS	5.6
30	447625	AW505364	Hs.19074	Immunoglobulin superfamily, member LATS (large tumor suppressor, Droso	ig:TM;SS	5.5
	408056	AA312329	Hs.42331	ephrin-A4	pkinase,pkinase_C,UBA,Pol	5.5
	445960	AI268399	Hs.140489	ESTs, Weakly similar to UN1_HUMAN	Ephrin;TM;SS zf-C2H2,bZiP,none	5.5 5.5
	406874	AW161706	Hs.180842	ribosomal protein L13	Ribosomal_L13e;SS	5.4
0.5	418558	AW082266	Hs.86131	Fas (TNFRSF6)-associated via death	death,DED:SS	5.4
35	414638	W03516	Hs.76698	stress-associated endoplasmic retic	TM:SS	5.4
	409190	AU076536	Hs.50984	sarcoma amplified sequence	transmembrane4;TM;SS	5.4
	429150	AF120103	Hs.197366	smoothened (Drosophila) homolog	COX8,SHMT,MIF,GST_C,EF1G_	5.3
	453099	H62087	Hs.31659	thyroid hormone receptor-associated	WD40;TM;	5.3
40	414443 441283	AU077268	Hs.76144	platelet-derived growth factor race	ig.pkinase;TM;	5.3
40	414249	AA927670	Hs.131704	EST ₈	CUB,MAM,F5_F8_type_C,none	5.3
	451154	AI797994 AA015879	Hs.279929 Hs.33536	gp25L2 protein	Sulfotransfer, EMP24_GP25L	5.3
	406655	M21533	H\$.277477	ESTs major histocompatibility complex, c	TIMP,none	5.2
	406656	M16714	Hs.89643	major histocompatibility complex, c	ig.MHC_i;TM;SS	5.2
45	449224	AW995911	Hs.299883	hypothetical protein FLJ23399	transketolase.transket_py fn3;TM;	5.2 5.2
	422562	AI962060	Hs.118397	AE-binding protein 1	Zn_carbOpept.F5_F8_type_C	5.2 5.2
	436127	W94824	Hs.11565	RIKEN cONA 2010100012 gene	TM:SS	5.2
	428327	AW206236	Hs.28773	ESTs	cystatin,Coprogen_oxidas,	5.2
50	427080	AW068287	Hs.301175	ras-related C3 botulinum toxin subs	ras;TM;	5.2
50	414624	BE389320	Hs.23628	3 beta-hydroxy-delta 5-C27-steroid	none	5.2
	430281	A1878842	Hs.237924	CGI-69 protein	mito_carr,homeobox;TM;S	5.2
	426433	L38969	Hs.169875	thrombospondin 3	TSPN,tsp_3,EGF,toxin;TM	5.1
	432716 451564	A1762954 AU076698	Hs.205180	ESTs	LRR,UPAR_LY6;TM;	5.1
55	409340	BE174629	Hs.132760 Hs.321130	hypothetical protein MGC15729	sugar_tr,Condensation;TM=	5.1
	432680	T47384	Hs.278613	hypothetical protein MGC2771 interleron, alpha-inducible protein	aa_permeases,pyridoxal_de	5.1
	404913		144,0013	NM_024408*:Homo sapiens Notch (Dros	TMSS	5.1
	409485	880990	Hs.252136	ficolin (collagen/fibrinogen domain	EGF,ank,notch,metalthio,E Collagen,fibrinogen_C;TM=	5.1 5.1
	432078	BE314877	Hs.24553	hypothetical protein FLJ12541 simil	TM:SS	5.1
60	406687	M31126	Hs.352054	matrix metalloproteinase 11 (strome	hemopexin,Peptidase_M10;T	5.1
	423712	W46802	Hs.81988	disabled (Orosophila) homolog 2 (mi	PID,MACPF,ktl_recept_a,ts	5.0
	441595	AW206035	Hs.356457	ESTs	sugar_tr,none	5.0
	450435	AI695975	Hs.201805	ESTs	EGF_taminin_B,taminin_EGF	5.0
65	443177	BE268461	Hs.202	benzodiazapine receptor (peripheral	TapO_MBR;TM;SS	5.0
UJ	433435 426386	BE545277 AA748850	Hs.340959	Ts translation elongation factor, m	EF_TS,UBA;	5.0
	419913	AW270040	Hs.125830	bladder cancer overexpressed protei	none	5.0
	446696	AF279265	Hs.34455 Hs.298476	ESTs	EPH_lbd,fn3.pkinase,	5.0
	448997	AA130390	Hs.25549	solute carrier family 26, member 6 hypothetical protein FLJ20898	Sulfate_transp,STAS,xan_u	5.0
70	413891	8E271020	Hs.355753	tumor suppressor deleted in oral ca	TM;SS	5.0
	453143	AA382234	Hs.356289	protein tyrosine phosphatase, recep	none serpin;SS	5.0 5.0
	448249	AW855331	Hs.337124	ESTs	carb_anhydrase,UCH-1,UCH-	5.0 5.0
	412819	T25829	Hs.24048	FK506 binding protein precursor	FKBP;TM;SS	5.0 5.0
75	426059	BE292842	Hs.166120	interferon regulatory factor 7	IRF;SS	5.0
75	432295	BE091049	Hs.343665	ribosomal protein S15a	Ribosomal_S8,RNase_PH,KH-	5.0
	412540	C18341	Hs.73999	thyroid hormone receptor interactor	SH3,FCH;SS	5.0
	414465	AW270645	Hs.76194	ribosomal protein \$5	Ribosomal_S7;	5.0
	456655	AL376736	Hs.111779	secreted protein, ecidic, cysteine-	kazat;SS	5.0
80	421794	X86096	Hs.108371	E2F transcription factor 4, p107/p1	E2F_TDP.KOW.Ribosomal_L14	4.9
-	444824 438278	AA843575 BE409248	Hs.12056 Hs.57988	asialoglycoprotein receptor 1	tectin_c,Tropomyosin;TM	4.9
	418140	BE613836	Hs.83551	hypothetical protein FLJ22357 simil microfibrillar-associated protein 2	TFIIS,RNA_POL_M_15KD,UPF0	4.9
	429457	BE243065	Hs.202955	hypothetical protein FLJ20507	TM;SS	4.9
				Type and product to 2000!	Cys-protease-3C;TM;	4.9



	449475	A1348027	Hs.108557	hypothetical protein PP 1057	transmembrane4;TM;SS	4.9
	425274	BE281191	Hs.155462	minichromosome maintenance deficien	MCM:TM;	4.9
	442110 415209	AF113008 F00183	Hs.8102	ribosomal protein S20	Ribosomal_S10;TM;	4.9
5	451849	Al199261	Hs.172004 Hs.27191	tiin hypothetical protein from clone 247	none	4.9
-	421567	AJ272137	Hs.198265	matrix metalloproteinase 25	TM;	4.9
	427380	NM_005534	Hs.177559	interferon garmma receptor 2 (interf	hemopexin,Peptidase_M10;T fn3;TM;SS	4.9 4.9
	431303	AW241605	Hs.253928	ESTS	none	4.9
	432396	AW295956	Hs.11900	hypothetical protein FLJ14972	XEnt.zf-CCCH,G-patch,non	4.9
10	415021	RS4409	Hs.301693	Homo sapiens, clone IMAGE:3638994,	none	4.8
	430498	X02910	Hs.241570	tumor necrosis factor (TNF superfam	TNF;TM;SS	4.8
	449957	D31365	Hs.24220	hypothetical protein	TM:	4.8
	419603	BE262579	Hs.91566	PL6 protein	OMPdecasa;TM;SS	4.8
15	427588	L25081	Hs.179735	ras homolog gene family, member C	ras,none	4.8
13	421502 404854	AF111856	Hs.105039	solute earrier family 34 (sodium ph	Ribosomal_L20,Na_PI_cotra	4.8
	411281	BE392792	Hs.4786	Target Exon	;\$\$	4.7
	414045	NM_002951	Hs.75722	Homo sapiens cDNA: FLJ22849 fis, cl ribophorin II	cadherin	4.7
	431830	Y16645	Hs.271387	small inducible cytokine subfamily	gpdh.gpdh_C.piii_assembly IL8;SS	. 4.7 4.7
20	412896	AW804157	Hs.375570	major histocompatibility complex, e	ig,MHC_II_beta;TM;SS	4.7
	429305	AF095727	Hs.287832	myelin protein zero-like 1	ig_transmembrane4;TM;SS	4.7
	451698	Y16187	Hs.26880	endothelin converting enzyme-like 1	Peptidase_M13;TM;	4.7
	422687	AW068823	Hs.119206	Insutin-tike growth factor binding	zf-C2H2,ig.none	4.7
25	444542	A1161293	Hs.280380	aminopeptidase	NAD_binding.flavodoxin,FA	4.7
23	429833	NM_012079	Hs.288627	diacylglycerol O-acyltransferase (m	ACAT;TM;	4.7
	456376	AA663904	Hs.89862	TNFRSF1A-associated via death domai	death;TM;	4.7
	438568 456356	R98865	Hs.11135	major histocompatibility complex, c	MHC_II_elpha.ig,none	4.7
	420486	M74715 AF036365	Hs.89560 Hs.98303	iduronidase, alpha-L- caveolin 3	Glyco_hydro_39;SS	4.7
30	425123	AW205274	Hs.154695	phosphomannomutase 2	Caveofin;TM;	4.6
• -	439512	AA418287	Hs.58093	Homo sapiens, clone IMAGE:3163559,	PMM;SS laminin_EGF;TM;	4.6 4.6
	418424	Y13622	Hs.85087	latent transforming growth factor b	EGF,TB,spidertoxin,granut	4.6
	433350	BE563152	Hs.10362	Homo saplens cDNA: FLJ20944 fis, cl	zf-C3HC4,SPRY,none	4.6
25	432659	AA281633	Hs.278586	KIAA1108 protein	TBC:TM:	4.6
35	445417	AK001058	Hs.12680	a disintegrin-like and metalloprote	tsp_1,Reprolysin,Pep_M12B	4.6
	437408	AL359598	Hs.36606	Homo sapiens mRNA; cDNA DKFZp547B08	none	4.6
	427349	AA350154	Hs.177415	Finkel-Biskis-Reitly murine sarcoma	ubiquitin;TM;	4.6
	418918 421310	X07871 AW630087	Hs.89476	CD2 antigen (p50), sheep red blood	ig;TM;SS	4.6
40	427969	NM_001963	Hs.103315 Hs.2230	trinucleolide repeat containing 1	PHD	4.6
	447860	AF193807	Hs.131835	epidermal growth factor (beta-uroga Rhesus blood group, B glycoprotein	EGF,Idl_recept_b,EB;TM;	4.6
	418916	BE392781	Hs.89474	ADP-ribosylation factor 6	Ammonium_transp,FecCO;TM= arl,ras;TM;	4.6
	425720	AA382394	Hs.293984	hypothetical protein MGC13102	TM;SS	4.6 4.6
	419942	U25138	Hs.93841	potassium large conductance calcium	CaKB;TM;SS	4.6
45	403105			Target Exon	ISK_Channel;TM;SS	4.6
	418067	Al127958	Hs.83393	cystatin E/M	cystatin;SS	4.6
	427863	AF189712	Hs.181002		GTP_CDC;TM;	4.5
	458147	AW752597		gb:IL3-CT0214-161299-045-B06 CT0214	PMM.none	4.5
50	456799	AC004923	Hs.135187	unc93 (C.elegans) homolog B	TM;	4.5
50	427136 458766	AL117415 AW183618	Hs.173718 Hs.55610	a disintegrin and metalloproteinase	ig .	4.5
	445033	AV652402	Hs.72901	soluta carrier family 30 (zinc tran cyclin-dependent kinase inhibitor 2	Cation_efflux;TM;SS	4,5
	4412B1	BE501247	Hs.144084		ank;	4.5
	439720	AJ935202	Hs.31181	Homo sapiens cDNA: FLJ23230 fis, cl	Collagen, C4, none SDF, sugar_tr	4.5 4.5
55	410184	AW503667	Hs.59545	ring finger protein 15	SPRY,zi-B_box.zi-C3HC4;TM	4.5
	431760	NM_005317	Hs.268531	granzyme M (lymphocyte met-ase 1)	trypsin;TM;SS	4.5
	446990	AI354717	Hs.223908	ESTs	transmembrane4	4.5
	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial	IBR	4.5
60	426156 442941	BE244537	Hs.167382	natriuretic peptide receptor A/guan	ANF_receptor.guanylate_cy	4.5
00	451118	AU076728 AI862096	Hs.8887 Hs.60640	cysteine-rich, angiogenic inducer,	Cys_knot.tsp_1,vwc,tGFBP;	4.5
	457657	AW411509	Hs.352567	ESTS	EGF, vwc, TIL; SS	4.5
	437016	AU076916	Hs.5398	hypothetical protein PRO2121 guanine monphosphaté synthetase	UQ_con;TM;	4.4
	429497	AB028953	Hs.204121	KIAA1030 protein	PHD,SET,zf-CXXC,EGF,ank,n fn3:TM:	4.4
65	444090	\$69115	Hs.10306	natural killer cell group 7 sequenc	PMP22_Claudin;TM;SS	4.4
•	454005	AF039237	Hs.288600	hypothetical protein MGC3123	TM;SS	4.4
	412270	AC005262	Hs.73797	guarrine nucleotide binding protein	G-elpha.arf;TM;	4.4
	406729	AA069711		gb:zm52b11.a1 Stratagene fibroblast	filament,bZIP,Apolipoprot	4.4
70	404510			Homo sapiens cDNA FLJ11027 fis, clo	EGF,laminin_B,laminin_EGF	4.4
70	422311	AF073515	Hs.114948	cytokine receptor-like factor 1	tn3;TM;	4.4
	406973 407196	M34996	Hs.198253	major histocompatibility complex, c	ig.MHC_II_alpha;TM;SS	4.4
	404243	D11747	Hs.177415	Finkel-Biskia-Reilly murine sercorna	ERG4_ERG24,none	4.4
	443834	AJ741510	Hs.173548	NM_006778:Homo sapiens ring finger ESTs	zf-C3HC4,zf-B_box,TM;SS	4.4
75	446057	AI420227	Hs.366053		CUB,MAM,F5_F8_type_C,none	4.4
_	413661	AA071146	Hs.343354	ribosomal protein L18	Ribosomal I 18a I 15 TM-9	4.4
	414875	H42679	Hs.77522	major histocompatibility complex, c	Ribosomal_L18e,L15;TM;S ig,MHC_II_atpha;TM;SS	4.4
	439730	AF035292	Hs.6654	KIAA0657 protein	m3,ig;	4.3
0Λ	406257			Target Exon	7tm_1,none	4.3
80	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mR	ig:TM;	4.3
	414961	U27265	Hs.927	myosin-binding protein H	tn3,ig;TM;	4.3
	430265 429249	L36033	Hs.237358		n.8;5\$	4.3
	463249	X81479	Hs.2375	egf-like modute containing, mucin-l	7tm_2,EGF,GPS,S_locus_gly	4.3
					~~	

	433541	AW081538	Hs.220324	hypothetical protein FLJ13052	NAD_kinase;TM;	4.3			
	400575			NM_022146:Homo sapiens neuropeptide	7tm_1;TM;SS	4.3			
	427661	AA410292	Hs.104761	ESTs	wnt.none	4.3			
_	452056	AW955065	Hs.101150	Horno sapiens, clone IMAGE:4054156.	TM:	4.3			
5	433669	AL047879	Hs.194251	ESTs, Weakly similar to ALUZ_HUMAN	RNA_pol_L,RNA_pol_L,RasGA	4.3			
	422624	BE615578	Hs.76152	KDEL (Lys-Asp-Glu-Leu) endoptasmic	ER_tumen_recept_none	4.3			
	421680	AL031186	Hs.289106	Human DNA sequence from clone CTA-9	Collagen; TM; SS	4.3			
	422768	AA334108	Hs.159572	heparan sulfate (glucosamine) 3-0-s	none				
	437596	AA761490	Hs.351250	ESTs, Moderately similar to S55657	pkinase,WD40	4.3			
10	419285	D31887	Hs.89868	KIAA0062 protein		4.3			
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	Zip;TM;SS	4.3			
	410693	BE044206	16.01000		ion_trans;TM;SS	4.2			
	413100	BE065208		gb:ho40c08.x1 Soares_NFt_T_G8C_S1 H gb:RC1-BT0314-310300-015-b09 BT0314	C1q,Collagen,cystati	4.2			
	432497	AA551104		ESTs, Moderately similar to ALUC_HU	none	4.2			
15	423041	BE170842	Hs.123059	chloride channel Kb	none	4.2			
	449799	Al143466	Hs.125060	ESTs	CBS,voltage_CLC;TM;SS	4.2			
	438472	AW974907	Hs.86228	TRIAD3 protein	none	4.2			
	432179	X75208	Hs.2913		none	4.2			
	424488	AK000413	Hs.149227	EphB3	EPH_lbd.fn3.pkinase.SAMtT	4.2			
20	406809	AF000574	Hs.22405	hypothetical protein FLJ20406	XIInk,zf-CCCH,G-patch;TM=	4.2			
	407588	Z37544	Hs.37121	leukocyte immunoglobulin-like recep	ig,Gemini_mov;TM;SS	4.2			
	407228	M25079		phospholipase C, beta 3 (phosphatid	C2.PI-PLC-Y,PI-PLC-X,TM	4.2			
	450900	H61005	Hs.155376 Hs.37902	hemoglobin, beta	globin;TM;	4.2			
	410188	AL096739		ESTs	none	4.2			
25	458248	BE407379	Hs.107260	hypothetical protein OKFZp586H0623	Ricin_B_lectin,Glycos_tra	4.2			
23	403138	DE40/3/9	Hs.108082	ESTs, Weakly similar to 731636 hypo	C1q,Collagen;TM;SS	4.2			
	432074	AA525248	Un 140722	NM_006056:Homo sapiens G protein-co	7tm_1,HECT;TM;SS	4.2			
	438682		Hs.149723	ESTs	Y_phosphatase,none	4.2			
	401908	AA354489	Hs.375594	EBPSO-PDZ Interactor of 64 kD	none	4.2			
30	451287	AK002158	LL 20104	C17000154:gi[12003980]gb]AAG43830.1	TM;SS	4.2			
50	407904	W44735	Hs.26194	likely homolog of mouse immunity-as	TM;	4.2			
	403694	1144733	Hs.107260	Homo sapiens cDNA: FLJ21278 fis, cl	none	4.1			
	423461	A D020522		Target Exon	UDPGT-	4,1			
	425603	AB020527	Hs.128827 Hs.158329	solute carrier family 17 (sodium ph	sugar_tr;TM;	4.1			
35	421485	U52219 AA243499		G protein-coupled receptor 50	7tm_1;TM;SS	4.1			
	414509		Hs.104800	hypothetical protein FLJ10134	TM;SS	4.1			
	423313	AW161311	Hs.76294	CD63 antigen (melanoma 1 antigen)	transmembrane4;TM;SS	4,1			
	432171	NM_014269	Hs.126838	a disintegrin and metalloproteinase	disintegrin, Reprotysin, Pe	4.1			
	434652	AI202503 AF148713	Hs.343661	ESTs, Weakly similar to ALUB_HUMAN	WD40	4,1			
40	429592		Hs.125830	bladder cancer overexpressed protei	WD40,DUF6;	4.1			
•••	432982	A8029041	Hs.209646	KIAA1118 protein	Tropanin,Exo_endo_phos.IQ	4,1			
		AA531058	Hs.182248	truncated calcium binding protein	OPR,ZZ;TM;	4.1			
	424867	AJ024860	Hs.153591	Not56 (D. melanogaster)-like protei	TM;SS	4.1			
	441455	AJ271671	Hs.7854	zinciron regulated transporter-lik	Zip;TM;SS	4.1			
45	400785	********		C11000861:gij9938016 ref NP_084687.	TM;SS	4.1			
43	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	TM;SS	4.1			
	450785	AA852713	Hs.108885	Homo sapiens, alpha-1 (VI) collagen	vwa,Collagen;TM;\$S	4.1			
	424027	AW337575	Hs.201591	ESTs	7tm_2.HRM.none	4.1			
	435857	AF253468	Hs.3736	delta-like 4 homolog (Drosophila)	egf,dsl,eb;tm;ss	4.1			
50	437118 · 411410	AB037857	Hs.300591	CO9 partner 1	0008	4.1			
50		R20693	Hs.69954	taminin, gamma 3	laminin_B,laminin_EGF,lam	4.1			
	413902	AU076743	Hs.75613	CD36 antigen (collagen type i recep	E2F_TDP,CD36;SS	4.1			
	428938	AC002425	Hs.194660	ceroid-lipofuscinosis, neuronal 3,	CLN3;TM;SS	4.1			
	453094	AA740928	Hs.27356	ESTA	none	4.1			
55	440811	BE384713	Hs.74655	ESTs, Weakly similar to T34482 hypo	hormone_rec,zf-C4,none	4.0			
33	407287	AI578812	Hs.345139	gb:tu59d08.x1 NCI_CGAP_Gas4 Homo sa	ras,cadherin	4.0			
	428028	U52112	Hs.182018	Interleukin-1 receptor-associated k	death.pkinase;TM;	4.0			
	428469	BE549205	Hs.184488	flotitin 2	none	4.0			
	423114	AU076497	Hs.1614	cholinergic receptor, nicotinic, at	Neur_chan_LBD,Neur_chan_m	4.0			
60	426858	NM_004182	Hs.172791	ubiquitously-expressed transcript	DUF232:SS	4.0			
00	444626	AA320893	Hs.117062	hypothetical protein FLJ14497	pyr_redox;TM;SS	4.0			
	TABLE 30	NO.							
			C						
	Pkey:			et identifier number					
CAT number: Gene cluster number  65 Accession: Genhant accession numbers									
05	Accession	i. Geni	bank accessio	n numbers					
	Pkey	CAT Number	A						
	458147			AUM 40400 AVED 40000 AVED 400000 AVED					
	406729	1030220_1	WA1040101	AW848490 AW849062 AW752597 AW752699					
70	410693	0_0 1054267_1	AA069711						
, ,	413100		BE044206	AW797320 BE161676 AW797356 AW797352					
		1490226_1		BE065168 BE065313 BE065208					
	432497	852_71	AWd/4688	R94134 AASS1104 AA777322 A1033094 BE247143					
	7401 P 44	<b>v</b> .							
75	TABLE 30								
, ,	Pkey:	Uniq	tue number corresponding to an Eos probeset uence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Durham, et al." refers to the publication emitted "The DNA						
	Ref:	Sequ	ience source.	rne r digit numbers in this column are Genbank Id	entifier (GI) numbers. "Dunham, et al." refer	rs to the publication entitled "The DNA			
	Ch A	acqu	RUCA OI UMILIA	n Chilomosonie 22 Donnam, et al. (1995) <u>Mature</u> 40	2:489-495.				
	Strand:	Indic	ates DNA stra	nd from which exons were predicted.					
Nt. position: Indicates nucleotide positions of predicted exons.									
50	OL:	0.4		44.		•			
	Pkey	Ref	Strand	Nt_position					
	401699	3176654	Minus	33285-34084					
	404864	5263010	Plus	94495-94661,95055-95195,97396-97506,9760					

	402241	7690131	Minus	125073-125206,130996-131125
	404913	7341740	Ptus	97717-97976
	404854	7143420	Plus	14260-14537
_	403105	8980016	Minus	145287-145744
5	404510	9588566	Minus	89583-89725.90402-90555.91428-91673
	404243	5672609	Plus	74695-75123
	406257	7417784	Plus	55821-56037
	400575	9886575	Plus	131603-132095
	403138	9211494	Minus	164684-165066,167757-168651
10	401908	8698760	Minus	126888-127024
	403694.	7107765	Plus	142925-143080,165505-166186,167486-16763
	400785	8131682	Plus	43113-43967

TABLE 31A: ABOUT 189 GENES DOWN-REGULATED IN QLIOMA COMPARED TO NON-MALIGNANT ADULT BRAIN TISSUE
Table 31A lists about 189 genes down-regulated in glioma compared to non-malignant adult brain tissue. These were selected as for Table 30A, except that the numerator was set to
the 90th percentile value amongst various gliomas, the numerator was greater than
or equal to 50 units, and the ratio was greater than or equal to 2.5 (i.e. 2½-fold downregulation in brain tumor vs. normal brain).

Pikey:

Exacon:

UnigenelD:

UnigenelD:

Unigene title:

Protein Domains:

R1: 15

20

25	RT:	tt: non-matignant adult brain tissue vs. glioma				
23	Pixey	ExAccn	UniGene ID	Unigene Title	Protein Domains	R1
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	F420_oxidored;TM;SS	14.5
	432874	W94322	Hs.279651	melanoma inhibitory activity	SHETMESS	8.3
~~	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	SCP,LCCL;TM;SS	· 8.2
30	426300	U15979	Hs.169228	delta-like homotog (Orosophila)	EGF, larninin_EGF; TM; SS	8.2
	447990	BE048821	Hs.20144	small inducible cytokine subfamily	IL8:SS	7.3
	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HU	GONF, TPR	7.1
	411602	L01406	Hs.767	growth hormone releasing hormone re	7tm_2,HRM;TM;SS	6.1
25	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneur	sugar_tr;TM;SS	6.0
35	426488	X03350	Hs.4	alcohol dehydrogenase 1B (class I),	adh_zinc;TM;	5.9
	447656	NM_003726	Hs.19126	src kinase-associated phosphoprotei	SH3,PH;TM;	5.3
	436950	L05779	Hs.113	epoxide hydrotase 2, cytoplasmic	abhydrolase,Hydrolase;TM=	5.2
	406837	R70292	Hs.156110	immunoglobulin kappa constant		4.9
40	410387 432855	AJ277367	Hs.47094	ESTs .		4.8
40		AF017988	Hs.279565	secreted frizzled-related protein 5	Fz,NTR:TM:SS	4.7
	441499 421481	AW298235 AW391972	Hs.101689	ESTs	T1100	4.6
	420255	NM 007289	Hs.104696 Hs.1298	KIAA1324 protein	TM;SS	4.5
	407230	AA157857	Hs.182265	membrane metallo-endopeptidase (neu keratin 19	Peptidese_M13;TM;SS	4.5
45	412445	X51362	Hs.73893	dopamine receptor D2	filament,bZIP;\$S	4.4
	413966	AA133935	Hs.173704	ESTs, Moderately similar to A53959	7tm_1;TM;SS	4.3
	415165	AW887604	Hs.78065	complement component 7	kli_recept_a.sushi,tsp_1,	4.2 4.2
	420103	AA382259	Hs.95197	aldehyde dehydrogenase 1 family, me	aldedh;TM;	4.2
	426723	AW003069	Hs.183860	ESTs	GNT-1;TM;SS	4.1
50	409081	AJ010277	Hs.50403	T-box 19	T-box:TM;	4.0
	407142	AA412535	110/04 -00	gb:zt99b10.s1 Soares_testis_NHT Hom	Na_sutph_symp;TM;	4.0
	414449	AA557660	Hs.76152	decorin	LRRNT, LRR, LRR, LRRNT	4.0
	444784	O12485	Hs.11951	ectonucleotide pyrophosphatase/phos	Somatomedin_B, Endonucleas	3.9
	420321	D78761	Hs.96657	hyothetical protein	tsp_1;SS	3.8
55	401700			Target Exon	TNC	3.8
	418807	NM_004944	Hs.88646	deoxyribonuclease Hike 3	Exo_endo_phos;TM;SS	3.8
	406746	AA580395	Hs.279860	tumor protein, translationally-cont	TCTP;TM;	3.7
	449077	AW262836	Hs.252844	ESTs		3.7
60	415718	F30631	Hs.200237	ESTs	isoamytase_N	3.7
UU	402449	41500045		Target Exon	pkinase,LRR,LRRCT;TM;SS	3.6
	457489	AI693815	Hs.127179	cryptic gene	TM;SS	3.6
	406743 416950	AA911568	Hs.279860		TCTP;TM;	3.6
	451554	AL049798	Hs.80552	dermatopontin		3.6
65	440708	AJ474866 AF038962	Hs.193237 Hs.7381	ESTs	Ed autoEst on to AB	3.6
05	426095	AJ278023	Hs.89986	voltage-dependent anion channel 3 ESTs	Euk_parin,Enterotoxin_A,P	3.5
	406742	AJ468091	Hs.279860	tumor protein, translationally-cont	WD40,none TCTP;TM;	3.5
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, c	VHS,ENTH,UIM;SS	3.5 3.4
	439457	AF086274	110.100	gb:Homo sapiens full length insert	THO,ENTH, OIM, GG	3.4
70	408796	AA688292	Hs.170345		hormone_rec.zf-C4	3.4
	440659	AF134160	Hs.7327	claudin 1	PMP22_Claudin;TM;SS	3.4
	415042	NM_006759	Hs.77837	UDP-glucose pyrophosphorylase 2	UDPGP:SS	3.4
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group	hormone_rec,zf-C4,none	3.3
	445234	AW137636	Hs.146059		14-3-3.none	3.3
75	430511	BE018156	Hs.2575	calpain 1, (mu/l) large subunit	efhand, Peptidase_C2, Calpa	3.3
	420485	AF218586	Hs.288835	cell death-inducing DFFA-like effec	7tm_1.CIDE-N;TM;SS	3.3
	413687	AI522318	Hs.103819	ESTs	TM;SS	3.3
	428928	8E409838	Hs.194657	cadherin 1, type 1, E-cadherin (epi	cadherin,Cadherin_C_term,	3.3
80	409738	BE222975	Hs.56205	insulin induced gene 1		3.3
٥v	442046	AA974575	Hs.287385		zl-C2H2,SET;TM;	3.2
	413127	BE066529		gb:RC3-BT0333-300300-017-a12 BT0333		3.2
	429350	AJ754634	Hs.131987		MANETHE	3.2
	427980	AA418305	Hs.303205	EST	LRR,none	3.2

	424498	AB033043	Hs.149377	hypothetical protein DKFZp761L0424	AIP3:TM:SS	3.2
	435684 402632	NM_001290	Hs.4980	LIM domain binding 2	UM_bind;TM;	3.2
	431130	NM_006103	Hs.2719	Target Exon HE4: epididymis-specific, whey-acid	ig;TM;SS wap;TM;SS	3.1
5	410636	AA088177	Hs.172870	ESTs	TM:SS	3.1 3.1
	452658	N88604	Hs.30212	thyroid receptor interacting protei	PCI:TM:	3.1
	453180	N46243	Hs.110373	ESTs, Highly similar to T42626 secr	laminin_G.URRCT,none	3.1
	430319	AJ480214	Hs.356075	ninjurin 2	TM:SS	3.1
10	438424 456063	AI912498 NM_006744	Hs.25895	hypothetical protein FLJ14996	C2;TM;	3.1
10	429798	AL11757B	Hs.76461 Hs.222909	retinol-binding protein 4, Intersti	lipocatin,TGF-beta,TGFb_p	3.1
	417677	NM_016055	Hs.82389	DKFZP434C128 protein CGI-118 protein	TM:	3.1 3.1
	443792	A1763073	Hs.204873	ESTs		3.1
1.5	445861	BE293423	Hs.11809	single ig IL-1R-related molecule	TIR:TM;	3.1
15	407815	AW373860	Hs.183850	hypothetical protein FLJ20277	LRR,none	3.1
	456689	NM_002251	Hs.117780	potassium voltage-gated channel, de	ion_trans,K_tetra;TM;SS	3.1
	446492 427706	AW205115 AW971225	Hs.161287 Hs.293800	ESTs Weakly similar to ALU1_HUMAN	SPRY_zf-8_box_PAAD_D	3.1
	458008	AA809314	Hs.123295	ESTS	SCAN,zf-C2H2,none	3.0 3.0
20	449708	A1694598	Hs.202126	ESTs	SOUZE CENTENDE	3.0
	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein	TM;SS	3.0
	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	FMO-like.pyr_redox;TM;S	3.0
	425280	U31519	Hs.1872	phosphoenotpyruvate carboxykinase 1	PEPCK:TM:	3.0
25	453177 416781	AW389509 AF072928	Hs.223747 Hs.79877	ESTS	zi-C2H2,none	3.0
	447582	BE293520	Hs.18910	myotubularin related protein 6 prostate cancer overexpressed gene	sugar_tr,TM;SS	3.0 3.0
	417365	050683	Hs.82028	transforming growth factor, bela re	pkinase.WD40;TM;	3.0
	452540	AW161048	Hs.150549	ESTs. Wealty similar to T33997 hypo	p	2.9
20	430233	AW367902	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N1D	PH,Ets,CH,spectrin,Ca_cha	. 2.9
30	418127	BE243982	Hs.83532	membrane cofactor protein (CD46, tr	sushi;TM;SS	2.9
	404445 423323	AJ951628	Hs.127007	Target Exon	1	2.9
	452093	AA447453	Hs.27860	potassium channel, subfamily K, mem Homo sepiens mRNA; cDNA DKFZo586M07	ion_trans;TM;SS	2.9 2.9
	427981	BE275986	Hs.181311	asparaginyl-IRNA synthetase	7tm_1,none tRNA-synt_2,tRNA_enti,tRN	2.9
35	452242	RS0956	Hs.159993	gycosyltranslerase	20013jn	2.9
	440232	AJ766925	Hs.112554	ESTs		2.9
	444634	AW611988	Hs.197813	ESTs	CKS	2.9
	445889 414483	BE465186 R25513	Hs.266958 Hs.10683	ESTs EST-	TM;	2.9
40	453500	AJ478427	Hs.43125	ESTs esophageal cancer related gene 4 pr	TM:SS	2.9 2.9
	419768	T72104	Hs.93194	apolipoprotein A-I	Apolipoprotein;SS	2.9
	427804	AL049654	Hs.180871	protein kinase C, alpha binding pro	POZ:SS	2.9
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2,	C2,PI3_PI4_kinase,PI3Ka,P	2.9
45	430699	AW969847	Hs.292718	ESTs, Wealdy similar to RET2_HUMAN	Repocatin:SS	2.9
45	427842 432834	AW936961 F06459	H- 200112	gb:RC1-DT0029-160200-013-a12 DT0029	efhand,mito_carr,none	2.8
	421435	AW972072	Hs.289113 Hs.372167	cytochrome b5 reductase 1 (B5R.1) ESTs	NAD_binding,FAD_binding_6	2.8
	402458	***************************************	113.572.101	C1002064;gij11993050jgbjAAG42574.1j	TM:SS	2.8 2.8
50	410036	R57171	Hs.57975	calsequestrin 2 (cardiac muscle)	Calsequestrin;SS	2.8
50	412570	AA033517	Hs.74047	electron-transfer-flavoprotein, bet	ETF_beta:SS	2.8
	459439 438622	AW402931	Hs.352411	gb:UI-HF-BK0-abd-a-01-0-UI.r1 NIH_M	•	2.8
	417023	L03151 AA192278	Hs.301596	gb:Home sapiens cell-type T-cell im		2.8
	453281	W46280	Hs.55940	ESTs, Moderately similar to S65657 ESTs, Weakly similar to A25704 syna		2.8 2.8
55	403028			Target Exon	trypsin.trefoil	2.8
	449029	N28989	Hs.22891	solute carrier family 7 (cationic a	aa_permeases;TM;SS	2.8
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) h	EGF,cadherin,laminin_G;TM	2.8
	406918 435213	M88357 AA092510	U- F00F	gb:Homo sepiens ONA-binding protein	zi-CZH2,KRAB,zi-BED,TM;	2.7
60	443990	AW205085	Hs.5985 Hs.39557	non-kinase Cdc42 effector protein S ESTs	TM;	27
	451698	Y16187	Hs.26880	endothelin converting enzyme-like 1	Peptidase_M13;TM;	27 27
	431713	AK000388	Hs.267997	EHM2 gene	Band_41;TM;	27
	431469	N49424	Hs.124159	ESTs .	SH3	2.7
65	400386	AF075290		gap junction protein, alpha 3, 46kD	connexin;TM;SS	2.7
03	406684	X16354	Hs.50964	carcinoembryonic antigen-related ce	ig:TM:SS	27
	449874 403213	AA135688	Hs.10083	Homo sapiens, clone IMAGE:4139786,	TM;	27
	459665	BE159784	Hs.47647	NM_019595:Homo sapiens intersectin gb:MR0-HT0408-220300-001-h06 HT0408	SH3,ethand,C2,PH,RhoGEF;T	2.7 2.7
	421823	N40850	Hs.28625	ESTs		27
70	422693	BE300073	Hs.279860		TCTP,none	27
	454906	AJ219323	Hs.101077	ESTs, Weakly similar to T22363 hypo	TM;	2.7
	447075	AV662037	Hs.124740		TM;	2.7
	450273	AW296454	Hs.24743	hypothetical protein FLJ20171	пт,лопе	2.7
75	434340 436972	AJ193043 AA284679	Hs.128685 Hs.25640	ESTs, Weakly similar to T17226 hypo claudin 3	DIADOS CIMATANOS	27
	441379	AW175787	Hs.334841		PMP22_Claudin;TM;SS TM;	2.7 2.7
	421143	AB024536	Hs.102171	immunoglobulin superfamily containi	ig,LRR,LRRNT,LRRCT;TM;S	27
	422558	NM_006420		brefeldin A-Inhibited guarrine nucle	Sec7,none	2.7
80	428900	AA437189	Hs.352324	Human DNA sequence from clone RP1-6	SS	2.7
80	421153	AF009267	Hs.102238			2.7
	427074 448133	AA527435 AA723157	Hs.178589 Hs.73769	hepatocethdar carcinoma antigen ge folate receptor 1 (aduli)	efhand;TM;	26
	419158	AF031475	Hs.89648	arginine vasopressin (neurophysin I	Folate_rec,MIP;TM;SS hormone5,hormone4;SS	2.6 2.6
					INTERNATION, INTERNATION, CONTRACTOR	20

	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564807	0.1 7.714.00	2.6
	437176 435075	AW176909 R51094	Hs.42346 Hs.12400	calcineurin-binding protein calsarc ESTs	Galactosyl_T;TM;SS	2.6 2.6
	403153	1034	HS. 12400	Target Exon		26
5	400387	AF133131		double homeobox, 5		2.6
	425940	AB023184	Hs. 163990	KIAA0967 protein	PDZ;S\$	2.6
	416157	NM_003243	Hs.342874	transforming growth factor, beta re	zona_pellucida:TM;SS	2.6
	452554	AW452434	Hs.58006	ESTs, Weakly similar to ALU5_HUMAN	HLH,PAC,PAS,none	2.6
10	453247 407744	T80198 A8020629	Hs.111806 Hs.38095	ESTs ATP-binding cassette, sub-family A	wra, Cache, none ABC_tran, PRK; TM; SS	2.6 2.6
10	432877	AW974111	Hs.292477	ESTs	Els,SAM_PNT,none	2.6
	450115	AI591038	Hs.38132	ESTs	code and the brains	2.6
	406337			C14000021:pij7242973jdbjjBAA92547.1	Peptidase_M22	2.6
1.5	430877	NM_005269	Hs.2693	glioma-associated oncogene homolog	zi-C2H2;\$\$	2.6
15	453874	AW591783	Hs.36131	collagen, typo XIV, alpha 1 (unduli	NAS 11 Mars 8- 14 1 MA	2.6
	450493 427620	M93718 NM_003705	Hs.166373 Hs.179866	nitric oxide synthase 3 (endothelia	NAD_binding.fiavodoxin.FA	26 26
	446585	AV659397	Hs.299668	solute carrier family 25 (mitochond ESTs, Wealdy similar to I38022 hypo	ethand,mito_carr,TM;SS=	2.6
		BE208189	Hs.174031	cytochrome c oxidase subunit VIb	tubulin,FKBP,COX68,7tm_1,	2.6
20	428111	S76617	Hs.2243	B lymphoid tyrosine kinase	SH2.SH3.pkinase;SS	2.6
	440133	AI056255	Hs.133349	ESTS		2.6
	419693	AA133749	Hs.301350	FXYD domain-containing ion transpor	ATP1G1_PLM_MAT8;TM;SS	2.6
	417103 419100	Z33905 AA464362	Hs.81218 Hs.6748	hypothetical protein MGC3597	TPR_zI-C3HC4,PHD;TM;SSo	26 26
25	449925	AL342493	Hs.24192	hypothetical protein PP1665  Homo sapiens cDNA FLJ20767 fis, clo	squash,GOPD;TM;	2.6
	430937	X53463	Hs.2704	glutathione peroxidase 2 (gastroint	GSHPx;SS	26
	425640	U34051	Hs.158460	cyclin-dependent kinase 5, regulato	CDK5_activator,TM;	26
	409021	AA156640	Hs.49881	fatty acid binding protein 3, muscl	lipocalin,none	2.6
30	400538	45440343	14 000455	ENSP00000239776*:BA425A6.2 (similar	TM:SS	. 2.6
30	446947 408310	AF146747 AW179023	Hs.232165 Hs.191705	polycythemia rubra vera 1; cell sur ab:PM3-ST0038-170899-001-e08 ST0036	TM;SS	2.6 2.6
	433032	AI084066	Hs.20072	myosin regulatory light chain inter	Band_41;	2.6
	419389	AI074951	Hs.319095	ESTs	DPPIV_N_term,none	2.6
	453145	R63438	Hs.183454	Homo sapiens cDNA FLJ14883 fis, do	STT3;TM;SS	2.6
35	443460	AL050275	Hs.9383	DKFZP566D213 protein	EGF, taminin_EGF, EB; TM; S	2.6
	421903	AW079940	Hs.15951	ESTs, Wealdy similar to S32436 coll	\$S	2.5
	421757 428475	Z20897 AF172940	Hs.296259 Hs.184542		Arylesterase;SS	2.5 2.5
	424657	AA344719	14.104542	gb:EST50901 Gall bladder II Homo sa		2.5
40	432862	AW004958	Hs.236720		TM;SS	2.5
	427195	W27230	Hs.173912	eukaryotic translation initiation f	DEAD heficase_C;	2.5
	447770	AB032417	Hs.19545	frizzled (Drosophila) homotog 4	Fz,Frizzled,7tm_2;TM;SS	2.5
	456523	AJ083668	Hs.50601	hypothetical protein MGC10986	pkinase,none	2.5
45	451846 432906	T65840 BE265489	Hs.11762 Hs.3123	ESTs lethal giant larvae (Drosophila) ho	WD40:TM;	2.5 2.5
	453876	AW021748	Hs.110406		110-10,1111,	2.5
	441488	AW450935	Hs.7862	hypothetical protein FLJ20312	TM;	2.5
	444669	F18939	Hs.153827			2.5
50	452497	AA732153	Hs.27865	Homo sapiens cDNA: FLJ21333 ffs, cl		2.5
50	TABLE 3	1D:				
	Pkey:		ique Eos probe	set Identifier number		
	CAT nur		ne cluster num			
	Accessio	n: Ge	nbank accessio	on numbers		_
55						-
	Pkéy 439457		Accession	INCO 434 INCOC47		
	413127	23338_1 151610_1		W69434 W69517 BF330853 BF747375 BE066356 BE066292 BF3:	10000 RE747142 REAGEA10 RE742510 REA	66520 BER66208 BE742516 BE746603
		10.0.0_1	BE066274		2300 B/ 747 142 DE0024 19 D/ 1423 10 DE0	3023 DE00230 Br (423 to Br (4000)
60	427842	1164138_1		AW936961 AA416706 R29415		
	438622	46171_1		3155 L03161		
	424657	896375_1	AW963487	7 AA365077 AA344719		
	TABLE 3	110-				
65	Pkey:		ique quimber o	orresponding to an Eos probeset		
	Ref:	Se	quence source	. The 7 digit numbers in this column are Genbank	Identifier (GI) numbers. "Dunham, et al." re	ders to the publication entitled 'The DNA
		se	quence of hum	an chromosome 22° Dunham, et al. (1999) Nature	402:489-495.	•
	Strand:			and from which exons were predicted.		
70	Nt_posit	ion: Inc	Sicates nucleof	de positions of predicted exons.		
70	Pkey	Ref	Strand	Nt_position		
	401700	3176654	Minus	35416-35534		
	402449	9796674	Plus	59867-60039,62588-62828,63465-63623,649	2	
75	402632	9931268	Plus	101166-101419		
75	404445	7596866	Minus	31112-31423		
	402458		Plus	170479-171134		
	403028 403213	7670577 7630897	Minus Minus	114150-114272 162572-162739,164442-164540		
	403153		Minus	42232-43389		
80	406337	9213455	Plus	90117-90337		
	400538		Plus	8752-9822		

TABLE 32A: ABOUT 68 GENES UP-REGULATED IN GLIOMA COMPARED TO NORMAL ADULT TISSUES AND TO NON-MALIGNANT BRAIN TISSUES THAT ARE LIKELY TO ENCODE PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES, PEPTIDES, OR ANTIBOCIES

Table 32A lists about 68 genes up-regulated in glioma compared to normal adult issues and to non-matignant brain issues that are fixely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetric/Eos-Hu03 GeneChip® array as follows: the ratio of "average" glioma to "average" normal adult issues was greater than or equal to 2.5, the ratio of "average" glioma to "average" normalignant brain issues was greater than or equal to 2.0, the "average" glioma tered was set to the 98th percentile value amongst various non-matignant tissues, the "average" normal adult issue level was set to the 85th percentile value amongst various non-matignant tissues, the "average" glioma value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of having an encogenic function or of transducing an intracefular signal, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Predicted protein domains are noted. 5

10

Pkey: ExAccn: Unique Eas probeset identifier number

Exemplar Accession number, Genbank accession number Unigene number Unigene gene title Predicted Protein Domains

UnigenelD: Unigene Title: Protein Domains: 15

R1: glioma vs. normal adult tissues and non-matignant brain tissues that are likely to encode proteins

	Pkey	ExAcen		Unigene Title	Protein Domains	R1
20	424343	AW956360	Hs.4748	adenytate cyclase activating polype	7tm_2,HRM	8.8
20	418506	AA084248	Hs.85339	Unknown protein for MGC:29643 (form		7.8
	456723	243902	Hs.4748	adenylate cyclase activating polype	7tm_2,HRM	7.5
	430228	AW950939	Hs.6382	ESTs, Highly similar to T00391 hypo		7.1
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	ASC;TM;	6.3
0.0	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322,	TM;	6.0
25	414825	X06370	Hs.77432	epidermal growth factor receptor (a	Furin-like pkinasa, Recep_	6.0
	423779	AW071837	Hs.57971	ESTs	TNFR_c6	5.5
	409638	AW450420	Hs.21335	ESTs	7tm_2,HRM	5.3
	442613	AI004002	Hs.130522	Kv channel-interacting protein 1	Neur_chan_LBD,Neur_c	5.2
20	436456	AW292677	Hs.248122	G protein-coupled receptor 24		· 5.1
30	424340	AA339036	Hs.7033	ESTs	fig_chan,ANF_receptor,non	5.0
	425115	R44664	Hs.123956	ESTs	7tm_1	4.7
	446809	AW590171	Hs.101413	ESTs	CaMBD,SK_channel,CaMBD,SK	4.4
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 k	ubiquitin;SS	4.4
2.5	454360	L78207	Hs.54470	ATP-binding cassette, sub-family C	ABC_tran_ABC_membrane_PRK	4.2
35	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity I	ig:TM;SS	4.2
	428141	D50402	Hs.182611	solute carrier family 11 (proton-co	Nramp;TM;	4.1
	435472	AW972330	Hs.283022	triggering receptor expressed on my	ig:TM:SS	4,1
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQ	ion_trans,KCNQ1_channel;T	3.8
40	448204	AI475124	Hs.170561	ESTs	lig_chan,S8P_bac_3	3.7
40	433290	R20077	Hs.302185	Homo saplens clone 23818 mRNA seque	lig_chan,SBP_bac_3,ANF_re	3.6
	408243	Y00787	Hs.624	interleukin 8	HLH,PAS,IL8;TM;	3.6
	415849	R20529	Hs.6806	ESTs	7tm_2,GPS,Gal_Lectin,HRM,	3.5
	451099	RS2795	Hs.25954	Interleukin 13 receptor, alpha 2	fn3;TM;SS	3.4
	445070	NM_000677	Hs.258	adenosine A3 receptor	7tm_1;TM;SS	3.4
45	428037	N47474	Hs.89230	polassium intermediate/small conduc	CaMBD,SK_channel	3.2
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	kfl_recept_a,PKD,MHC_I;TM	3.1
	447143	AW292408	Hs.152290	ESTs, Highly similar to JC2463 vaso		3.0
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	SRCR_Lysyl_exidase;TM;S	3.0
	424441	X14850	Hs.147097	H2A histone family, member X	histone,C8FO_NFYB_HMF;TM=	3.0
50	446057	AJ420227	Hs.366053	Trp-p8 transient receptor potential		2.9
	438204	AI589645	Hs.128690	ESTs	7tm_1	29
	431674	AA098901	Hs.301642	G-protein coupled receptor	GCV_H	2.9
	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, do		2.9
	415209	F00183	Hs.172004	titin		2.8
55	438537	AK000511	Hs.6294	hypothetical protein DKFZp434L1435	tRNA-synt_1;TM;	28
	431053	\$40369	Hs.249141	Glutamate receptor subunit	lig_chan,ANF_receptor,TM=	2.8
	408482	NM_000676	Hs.45743	adenosine A2b receptor	7tm_1;TM;SS	2.8
	414774	X02419	Hs.77274	plasminogen activator, urokinase	kringle,trypsin,plant_thi	2.8
	426865	D63476	Hs.172813	PAK-interacting exchange factor bet	SH3,PH,RhoGEF,Terpene_syn	2.8
60	430897	U71092	Hs.248122	G protein-coupled receptor 24	7tm_1;TM;	2.7
	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sap	EGF,metalthio,integrin_B,	2.7
	409552	AL119675	Hs.54929	phosphorylase kinase, gamma 1 (musc	pkinase,Bac_CNA_binding;T	2.7
	412817	AL037159	Hs.74619	proteasome (prosome, macropain) 26S .	PC_rep:TM;	27
	429150	AF120103	Hs.197366	smoothened (Drosophila) homolog	COXB,SHMT,MIF,GST_C,EF1G_	2.7
65	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C	ABC_tran,ABC_membrane;TM=	2.7
	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion mol	EGF,lectin_c,sushi;TM;S	2.7
	432074	AA525248	Hs.149723	ESTs	Y_phosphatase	2.6
	402154			NM_031896*:Homo sepiens calcium cha	PMP22_Claudin;TM;SS	2.6
	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (spe	zona_oellucida;TM;SS	2.6
70	419913	AW270040	Hs.34455	ESTs	EPH_fbd,fn3,pkinase,	26
	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integr	MIP:TM:SS	2.6
	412070	AW893260		gb:CM2-NN0010-100300-111-e09 NN0010	7tm_2,HRM	2.6
	422676	D28481	Hs.1570	histamine receptor H1	7tm_1:TM:SS	2.6
	422311	AF073515	Hs.114948	cytokine receptor-like factor 1	th3.TM:	2.6
75	444381	BE387335	Hs.283713		Collagen;TM;SS	2.6
	419972	AL041465	Hs.182982	golgin-67	-constant i wide	2.6
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarbo	TM:SS	2.6
	421997	R66740	Hs.110613			2.6
	430181	AF065314	Hs.234785		aa_permeases.pyridoxal_de cNMP_binding,lon_trans;TM	2.5
80	426318	AA375125	Hs.147112		EPH_tbd.pkinase,fn3,SAM.n	2.5 2.5
	434808	AF155108	Hs.256150		TM;	2.5
	418843	AJ251016	Hs.89230	potassium intermediate/small conduc	CaMBD.SK_channetTM;SS=	2.5
	410290	AA402307	Hs.322844		Sema PSt TIG integrin_B;T	2.5
				Aboutone beams are chooses.	oana, ro, no, magin_b,	23

408359 R3	38438 Hs.182575	cell division cycle 258 SLC15A2 Solute carrier family 15 (H Homo sapiens emino acid transport s	Rhodanese;SS PTR2;TM; Aa_trans;TM;	2.5 2.5 2.5
-----------	-----------------	-------------------------------------------------------------------------------------------------------	------------------------------------------	-------------------

5 TABLE 328:

Unique Eos probeset identifier number Gene cluster number Pkey: CAT number:

Accession: Genbank accession numbers

10

 Pkøy
 CAT Number 2580163_1
 Accession AI926361 AA834879 AA828995

 412070
 287551_1
 AGCESSION AI926361 AA834879 AA828995

 412070
 287551_1
 BG820657 AW890808 BF904755 AW893260 BI034684 BF963423 BF961550 M85689

TABLE 32C:

30

15

Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA Pkey: Ref:

sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Indicates DNA strand from which exons were predicted.

Strand:

Nt_position: Indicates nucleotide positions of predicted exons. 20

Ref 8516165 Nt_position 125299-125494 Pkey 402154 Strand Minus

#### 25 TABLE 33A: ABOUT 798 GENES UP-REGULATED IN KIDNEY CANCER

TABLE 33A: ABOUT 798 GENES UP-REGULATED IN KIDNEY CANCER
Table 33A issts about 798 genes up-regulated in kidney cancer compared to normal adult tissues. These were selected from 59680 probesets on the Aflymetrix/Eos Hu03 GeneChip
array such that the ratio of "average" kidney cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" kidney cancer level was set to the 90th
percentile amongst various kidney cancers. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove genespecific background levets of non-specific hybridization, the 15th percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the
denorminator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
EXACOT: Exemplar Accession number, Genbank accession number

ExAcon: UnigenelD: Unigene Title:

Unigene number
Unigene gene title
Ratio of tumor to normal tissue 35 R1:

	Pkey	ExAcon	UniGenelD	Unigene Title	04
	421471	U90545	Hs.104635	solute carrier family 17 (sodium phospha	R1 1007.4
	445178	A1792241	Hs.129614	kidney-specific membrane protein	438.0
40	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	338.4
-10	421727	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3	323.6
	440304	BE159984	Hs.125395	ESTs	295.0
	436878	BE465204	Hs.47448	ESTs	258.8
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	258.6
45	421155	H87879	Hs.102267	hysyl oxidase	251.8
	426471	M22440	Hs.170009	transforming growth factor, stoha	224.6
	421478	AI683243	Hs.97258	ESTs	212.6
	424086	AJ351010	Hs.102267	lysyl oxidase	199.2
	428296	NM_003058	Hs.183572	solute carrier family 22 (organic cation	186.4
50	426890	AA393167	Hs.41294	ESTs	183.4
	441031	AJ110684	Hs.7645	fibrinogen, B beta polypeptide	174.0
	411642	NM_014932	Hs.71132	neuroligin 1	172.4
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	161.4
	425984	AW836277	Hs.165636	hypothetical protein DKFZo761C07121	151.0
55	438966	AW979074		gb:EST391184 MAGE resequences, MAGP Homo	135.0
	453165	\$74727	Hs.32042	aspartoacytase (aminoacytase 2, Canavan	134.8
	453160	AI263307	Hs.146228	ESTs	132.6
	452431	U88879	Hs.29499	toli-like receptor 3	130.6
	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	120.4
60	420642	AKD01520	Hs.99545	Homo sapiens cDNA FLJ10658 fis, clone NT	112.6
	407975	X89426	Hs.41716	endothelial cell-specific molecule 1 (NO	111.8
	431708	A1698136	Hs.108873	ESTs	109.8
	446460	AW013999	Hs.150164	ESTs	103.6
65	443450	N66045	Hs.133529	ESTs	103.0
03	432865	AI753709	Hs.152484	ESTs	101.4
	442438	AA995998		gb:os26b03.s1 NCI_CGAP_Kid5 Horno sepiens	98.8
	433447	U29195	Hs.3281	neuronal pentraxin II	98.5
	440311	A1733079	Hs.125407		98.2
70	415076	NM_000857		guanylate cyclase 1, soluble, beta 3	97.0
70	437157	BE048860	Hs.120655		94.4
	453319	A1985369	Hs.20117	ESTs	91.4
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	90.2
	439169	Af912122	Hs.41095	ESTs	85.6
75	431870	AW449902	Hs.105500		84.4
15	438993	AA828995	00046	gb:od77b08.s1 NOI_CGAP_Ov2 Homo sapiens	83.8
	445279	R41900	Hs.22245	ESTs	82.4
	451592	A1805416	Hs.213897		79.4
	422966 423109	AV648419 M59305	Hs.122613 Hs.123655		78.8
80	415989	AI267700			78.0
00	422544	AB018259	Hs.111128 Hs.118140		77.0
	425878	AW964806	Hs.38085	ESTs, Weakly similar to putative glycine	74.8
	429352	AK001512	Hs.200097		74.8
	42332	WWW1912	ms.200097	hypothetical protein FLJ 10650	73.0

	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	72.2
	441665 435094	Al301355 Al560129	Hs.151285 Hs.277523	ESTs EST	71.6 71.2
_	403345		- 4.21 / 320		69.6
5	430440	X52599	Hs.2561	nerve growth factor, beta polypeptide	69.0
	440482	AA886658	Hs.50873	ESTs	67.6
	457100 420637	AA417878 AW976153	Hs.48401	ESTs, Weakly similar to ALUB_HUMAN ALU S gb:EST388262 MAGE resequences, MAGN Homo	67.0 65.2
	407905	AW103655	Hs.252905	ESTs	63.2
10	422998	AK000588	Hs.122939	hypothetical protein FLJ20581	61.8
	432267	AK000872	Hs.274227	Homo sapiens cONA FLJ10010 fis, clone HE	61.2
	449448 431941	D60730 AK000106	Hs.57471 Hs.272227	ESTS	60.6
	419752	AA249573	Hs.152618	Homo saplens cDNA FLJ20099 fis, clone CO ESTs	59.8 58.4
15	449579	AW207260	Hs.134014	prostate cancer associated protein 6	58.2
	408609	AA330431	Hs.640	calcitonin receptor	57.4
	451009	AA013140	Hs.115707	ESTs	57.2
	435610 411893	AI862767 R82845	Hs.114157 Hs.273789	ESTs, Weakly similar to putative p150 [H ESTs	56.4
20	415227	AW821113	Hs.72402	ESTs .	56.2 55.2
	433859	AW898758	Hs.163925	ESTs	55.0
	450459	AI697193	Hs.299254	ESTs	54.4
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	53.4
25	421831 438817	AA298836 A1023799	Hs.22026 Hs.163242	ESTs ESTs	52.8 52.1
	449101	AA205847	Hs.23016	G protein-coupled receptor	52.0
	410025	BE220489	Hs.113592	ESTs	51.8
	423685	BE350494	Hs.49753	Homo sapiens mRNA for KIAA1561 protein,	48.0
30	436751	AA732217	Hs.294054	ESTs	46.6
50	445424 444059	A8028945 R69743	Hs.12696 Hs.75442	cortactin SH3 domain-binding protein albumin	45.4 44.8
	442671	AI005668	Hs.134779	EST	44.4
	445657	AW612141	Hs.279575	ESTs	44.3
35	452891	N75582	Hs.212875	ESTs, Wealdy similar to KIAA0357 [H.sapi	44.0
33	423735 422553	AA330259 Al697720	Un 1714EE	gb:EST33963 Embryo, 12 week ti Homo sapi ESTs	43.8
	452461	N78223	Hs.171455 Hs.108106	transcription factor	43.6 42.8
	408430	879876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	42.6
40	452240	AI591147	Hs.61232	ESTs	41.7
40	445186	AW614544	Hs.123641	protein tyrosine phosphatase, receptor t	41.4
	452788 419287	AW294571 X91906	Hs.135040	ESTS  chlorida channal E (anchesEthionia 7 V	41.4
	428822	W28418	Hs.89872 Hs.301148	chloride channel 5 (nephrofithiasis 2, X potassium voltage-gated channel, lsk-rel	40.6 40.2
	412359	AW837985	110.0011140	gb:QV3-LT0048-140200-083-e05 LT0048 Homo	40.0
45	434208	T92641	Hs.127648	hypothetical protein PRO2176	39.2
	442168	AJ253165	Hs.146022	ESTs	38.8
	400792 445900	AA635062 AF070526	Hs.50094 Hs.13429	Homo sapiens mRNA; cDNA DKFZp43400515 (f Homo sapiens clone 24787 mRNA sequence	38.6
	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked moi	38.4 38.4
50	428795	R45503	Hs.97469	ESTs, Wealdy similar to 149698 alpha-1,3	37.6
	406411				37.6
	423657 417218	AL045128	Hs.1691	glucan (1,4-alpha-), branching enzyme 1	37.5
	448788	AA005247 AI570286	Hs.285754 Hs.107070	met proto-oncogene (hepatocyte growth fa ESTs	37.2 37.2
55	441826	AW503603	Hs.129915	phosphotriesterase related	37.0
	409263	AA069573	Hs.50319	ESTs	36.8
	425577	BE464496	Hs.280977	ESTs	36.2
	452249 435986	8E394412 AA703158	Hs.61252 Hs.187848	ESTs ESTs	34.8 34.4
60	417236	Al908497	Hs. 170737	Homo sapiens cDNA: FLJ23251 fis, clone C	33.6
	440234	AW117264	Hs.126252	ESTs	33.8
	435334	R94223	Hs.117747	ESTs	33.2
	410153 424871	BE311926 NM_004525	Hs.15830 Hs.153595	Homo sapiens cDNA FLJ12691 fis, clone NT	33.1
65	420908	AL049974	Hs.100261	low density lipoprotein-related protein Homo sapiens mRNA; cDNA DKFZp564B222 (fr	32.8 32.4
	423992	AW898292	Hs.137206		32.4
	451050	AW937420	Hs.69662	ESTs	32.0
	449034	AI624049		gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapiens	31.6
70	434539 431595	AW748078 AA508196	Hs.214410		31.0
. •	449625	NM_014253	Hs.23796	gb:nh60f07.s1 NCI_CGAP_Pr8 Homo sapiens odz (odd Oz/ten-m, Drosophila) homolog 1	30.6 30.5
	448243	AW369771	Hs.77496	small nuclear ribonucleoprotein polypept	30.4
	413573	A1733859	Hs.149089	ESTs	30.2
75	421037	A1684808	Hs.197653		30.2
, ,	449353 416548	AA001220 H62953	Hs.271369	ESTs gb:yr47f06.r1 Soares fetal liver spleen	30.2
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	29.6 29.6
	422420	U03398	Hs.1524	turnor necrosis factor (ligand) superlami	29.6
80	459508	R83265	Hs.205956	ESTs	29.2
30	414245 424565	BE148072 AW102723	Hs.75850 Hs.75295	WAS protein family, member 1 guanylate cyclase 1, soluble, alcha 3	28.8
	445925	A1733820	Hs.145664		28.6 28.4
	412616		Hs.291033		28.0

	424638	AI472106	Hs.49303	Homo sapiens cDNA FLJ11663 fs, clone HE	27.6
	445885	AJ734009	Hs.127699	KIAA1603 protein	27.6
	410247	AF181721	Hs.61345	RUŽS	27.4
_	406414				27.2
5	435951	AF269162	Hs.41267	c21orf7 form A-D	27.2
	458680	N73773	Hs.282950	ESTs	27.0
	419948	AB041035	Hs.93847	NADPH oxidase 4	26.4
	423276	AC003034	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	26.3
10	427457	AW779105	Hs.164682	ESTs, Wealty similar to ORF2 consensus s	26.0
10	446346	AI290205		gb:qi79g06.x1 Soares_NhHMPu_S1 Homo sapi	26.0
	448595	AB014544	Hs.21572	KIAA0644 gene product	25.8
	419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	25.6
	433242	AB040938	Hs_113940	KIAA 1505 protain	25.6
15	453118	AW195849	Hs.252757	EST ₅	25.6
15	412209	AW901456		gb:RC0-NN1012-270300-031-c07 NN1012 Homo	25.2
	429710	Al337113	Hs.146025	Homo sapiens cDNA: FLJ23594 ffs, clone L	25.2
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	24.6
	436788	AA766908	Hs.259047	ESTS	24.4
20	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fs, clone C	24.4
20	419172	AW338625	Hs.22120	ESTs	24.3
	436061	A1248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	24.2
	413823	AA825721	Hs.246973	ESTs .	24.0
	407615	AW753085		gb:PM1-CT0247-151299-005-a03 CT0247 Homo	23.8
25	452466	N84635	Hs.29664	Human DNA sequence from clone 682J15 on	23.8
23	432809	AA565509	Hs.131703	ESTs	23.7
	440102	AI672443	Hs.131190	ESTS	23.6
	451559	AL119980	Hs.128857	EST _{\$}	23.2
	410811	AW805687	Hs.300648	EST ₈	23.0
30	416778	M16505	Hs.79876	steroid suffatese (microsomal), erylsulf	23.0
50	453628 401352	AW243307	Hs.170187	EST8	22.8
	451561	METOLO	11- 177/00	ESTs	22.6
	401976	N52812	Hs.177403	£315	22.6
	410658	AW105231	U- 400036	PAT-	22,4
35		N49776	Hs.192035 Hs.121773	ESTs STATE	22.4
55	416220 424073	U03493	Hs.138959	ESTs	22.2
	444575	AI264847		gap junction protein, alpha 7, 45kD (con	22.0
	444144	BE159397	Hs.22545 Hs.7736	Homo sapiens cDNA FLJ12935 fis, clone NT	22.0
	438504	AW665281	Hs.224625	hypothetical protein	21.8
40	439157	AA912737	Hs.20160	ESTs ESTs	21.2
70	429006	AA443143	Hs.50929		20.8
	442006	AW975183	Hs.292663	Homo sapiens cDNA FLJ 13842 fis, clone TH ESTs	20.5
	409569	AW573153	Hs.256216	ESTs	20.2
	421160	AL080215	Hs.102301		19.8
45	404200	ALVOVE13	113.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f	19.8
	446591	H44186	Hs.15456	POZ domain containing 1	19.6
	420218	AW958037	Hs.22437		19.2
	408390	AA054222	Hs.40400	Homo sapiens cDNA: FLJ23366 fis, clone H ESTs	18.9
	444038	AW134509	Hs.135077	ESTs	18.8
50	446443	AV659082	Hs.134228	ESTs	18.8 18.8
• •	442204	AI635450	Hs.21914	ESTs	18.4
	451177	AI969716	Hs.13034	ESTs	18.2
	453931	AL121278	Hs.25144	ES7s	18.1
	437212	AJ765021	Hs.210775	ESTs	18.1
55	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfami	18.0
	451659	BE379761	Hs.14248	ESTs. Wealthy similar to ALUS_HUMAN ALU S	17.8
	423909	AJ223183	Hs.135194	immunoglobulin superfamily, member 6	17.6
	441082	AW444804	Hs.202655	ESTs	17.6
	446259	AA425204	Hs.42278	Homo sapiens cDNA FLJ13391 fis, clone PL	17.6
60	423609	AA328348	Hs.218289	ESTs	17.4
	428301	AW628666	Hs.98440	ESTs	17.4
	446364	AB006624	Hs.14912	KIAA0286 protein	17.4
	419983	W55958	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (I	17.0
	424929	AI640761	Hs.224988	ESTs	17.0
65	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-recept	17.0
	449122	AI631310	Hs.196955	ESTs	17.0
	409519	AA075368		gb:zm86h10.r1 Stratagene ovarian cancer	18.8
	410947	AK000305	Hs.67055	hypothetical protein FLJ20298	16.8
70	418053	AA211493		gb:zn55d06.s1 Stratagene muscle 937209 H	16.8
70	433225	AW816515	Hs.173540		16.8
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	16.6
	421002	AF116030	Hs.100932	transcription factor 17	16.5
	419296	AA236115	Hs.120785		16.2
75	421659	NM_014459	Hs.106511	protocadherin 17	16.0
75	417589	T82075	Hs.13911	ESTs	16.0
	446057	A1420227	Hs.149358	ESTs .	15.8
	434638	AA083764	Hs.241334		15.6
	446797	A1682536	Hs.163495		15.6
80	443718	AI083580	Hs.221373	ESTa	15.4
OU	409748	A1670776	Hs.20961	ESTs	15.2
	443211	A1128388	Hs.143655		15.0
	428911	Z43846	Hs.194478		14.9
	444692	AW779922	Hs.145047	ESTs	14.8

	445436	AI224105	Hs.151408	ESTs	14.6
	408684	R61377	Hs.12727	hypothetical protein FLJ21610	14.5
	405943 406291				14,4
5	458679	AW975460	Hs.143563	ESTs	14.4
-	450152	Al138635	Hs.22968	EST8	14.4 14,4
	403899			20.0	14.2
	454490	AW797778		gb:CM2-UM0041-250200-104-d02 UM0041 Homo	14.2
• •	451807	W52854	Hs.27099	DKFZP564J0863 protein	14.0
10	452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sapien	13.8
	447499	AW262580	Hs.147674	KIAA1621 protein	13.8
	406598	41000404			13.6
	430939	AJ269471	Hs.187018	ESTs	13.4
15	443316 408034	AJ478463 N26639	Hs.18443	ESTs	13.4
13	428508	BE252383	Hs.42192 Hs.184568	Human EST clone 251800 mariner transposo SB8i31 protein	13.2
	447934	AW631440	Hs.165596	ESTs	13.2 13.2
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	13.1
	438199	AW016531	Hs.122147	ESTs	13.0
20	415511	AJ732617	Hs.182362	ESTs	12.9
	426920	AA393351	Hs.132121	ESTs	12.8
	447311	R37010	Hs.33417	Homo sapiens cDNA: FLJ22806 fis, clone K	12.6
	423321	AB013885	Hs.126926	beta-ureidopropionase	12.5
25	403622	41.350055	11. 07700		12.4
25	439759 422317	AL359055 NM_001147	Hs.67709	Homo sapiens mRNA full length insert cDN	12.4
	428637	AW979268	Hs.115181	angiopoletin 2	12.2
	445717	AW664658	Hs.149332	gb:EST391378 MAGE resequences, MAGP Homo ESTs	12.2 12.2
	418413	R95735	Hs.117753	ESTs, Wealthy similar to antigen of the m	12.2
30	405336			Corot troomy animal as assignment to the	12.0
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	12.0
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	12.0
	414923	AW445008	Hs.77637	homeo box A4	11.9
35	432009	AL137424		gb:Homo sapiens mRNA; cDNA DKFZp761G2123	11.8
33	433326	Al379486	Hs. 159430	ESTs	11.8
	453955 407510	AW579207 U96191		gb:RC1-DT0029-120100-011-h01 DT0029 Homo	11.8
	433231	AB040926	Hs.143552	gb:Human trophoblast hypoxia-regulated f	11.6
	451651	AI097337	Hs.88977	KIAA1493 protein hypothetical protein dJ511E16.2	11.6
40	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	11.6 11.4
	405609			A STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STA	11.4
	418912	NM_000685	Hs.89472	angiotensin receptor 1	11,4
	421306	AA806207	Hs.125889	ESTs	11,4
45	428721	X02158	Hs.2303	erythropoietin	11.4
43	419255	AA235672	Hs.87491	EST8	11.4
	450006	AI241555	Hs.60171	ESTs	11.3
	435420 449802	AI928513 AW901804	Hs.59203	ESTs	11.2
	424647	W67751	Hs.23984 Hs.137308	hypothetical protein FU20147 ESTs	11.2
50	435758	AJ242163	Hs.22670	chromodomain helicase DNA binding protei	11.0 11.0
	404347			and the second second second second	10.8
	438664	AJ911173	Hs.213722	ESTs	10.8
	429125	AA446854	Hs.271004	ESTs	10.7
55	416560	R02818	Hs.14102	ESTs	10.6
23	429945	NM_006729	Hs.226483	diaphanous (Drosophila, homolog) 2	10.6
	435085 442409	AW130284	Hs.192752	ESTs, Moderately similar to NSO1 protein	10.6
	450644	BE208843 AW505496	Hs.129544	ESTs. Weakly similar to ORF YLL027w (S.c	10.6
	448298	AW137134	Hs.281215 Hs.187203	ESTs ESTs	10.6
60	404115	A.V. 101	19.101200	2015	10.4 10.2
	406242				10.2
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	10.2
	452588	AA889120	Hs.110637	homeo bax A10	10.2
65	457233	AI355009	Hs.221698	ESTs	10.2
65	416185	AW975861	Hs.291995	ESTs	10.2
	446152	AI292036	Hs.150028	ESTs	10.1
	446298 423637	AF187813 AL137279	Hs.14637	kidney- and liver-specific gene	10.1
	442405	BE465247	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (f	10.0
70	419213	AW749146	Hs.129530	ESTs gb:PM0-BT0340-170100-004-e03 BT0340 Homo	9.9
. •	420840	AI915838	Hs.294008	ESTs	9.8
	423355	AA324856	Hs.257510		9.8 9.8
	444929	AI685841	Hs.161354		9.8
75	423811	AW299598	Hs.50895	homeo box C4	9.8
75	433527	AW235613	Hs.133020	ESTs .	9.6
	429975	A1167145	Hs.165538		9.6
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	9.5
	433703 417404	AA210863 NM_007350	Hs.3532	nemo-like kinase	9.2
80	451621	AI879148	Hs.82101 Hs.26770	pleckstrin homology-like domain, family	9.2
	406992	S82472	1520110	fatly acid binding protein 7, brain gb:beta-pol=DNA polymerase beta (exon a	9.2 9.2
	419699	AA248998	Hs.31246	ESTs	9.2 9.2
	443740	R56434	Hs.21062	ESTs	9.2

				POT-	
	422728 436961	AW937826	Hs.103262	ESTs ESTs	9.2
	431385	AW375974 BE178536	Hs.156704 Hs.11090		9.2 9.1
	411411	AA345241	Hs.55950	high affinity immunoglobulin epsiton rec ESTs, Wealdy similar to KIAA1330 protein	9.1
5	424115	AA335497	Hs.293965	ESTs	9.0
	402045				9.0
	433426	H69125	Hs.133525	ESTs	9.0
	425493	AW363582	Hs.75323	prohibitin .	9.0
10	447641	BE619186		gb:601472933F1 NIH_MGC_68 Horno sapiens c	9.0
10	407942	AA378608	Hs.5894	hypothetical protein FLI 10305	8.8 8.8
	423126	AA322245	Hs.290165	ESTs	8.8
	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodieste	8.7
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	8.6
15	443647	AV653846	Hs. 126261	Homo sepiens Chromosome 16 BAC clone CIT	8.6
	401439				8.6
	449532	W74653	Hs.271593	ESTs	8.6
	453197 448450	AI916269 BE612490	Hs.109057	ESTs, Wealdy similar to ALUS_HUMAN ALU S	8.6
20	425176	AW015644	Hs.301430	gb:601451884F1 NIH_MGC_66 Homo sapiens c ESTs, Moderately similar to TEF1_HUMAN T	8.5 8.4
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	8.4
	402921			and the same (1) breshief.	8.4
	428133	AW167727	Hs.11873	ESTs .	B.4
25	419603	AA243642	Hs.137422	ESTs	8.4
25	452644	AW452616	Hs.212481	ESTs	8.4
	452259 409695	AA317439 AA296961	Hs.28707	signal sequence receptor, gamma (translo	8.4
	418076	R61388	Hs.6724	gb:EST112514 Adrenal gland tumor Homo sa ESTs	8.3 8.3
	402696		13.0124	2010	8.3
30	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	8.3
	413998	AW103807	Hs.243933	ESTs	8.2
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (93720	8.2
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone C	8.2
35	450001 435496	NM_001044 AW840171	Hs.406 Hs.265398	solute carrier family 6 (neurotransmitte	8.1
55	413627	BE182082	Hs.246973	ESTs, Weakly similar to transformation-r ESTs	8.0 8.0
	415713	AW968573	14.240310	gb:EST380649 MAGE resequences, MAGJ Homo	8.0
	426695	AW118191	Hs.112729	ESTs	8.0
40	452284	AW451426	Hs.252740	ESTS	8.0
40	454933	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	8.0
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	8.0
	418882 444107	NM_004996 T46839	Hs.89433 Hs.10319	ATP-binding cassette, sub-family C (CFTR	6.0
	445740	T78281	Hs.13226	UDP glycosytransferase 2 family, polype Homo sapiens clone 25181 mRNA sequence	7.9 7.9
45	433190	M26901	Hs.3210	renin	7.8
	432777	AA564991	Hs.269477	ESTs	7.8
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	7.7
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	7.7
50	434032	AW009951	Hs.206892	ESTs	7.7
50	419750 439024	AL079741 R96696	Hs.183114 Hs.35598	Homo sapiens cDNA FLJ14236 fis, clone NT ESTs	7.6
	437205	AL110232	14.0000	gb:Homo sapiens mRNA; cDNA DKFZp564D2071	7.6 7.4
	446030	AF131805	Hs.13544	Homo sapiens clone 24850 mRNA sequence	7.4
	448311	AW007294	Hs.149795	ESTs, Wealdy similar to ALU1_HUMAN ALU S	7.4
55	452883	X80031	Hs.150318	ESTs .	7.4
	448253	H25899	Hs.201591	ESTs	7.4
	406030 437084	AI911516	Hs.127811	ESTs	7.4
	435013	H91923	Hs.110024	NADH:ubiquinons oxidoreductase MLRQ subu	7.3 7.3
60	432143	AL040183	Hs.123484	ESTs, Weakly similar to The KIAA0149 gen	7.3 7.3
	409594	AA076118		gb:zm18e06.s1 Stratagene pancreas (93720	7.2
	425151	AA351814	Hs.298678	ESTs	7.2
	448582	A1538880	Hs.94812	EST6	7.2
65	455068 406504	A1807894	Hs.27910	centrosomal protein 2	7.2
05	428395	AA427992	Hs.104885	CCTs. Wookhy slowlers to sing forms and	7.2
	421102	AI470093	Hs.89217	ESTs, Weakly similar to zinc finger prot ESTs	7.2 7.2
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	7.1
70	410534	AW905138		gb:QV0-NN1071-280400-207-g07 NN1071 Homo	7.1
70	415084	M19267	Hs.77899	tropomyosin 1 (alpha)	7.0
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	7.0
	439416	W58294	Hs.56254	ESTs	6.9
	420036 423349	R60336 AF010258	Hs.52792 Hs.127428	Homo sapiens mRNA; cDNA DKFZp586(1823 (f homeo box A9	6.8
75	413070	AA126776	113.14/420	gb:zn88c11.s1 Stratagene lung carcinoma	6.8
	449361	AW207890	Hs.201918	ESTs	6.8 6.8
	459309	AA040620	Hs.109144		6.8
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	6.8
80	416462	W92845		gb:zh80f05.r1 Soares_fetal_liver_spleen_	6.8
30	447835	AW591623	Hs.164129	ESTs	6.7
	403563 427897	NM_017413	Hs.181060	apelin; peptide ligand for APJ receptor	6.7
	422063	BE156476	- 10 1000	gb:QV0-HT0368-040100-082-c05 HT0368 Homo	6.5 6.6
					4.0

	455375	A14/07200C			
	455275 441350	AW977806 AB020690	Hs.7782	gb:EST389810 MAGE resequences, MAGO Homo	6.6
	445575	Z25368	Hs.172004	paraneoplastic antigen MA2 titin	6.6 6.6
	446075	AW451457	Hs.279179	ESTs	6.6
5	405963		VI3.210114	20.0	6.6
	423049	X59373	Hs.188023	ESTs	6.6
	436456	AW292677	Hs.65909	ESTS	6.5
	420273	AI652864	Hs.197257	ESTs	6.5
10	420831	AA280824	Hs.190035	ESTs	6.4
10	423739	AA398155	Hs.97600	ESTs	6.4
	441559	AA938448	Hs.259733	ESTs	6.4
	433999	AA778212	Hs.191869	EST8	6.4
	439703 433757	AF086538 AI949974	Hs.196245	ESTs	6.4
15	422095	AI868872	Hs.152670 Hs.288968	ESTs	6.3
	415138	C18356	Hs.78045	cerufoplasmin (ferroddase) lissue factor pathway inhibitor 2	6.3 6.3
	448515	H68441	Hs.13528	Homo sapiens cDNA FLJ14054 fis, clone HE	6.3
	443595	AF169312	Hs.9613	PPAR(gamma) engiopoietin related protein	6.3
~~	429357	AA779725	Hs.164589	ESTs	6.3
20	404939				6.3
	417071	N58820	Hs.275133	ESTs	6.2
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed prot	8.2
	403111	44447020	11- 22402	POT- 15-41 -1- 7 A 4 0040000 0 D0000	6.2
25	448796 442353	AA147829 BE379594	Hs.33193 Hs.49136	ESTs, Highly similar to AC007228 3 BC372 ESTs	6.2
	451110	A1955040	Hs.301584	ESTs	6.2
	420092	AAB14043	Hs.88045	ESTs	6.1 6.1
	441801	AW242799	Hs.211874	ESTs	6.0
	407500	U43279		gb:Human nucleoporin nup 36 mRNA, comple	6.0
30	450864	R64139	Hs.205225	ESTs	6.0
	455711	BE069465		gb:RC2-BT0388-290100-012-a11 BT0388 Homo	6.0
	405394				6.0
	436476	AA326108	Hs.53631	ESTs, Weakly similar to enhancer-of-spli	6.0
35	454392	BE260893		gb:601150677F1 NIH_MGC_19 Homo sepiens c	6.0
33	414575 435767	H11257 H73505	Hs.295233	ESTs	5.9
	445495	BE622641	Hs.117874 Hs.38489	ESTs ESTs	5.9
	428372	AK000684	Hs.183887	hypothetical protein FLJ22104	5.9 5.9
	436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.9
40	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	5.9
	402421				5.8
	417038	T85230		ģb:yd33f02.r1 Soares fetal liver spiesn	5.8
	438461	AW511956	Hs.293261	ESTs	5.8
45	440870	AJ587284	Hs.150539	Homo sepiens cDNA FLJ13793 fis, clone TH	5.8
43	452281	T93500	Hs.28792	Homo sapiens cONA FLJ11041 fis, clone PL	5.8
	417280 437259	AW173116 AI377755	Hs.262206	ESTs	5.7
	425717	X07282	Hs.120695 Hs.171495	ESTs	5.7
	443614	AV655386	Hs.7645	retinoic acid receptor, beta fibrinogen, B beta polypeptide	\$.7 5.7
50	450625	AW970107	113.70-3	gb:EST382188 MAGE resequences, MAGK Homo	5.6
	425305	AA363025	Hs.155572	Human clone 23801 mRNA sequence	5.6
	430371	D87466	Hs.240112		5.6
	430499	AW969408	Hs.231991	ESTs	5.6
55	427920	Z11502	Hs.181107	annexin A13	5.6
در	449318 407864	AW236021	Hs.108788	ESTs. Weakly similar to zeste [D.melanog	5.6
	410754	AF069291	Hs.40539	chromosome 8 open reading frame 1	5.5
	415286	T63840 AW249540	Hs.72548	gb:yc16b10.s1 Stratagene lung (937210) H ESTs	5.5
	443297	AI049864	Hs.133029		5.5 5.5
60	440138	AB033023	Hs.6982	hypothetical protein FLJ10201	5.5
-	441006	AW605267	Hs.7627	CGI-60 protein	5.4
	409348	AI401535	Hs.146090	ESTs	5.4
	449679	AJ823951	Hs.296668		5.4
65	408938	AA059013	Hs.22607	ESTs	5.4
UJ	456411	AA603305	14- 4-00	gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	5.4
	443756	AW089799	Hs.153665		5.4
	422232 424574	D43945 BE408618	Hs.113274		5.4
	424834	AK001432	Hs.150748 Hs.153408		5.3
70	440589	BE397763	Hs.194478		5.3 5.3
	425782	U66468	Hs.159525		5.3
	450236	AW162998	Hs.24684	KIAA1376 protein	5.3
	418110	R43523	Hs.217754		5.3
75	427061	AB032971	Hs.173392	KIAA1145 protein	5.3
75	413841	M34276	Hs.75578	plasminogen	5.3
	432358	AI093491	Hs.72830	ESTs	5.2
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	5.2
	438475	W03856	Hs. 13188	ESTs, Highly similar to Gene product wit	5.2
80	443305 413930	AJ050693 M86153	Hs.133318 Hs.75618	ESTs RAB11A, member RAS oncogene family	5.2
	451859	H44491	Hs.252938		5.1
	429826	N93266	Hs.40747	ESTS	5.1 5.1
	436032	AA150797	Hs.109276		5.1
					5

	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	5.1
	438297	AW515196	Hs.258238	ESTs, Moderately similar to ALU1_HUMAN A	5.1
	421126	M74587	Hs. 102122	insufin-like growth factor binding prote	5.1
5	440238	AW451970	Hs.155644	paired box gene 2	5.1
ر	426651 425813	AU076645 AA364138	Hs.171683 Hs.210553	nuclear receptor subtamily 1, group H, m ESTs, Wealthy similar to hypothetical pro	5.0 5.0
	432328	AI572739	Hs.195471	6-phosphotructo-2-kinase/fructose-2,6-bi	5.0
	430682	AW971949	Hs.291252	ESTs	5.0
10	410049	AW579475		gb:RC0-DT0076-110100-031-d10 DT0076 Homo	5.0
10	429222	AI457692	Hs.99164	ESTs	5.0
	446317 409506	AI287367 NM_006153	Hs.150906 Hs.54589	ESTs NCK adaptor protein 1	5.0 5.0
	407768	AW002841	Hs.29475	ESTs	5.0
	437938	AI950087		gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapien	5.0
15	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfami	4.9
	426215 448570	AW963419 AI923944	Hs.155223 Hs.30913	stanniocalcin 2 ESTs	4.9 4.9
	445034	AW293376	Hs. 160323	ESTs	4.9
~~	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	4.8
20	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	4.8
	438492 446417	AW340048 AJ299050	Hs.293188	ESTS	4.8
	409578	BE041386		gb:qn14d12.x1 NCI_CGAP_Lu5 Homo sapiens gb:hk88c02.x1 NCI_CGAP_Lu21 Homo sapiens	4.8 4.8
	447269	NM_004861	Hs.17958	cerebroside (3'-phosphoadenyly/sulfate:g	4.8
25	413795	AL040178	Hs.142003	ESTs	4.8
	422357	AF016272	Hs.115418	cadherin 16, KSP-cadherin	4.8
	452208 422711	AA024792 D60641	Hs.31895 Hs.21739	ESTs, Weakly similar to 89 [H.sapiens] Homo sapiens mRNA; cDNA DKFZpS86I1518 (/	4.7 4.7
	441392	AW451831	Hs.222119	ESTs, Weakly similar to K1CQ_HUMAN KERAT	4.7
30	439221	AA737106	Hs.32250	ESTs	4.7
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PL	4.7
	417355	D13168	Hs.82002	endothelin receptor type 8	4.7
	414700 402739	H63202	Hs.38163	ESTs	4.7 4.6
35	403170				4.6
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	4.6
	408380	AF123050	Hs.44532	diubiquitin	4.6
	427899	AA829286	Hs.181062	serum amyloid A1	4.5
40	446302 414812	AJ285848 X72755	Hs.149757 Hs.77367	ESTs	4.5 4.4
70	424063	NM_002019	Hs.138671	monokine induced by gamma interferon fms-related tyrosine kinase 1 (vascular	4.4
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	4.4
	421298	AW172431	Hs.13012	ESTs	4.4
46	420789	AI670057	Hs.199882	ESTs .	4.4
45	453558	AI417023	Hs.40478 Hs.63908	ESTS	4.4
	453745 451762	AA952989 AF222980	Hs.26985	Homo sapiens HSPC316 mRNA, partial cds disrupted in schlzophrenia 1	4.4 4.4
	410334	AW979261	Hs.291993	ESTs	4.4
50	457030	Al301740	Hs.173381	dihydropyrimidinase-like 2	4,4
50	452194	AI694413	Hs.298262	ESTs, Weakly similar to dJ88J8.1 [H.sapi	4.3
	410407 401157	X66839	Hs.63287	carbonic anhydrase IX	4.3 4.3
	432004	BE018302	Hs.2894	placental growth factor, vascular endoth	4.3
	426866	U02330	Hs.172816	neuregulin 1	4.3
55	446115	AI733075	Hs.292682	ESTs, Wealdy similar to S69913 hypertens	4.3
	424704 446619	AI263293 AU076643	Hs.152096 Hs.313	cytochrome P450, subfamily IIJ (arachido	4.2
•	433578	BE336886	Hs.3416	secreted phosphoprotein 1 (osteopontin, adipose differentiation-related protein	4.2 4.2
	407065	Y10141		gb:H.sapiens DAT1 gene, partial, VNTR.	4.2
60	407182	AA312551	Hs.230157	ESTs	4.2
	416565	AW000960	Hs.44970	ESTs	4.2
	442230 440680	8E219088 AA903098	Hs.279547	ESTs gb:ok46f08.s1 NCI_CGAP_Lei2 Homo sapiens	4.2 4.2
	413802	AW964490	Hs.32241	ESTs	4.2
65	438370	AA843242	Hs.48523	ESTS	4.2
	432731	R31178	Hs.287820		4.2
	409745	AA077391	U- 50070	gb:7814E12 Chromosome 7 Fetal Brain cDNA	4.2
	441484 411213	AA935481 AA676939	Hs.58972 Hs.69285	ESTs neuropilin 1	4.2
70	453045	AW418979	Hs.224502		4.2 4.2
_	407999	AJ126271	Hs.49433	ESTs. Wealty similar to HYPOTHETICAL PRO	4.2
	409770	AW499536		gb:UI-HF-BR0p-aji-c-12-0-UI.rt NIH_MGC_5	4.1
	449856	AA203155	Hs.18200	ESTs	4.1
75	430808 412872	S69377 BE006341	Hs.247978		4.1
, ,	430719	AA488988	Hs.293796	gb:RC2-BN0127-240300-011-b05 BN0127 Homo ESTs	4.1 4.1
	409637	AA323948	Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (f	4.1
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	4.1
80	444670	H58373	Hs.37494	ESTS	4.1
30	448090 408830	At608821 AK001709	Hs.270289 Hs.48403	ESTs hypothetical protein FLJ10847	4.1 4.1
	419088	AI538323	Hs.77496	small nuclear ribonucleoprotein polypept	4.1
	416655	AW968613		BCL2/adenovirus E1B 19kD-interacting pro	4.1

	******	******			
	436772	AW975688	Hs.250867	zona pellucida glycoprotein 3A (sperm re	4.1
	442556	AL137761	Hs.8379	Homo sepiens mRNA; cONA DKFZp586L2424 (I	4.1
	459595	AL040421		gb:DKFZp434B0714_r1 434 (synonym: htes3)	4.1
5	438859	A1559626	Hs.164973	ESTs, Wealty similar to AF231024 1 proto	4.0
,	423279	AW959861	Hs.290943	ESTs	4.0
	441592	AW137071	Hs.127211	ESTs .	4.0
	411836	AW901879		gb:QV0-NN1021-280400-212-410 NN1021 Homo	4.0
	426384	A1472078		gb:tj85h03.x1 Soares_NSF_F8_9W_OT_PA_P_S	4.0
10	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	4.0
10	413583	AL120806	Hs.5888	ESTs	4.0
	415610	L44319		gb:HUMEST1D10 Human Brymus NSTH II Homo	4.0
	430009	AA894564	Hs.22242	ESTs	4.0
	449539	W80363	Hs.58446	ESTs	4.0
	438929	AW195515	Hs.253177	ESTs	4.0
15	416000	R82342	Hs.79856	ESTs	4.0
	429616	AI982722	Hs.120845	ESTs	4.0
	458471	AV648609	Hs.194240	ESTs	4.0
	453195	BE241876	Hs.32352	hypothetical protein DKFZp434K1210	4.0
	459045	AA910339	Hs.26216	Homo sapiens cDNA: FLJ22811 fis, clone K	3.9
20	438177	BE327015	Hs.281391	ESTs	3.9
	422438	AA445925	Hs.270896	ESTs	3.9
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fls, clone PL	3.9
	449611	AI970394	Hs.197075	ESTs	3.9
	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (f	
25	452881	AW135220	Hs.241921	ESTs	3.9
	414729	BE466928	Hs.281901	ESTs	3.9
	428816	AA004986	Hs.193852		3.9
	405908		**********	ATP-binding cassette, sub-family C (CFTR	3.9
	445452	H92975	Hs.246046	ESTe Weath similar to DETA LIBRARI DETA	3.8
30	447961	W32791	Hs.170405	ESTs. Wealdy similar to RET1_HUMAN RETIN	3.8
-	446639	AI016826	Hs.132501	ESTS	3.8
	401189	71010020	113, 132301	EST ₈	3.8
	429548	AW138872	Hs.135288	ESTs	3.8
	431523	N55759	Hs.163674		3.8
35	430014	H59354	Hs.182485	ESTs	3.8
55	429250	H56585		actinin, alpha 4	3.8
	451988	AF263928	Hs.198308	tryptophan rich basic protein	3.8
	437939	AW298600	Hs.27410	papillomavirus regulatory factor PRF-1	3.8
	427510	Z47542	Hs.141840	ESTs. Weakly similar to S59501 interfero	3.8
40	433522	AIB21730	Hs.179312	small nuclear RNA activating complex, po	3.8
40	443843		Hs.116524	ESTs	3.8
		AW878864	Hs.13528	Homo sapiens cDNA FLJ14054 fis, clone HE	3.7
	407305	AA715284		gb:rv35f03.r1 NCI_CGAP_Br5 Homo sapiens	3.7
	434613	AJ821826	Hs.187786	ESTs, Moderately similar to ALUB_HUMAN !	3.7
45	410276	AI554545	Hs.68301	ESTs	3.7
73	422504	AA311407		gb:EST182187 Jurket T-cells V Homo sapie	3.7
	421013	M62397	Hs.1345	mutated in colorectal cancers	3.7
	437949	U78519	Hs.41654	ESTs	3,7
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	3.7
50	409446	AI561173	Hs.67688	ESTs	3.7
50	415263	AA948033	Hs.130853	ESTs	3.7
	450206	A1796450	Hs.201600	EST8	3.7
	439444	AI277652	Hs.54578	ESTs	3.7
	437828	AW976806	Hs.291805	ESTs	3.7
55	453238	AA033991	Hs.269234	ESTs	3.7
"	420041	AB005142	Hs.94592	Idotho	3.7
	448458	AW614367	Hs.171054	ESTs	3.7
	435080	AI831760	Hs.155111	ESTs .	3.7
	444249	T87398	Hs.205816	ESTs	3.7
60	426595	AW971980	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	3.7
00	417715	AW969587	Hs.86366	EST8	3.7
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.6
	440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein	3.6
	430091	AB032958	Hs.233023	KIAA1132 protein	3.6
65	438030	X98427	Hs.122634	ESTa	3.6
05	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	3.6
	446638	AC002563	Hs.15767	citron (rho-interacting, sennerthreonin	3.6
	417860	AW408557	Hs.235498	Homo sapiens cDNA FLJ14075 fis, clone HE	3.6
	435794	H72108	Hs.13704	ESTs	3.6
70	449695	AA164569	Hs.34550	ESTs	3.6
70	411485	AW848125		gb:IL3-CT0214-301299-048-G04 CT0214 Homo	3.6
	426274	038122	Hs.2007	tumor necrosis factor (ligand) superfami	3.6
	458201	AI989961	Hs.233477	ESTs. Moderately similar to A Chain A, S	3.6
	440987	AA911705	Hs.130229	EST ₆	3.6
75	425178	H16097	Hs.161027	ESTs	3.6
75	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	3.6
	436091	AA704705	Hs.181044	ESTs, Wealdy similar to A Chain A, Human	3.6
	452671	AW861074	Hs.225833	EST8	3.6
	437222	AL117588	Hs.299963	EST\$	3.6
80	437809	AL137723	Hs.5855	Homo sapiens mRNA; cDNA DKFZp434D0818 (1	3.5
OU	411545	AW850818		gb:IL3-CT0220-091199-026-A03 CT0220 Homo	3.5
	414799	AJ752416	Hs.77326	insufin-like growth factor binding prote	3.5
	439882	AA847856	Hs.124565	ESTs	3.5
	419229	AI827237	Hs.282884	ESTs	3.5

	431889	AA521277	Hs.124945	ESTs	3.5
	422660	AW297582	Hs.237062	ESTs	3.5
	415122 444127	D60708 N63620	Hs.22245 Hs.13281	ESTs ESTs	3.5 3.5
5	416913	AW934714	113.10201	gb:RC1-DT0001-031299-011-a11 DT0001 Homo	3.5
	409044	Al129588	Hs.33033	ESTs	3.5
	453365	AA035211	Hs.17404	ESTs	3.5
	452355	N54926	Hs.29202	G protein-coupled receptor 34	3.5
10	423246 434131	AL119114 AI858275	Hs.23107 Hs.143659	ESTs ESTs	3.5 3.5
	425304	AA463844	Hs.31339	fibroblast growth factor 11	35
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.4
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	3.4
15	456311	AA225632	Hs.190016	ESTs	3.4
13	420737 448733	L08096 NM_005629	Hs.99899 Hs.187958	tumor necrosis factor (ligand) superfami solute carrier family 6 (neurotransmitte	3.4 3.4
	401811	14M_000025	115.107550	some come rainty of (new on a raint)	3.4
	404021				3.4
20	447175	AI365208	Hs.293606	ESTs	3.4
20	453743	AL120480		gb:DKFZp761K098_r1 761 (synonym: hamy2)	3.4
	455070 419546	AW854675 AA244199		gb:MR1-CT0258-290300-206-a01 CT0258 Homo gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sapiens	3.4 3.4
	449441	AI656040	Hs.196532	ESTs	3.4
	441606	R37263	Hs.21065	ESTs	3.4
25	446594	Al311917	Hs.16292	ESTs	3.4
	424564	AI432572	Hs.164221	ESTs	3.4
	413719 427914	BE439580 AA417350	Hs.75498 Hs.20575	small inducible cytokine subfamily A (Cy ESTs	3.4 3.4
	438257	AW474419	Hs.224794	ESTs	3.4
30	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoletin A;	3.4
	454690	AW854539		gb:MR1-CT0258-140100-203-d10 CT0258 Homo	3.3
	428046 407331	AW812795	Hs.155381	ESTs, Moderately similar to 138022 hypot	3.3
	440472	AJ570416 AA886169	Hs.99910 Hs.169071	phosphofructokinase, platelet ESTs	3.3 3.3
35	421893	NM_001078	Hs.109225	vascular cell adhesion molecule 1	3.3
	403797	_			3.3
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos	3.3
	410623 449338	AW958932 H73444	Hs.293833 Hs.394	ESTs adrenomedullin	3.3
40	441024	AW081530	Hs.137088	ESTs	3.3 3.3
	405257			20.2	3.3
	450396	AU077002	Hs.24950	regulator of G-protein signalling 5	3.3
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	3.3
45	444471 431689	AB020684 AA305688	Hs.11217 Hs.267695	KIAA0877 protein	3.3 3.3
43	452093	AA447453	Hs.27860	UDP-Gal:betaGicNAc beta 1,3-galactosyltr Homo sapiens mRNA; cDNA DKFZp586M0723 (f	3.3 3.3
	425236	AW067800	Hs.155223	stanniocalcin 2	3.3
	428824	W23624	Hs.173059	ESTs	3.2
50	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	3.2
50	425260 443830	L47726 AI142095	Hs.1870 Hs.143273	phenylalanine hydroxytase ESTs	3.2 3.2
	415245	N59650	Hs.27252	ESTs	3.2
	405953				3.2
55	430812	£10405	Hs.247992	DNA binding protein for surfactant prote	3.2
23	418946 424750	A1798841 D2 <del>99</del> 56	Hs.132103 Hs.152818	ESTs ubiquitin specific protease 8	3.2 3.2
	435342	AW979168	Hs.163270	ESTs	3.2
	458860	AW873557	Hs.212739	ESTs	3.2
60	430172	AA468591	Hs.161889	ESTs	3.2
OU	431842 451221	NM_005764 AI949701	Hs.271473 Hs.210589	epithelial protein up-regulated in card	3.2
	436211	AK001581	Hs.80961	ESTs polymerase (ONA directed), gamma	3.2 3.2
	433727	C16221	Hs.112608	ESTs	3.2
65	424897	D63216	Hs.153684	frizzled-related protein	3.2
65	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity ta, re	3.1
	418030 417919	BE207573 AI928203	Hs.86379	ESTs	3.1
	430437	AI768801	Hs.169943		3.1 3.1
	409663	AI743750	Hs.65862	ESTs	3.1
70	454024	AA993527	Hs.16281	hypothetical protein FLJ23403	3.1
	424980	L42172	Hs.154078		3.1
	421633 436002	AF121860 R68529	Hs.106260 Hs.120967		3.1 3.1
	437682	AA476652	Hs.94952	Homo sapiens cONA: FLJ23371 fis, ctone H	3.1 3.1
75	439451	AF085270	Hs.278554	heterochromatin-like protein 1	3.1
	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	3.1
	428479	Y00272	Hs.184572		3.1
	441285 456386	NM_002374 W28481	Hs.167	microtubule-associated protein 2 gb:47e1 Human retina cDNA randomly prime	3.1 3.1
80	451130	AI762250	Hs.211347		3.1
	439702	AW085525	Hs.134182	P ESTs	3.1
	453331	A1240665	Hs.8895	ESTs	3.1
	428841	AI418430	Hs.104935	5 ESTs	3.1

	449899	Al610700	U- 103380	ESTs	••
	436009	H57130	Hs.103280 Hs.120925	ESTs	3.1 3.1
	448966	AW372914	Hs.287462	Homo sapiens cDNA FLJ11875 fis, clone HE	3.1
E	408239	AA053401	Hs.271827	ESTs. Moderately similar to ALU7_HUMAN A	3.1
5	418526 401260	8E019020	Hs.85838	solute carrier tamily 16 (monocarboxylic	3.1 3.1
	450705	U90304	Hs.25351	iroquois-class homeodomain protein	3.1
	447233	AW246333	Hs.17901	Homo sapiens cDNA: FLJ21974 fis, clone H	3.1
10	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	3.0
10	403346 446319	AW207590	Hs.160711	ESTs	3.0 3.0
	432757	AF113013	Hs.278919	PRO0806 protein	· 3.0
	407921	AI378617	Hs.23100	Homo sapiens cDNA FLJ12592 fis, clone NT	3.0
15	414618 434398	AJ204600 AA121098	Hs.96978 Hs.3838	ESTs	3.0
13	440113	AF916532	Hs.188272	serum-inducible kinase ESTs	3.0 3.0
	424539	L02911	Hs.150402	activin A receptor, type I	3.0
	428945	AW192803	Hs.98974	ESTs .	3.0
20	458297 424405	R54033 AI076838	Hs.21245 Hs.12967	ESTs ESTs	3.0 3.0
	411290	AW835544	1 12.12.507	gb:QV4-LT0016-271299-068-f03 LT0016 Homo	3.0
	459068	BE464396	Hs.118468	<b>EST8</b>	3.0
	459065 437693	AI373532 AI754443	Hs.157910 Hs.185951	ESTs	3.0
25	429418	AI381028	Hs.99283	ESTs ESTs	3.0 3.0
	406117				3.0
	415492	R41674	Hs.16491	ESTs	3.0
	419854 453688	AW664873 AW381270	Hs.87836 Hs.194110	Homo sapiens PAC clone RP5-1087M19 from Homo sapiens mRNA; cDNA DKFZp434C0814 (f	3.0 3.0
30	408119	W26213		gb:22d10 Human retina cONA randomly prim	3.0
	438358	AL035992	Hs.210278	ESTs	3.0
	412372 431984	R65998 AL080239	Hs.118615 Hs.272284	ESTs Human DNA sequence from clone GS1-256O22	3.0
	403782	ALU00233	115.272204	Number Divi sequence von clone 931-230022	3.0 3.0
35	443183	R16258	Hs.6217	Homo sapiens cDNA FLJ12521 fis, clone NT	3.0
	456388 447922	W28557 292910	Hs.20019	gb:48d8 Human retina cDNA randomly prime hemochromatosis	3.0
	428857	AF008192	Hs.194283	putative GR6 protein	3.0 3.0
40	406991	582185		(NONE)	3.0
40	432596 453202	AJ224741	Hs.278461	matrilin 3	3.0
	414132	AW085781 AI801235	Hs.26270 Hs.48480	Homo sapiens cDNA FLJ11588 fis, clone HE ESTs	3.0 3.0
	409122	W07089	Hs.297873	ESTs	3.0
AS	405547				3.0
45	422219 417227	AW978073 T57776	Hs.191094	gb:EST390182 MAGE resequences, MAGO Homo	3.0
	448592	N69546	Hs.141706	ESTs ESTs	3.0 3.0
	421477	AF904743	Hs.104650	hypothetical protein FLJ10292	3.0
50	400368 455362	BE779978 AW902635	Hs.69149	proline-serine-threonine phosphatase int	3.0
20	443578	R97191	Hs.134106	gb:QV3-NN1024-100500-181-602 NN1024 Hamo ESTs	3.0 3.0
	419348	AA236645	Hs.98274	ESTs	3.0
	439138	A1742605	Hs.193696	EST8	3.0
55	449547 455180	H93543 AW863503	Hs.117963	ESTs gb:MR3-SN0009-180400-110-c12 SN0009 Homo	3.0 3.0
	444228	AV648612	Hs.282396	ESTs	3.0
	423496	U91963	Hs.129700	tolloid-like 1	3.0
	401707 419276	BE165909	Hs.134682	Homo sapiens cDNA: FLJ23161 fis, clone L	3.0 3.0
60	441677	AW271702	Hs.93739	ESTs	3.0
	459587	AA031956	Hs.188980	gb:zk15e04.s1 Soares_pregnant_uterus_NbH .	3.0
	431311 426326	AA502552 BE165753	Hs.188980 Hs.250528	ESTs ESTs, Weakly similar to unnamed protein	3.0 3.0
	412685	BE092186		gb:IL2-BT0734-200400-075-H05 BT0734 Homo	3.0
65	414752	BE503505	Hs.248689	ESTs	3.0
	407539	X91103		gb:H.sapiens mRNA for Hr44 protein.	3.0 3.0
	412379	AW947581		gb:RCO-MT0004-140300-031-d08 MT0004 Homo	3.0
70	407937	AW297944	Hs.242811		3.0
70	456976 417066	AI681882	Hs.270428		3.0
	406007	AA329572	Hs.172004	tiin	3.0 3.0
	416940	N75620	Hs.43157	ESTs	3.0
75	433322	H50621	Hs.134156	ESTS	3.0
, ,	406088 416573	R10356	Hs.18865	ESTs, Weakly similar to AC007228 2 BC372	3.0 3.0
	423130	AW897586	Hs.21213	ESTs	3.0
	412721	AW183165	Hs.95600	ESTs	3.0
80	418375 422992	NM_003081 AF016833	Hs.84389 Hs.122765	Synaptosomal-associated protein, 25kD	3.0
	406506	W-010079	113.166700	maliase-glucoamylase (alpha-glucosidase)	3.0 3.0
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	3.0
	422650	D42055	Hs.1565	neural precursor cell expressed, develop	3.0



	400325	M85292	Hs.247924	Homo sepiens endogenous HIV-1 related se	
	401078	AIZZEEDE	14-150004	COT-	3.0
	445645 445704	Al336596 Al337228	Hs.156294 Hs.197083	ESTs ESTs	3.0 3.0
5	427072	H38046	14.157000	gb:yp58c10.r1 Soares fetal liver spieen	3.0
			• •	0.1	
	TABLE 33				
	Pkey: CAT numb		ue Eos probes e cluster numb	et identifier number	
10	Accession		ank accession		
		-			
	Pkey	CAT number			
	407615 408119	1005404_1 1040172_1		NW753082 AW054744 AW753107 AW753087 8055 Z44031 AW954559 R17434	
15	409519	113722_1	AA075368		
	409578	1140976_1		W419449 AW663595	
	409594	114249_1		A975618 AA076220	
	409695 409745	114876_1 115237_1		A296889 AA076945 AA077528 AA077497 	960912 AA921874 AA286833 AA150722 BE152353 AW188822 BE152450
20	409770	1154048_1		AW499553 AW502138 AW499537 AW502136	
	410008	116812_1		8E142525 BE142527	
	410049	1172307_1		AW939654 AW939655	
	410534 410754	1207247_1 1219733_1		AW753008 R13818 Z43519 801569 AW801568	
25	411290	1237738_1			3 BE092535 BE092199 411485 1247181_1AW848125 AW848124 AW848203 AW848695
			AW848633	AW848693 BE350771	
	41 1545 41 1836	1249138_1 1260619_1		AW850833 AW851100	
	412209	1283610_1		AW901875 AW866247 BE011294 BE504813 AW901450 AW901441	
30	412359	129085_1		AW837938 AA101955 AW837913 AW837935	
	412379	1292479_1		AW947546 AW947545 AW947544	
	412685 412872	1321663_1 1333898_1		BE092157 AW983859 BE006307 BE006311	
	413070	134815_1		AA133984 BE148613 BE063475 AA358219	
35	415610	1540554_1		2851 T75057	
	415713	154859_1		AA167225 AA491129	
	416462 416548	1595954_1 1600181_1	W92845 H	6608 N72413	
4.0	416913	163001_1			BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
40	417038	164390_1		192508 T89190	
	418053 419213	171810_1		AW817839 AW817836	
	419546	182860_1 185766_1		AW749138 AW749123 AW749130 AA235142 AA244272 H57440	•
45	420637	195241_1		AA278945 AA747691	·
45	422063	210852_1		BE156473 BE156474 BE156475 AA302839	
	422219 422504	213547_1 217160_1		AW978072 AA807550 AA306567 AW958321 N23583 R70050	
	423735	231498_1		AA661806 AA502431 AW974633 AA649496	
50	426384	266211_1	AI472078	A377209 AA865807	
50	427072 428637	274884_1 293660_1		69645 AA397968 H38047	
	430183	31412_2		AA878419 AA431342 AA431628 AA676833 AI311783 TRER95 W68032 RED64:	393 BE064394 BE157228 BE183282 AI936370 AA552514 T67280 AA039909
	431595	335512_1		BE142920 AI280311 AI205616 D61709	330 0 C 0 3 C 1 0 C C 0 C 1 0 C C C C C C C C C C C
55	432009	34025_1		BE007148 T52277	
23	437205 437938	43463_1 44573_2	AL110232		7 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875
			AI820501	N820532 W87891 T85904 U71456 T82391 BE	E328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794
			AI560251	AW874068 AL134043 AW235363 AA663345 A	AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898
60	•				762688 AA988777 AA488892 A1356394 AW103813 A1539642 AA642789 AA856975 AW505512 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874
•					633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388
			H84729 H	50052 T92487 AI022058 AA780419 AA551005	5 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839
	420000	167426 4		A300207 AW959581 T63226 F04005	
65	438966 438993	467436_1 467651_1		I AA834841 AA828650 AA834879 A1926361	
•••	440680	500121_1		AW836693 BE160824 AW606818 AW582699	9 AW836768
	442438	542469_1		Al916584 R61781 T77332 F07756 F08149 F	07647
	446345 446417	673545_1 676384_1		AW235762 AI651268	
70	447641	73043 1		BE256910 BE264952 R26042	
	448450	76399_1		T05205 AA481187	
	449034	794817_1		AW117770 AI858360	
	450625 452453	84032_1 918300_1		7 AA513951 AA010406 AI902518 AI902516	
75	453743	979613_1		AW836448 AW176802	
	453955	989877_1	AW57920	7 AW936883 AW008026 N88905	
	454392	115882_1		AA078319 R85057 AWB03024 H85811 AA07	78293
	454490 454690	1217172_1 1229106_1		8 AW797781 AW797780 9 AWR54719 AWR54718 RF145ARN AWR5469	92 BE145866 AW816154 AW854698 AW854654 AW813335 AW854699
80	454933	1245515_1		1 AW845993 AW845989	ESONCOLLY ECCELOLLY INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT IN INCOMMENT I
	455070	1252209_1	AW85467	5 AW854685 AW854716 AW854690 AW8546	15 AW854624 AW854623 AW854641 AW854632 AW854695 AW854661
	455180 455275	1258558_1 1272255_1		3 AW863362	
	733613	1214200_1	V4431 (8)	6 AW887923 AW886321	

..........



	455362	1284507_1	AW902635 AV	902574 BE011167 BE	011329 AW902808 AW902651		
	455711	1352369_1	BE069465 BE				
	456386	18426931					
5	456388	18428391					
3	456411	185688_1		244095 AA244183			
	459587 459595	94893_1 969956_1	AA031956 AL040421				
	403030	505500_1	742010121				
• •	TABLE 330	<b>:</b>					
10	Pkey:			sponding to an Eos pro			
	Ref:					31) numbers. "Dunham, et al." refers to the publication entitled "The DNA	
	Strand:			from which exons were	m, et al. (1999) <u>Nature</u> 402:489-49	ъ.	
	Nt_position			ositions of predicted en			
15							
	Pkey	Ref		Nt_position			
	401078	3687273		105052-105171			
	401157 401189	9438289 9690246		114133-114247,11456 90815-90929	r-114043		
20	401260	8076883		86008-86355			
	401352	9931258	Minus	26064-26208			
	401439	8246737		92993-94026			
	401707 401811	2951946	Plus	21972-22104 107002-107209			
25	401976	6730720 3095020	Plus Minus	17594-17709,21068-2	175		
	402045	7923943	Plus	5964-6128			
	402421	9796341	Minus	46609-46662,46758-46	811,86293-86346,89776-89829,9	0048-90101,102817-102924	
	402696	7328818	Minus	23600-23731			
30	402739 402921	9212192	Plus Minus	60456-61019		0067 60472	
50	403095	7981303 8954339	Phys	150025-150240,15156	5858,57124-57309,59633-59761,5 4-151690	3331-00153	
	403111	8980970	Plus	175012-175159			
	403144	9454549	Minus	166200-166628			
25	403170	9838134	Plus	40955-41356			
35	403345 403346	8569726 8569726	Plus Plus	77890-78069 92752-93015			
	403563	8101139	Plus	2800-3501			
	403622	8569879	Plus	1941-2388,2580-2761			
40	4037B2	8078608	Plus	41326-41633			
40	403797	8099896	Minus	123065-125008			
	403899 404021	7381715 8655966	Minus Ptus	9144-9350 192534-193489			
	404115	9621489	Plus	232707-232982			
	404200	6010176	Minus	7066-7210			
45	404347	9838195	Plus	74493-74829			
	404939 405257	6862697 7329310	Plus Plus	175318-175476 73121-73273			•
	405336	6094635	Ptus	33267-33563			
	405394	6624123	Minus	31900-32373			
50	405547	1054740	Plus	124361-124520,1249			
	405609	5757553	Minus			47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469	<b>}</b>
	405908	6758795	Plus	97969-98715	8169-58296,6021 <b>5-60332</b> ,61482-	01/2/	
	405943	6758796	Plus	20605-20812			
55	405953	7960374	Minus	65101-65574			
	405963	8247786	Plus	4056-4699			
	406007 406030	8247802 8312328	Minus Minus	13484-13829 96123-96547		•	
	406088	9123919		65772-66270			
60	406117	9142932		54304-54584			
	406242	7417725		36736-36951			
	406291 406411	5686274 9256407		9562-9867 7400-7527			
	406414	9256407		49593-49850			
65	406504	7711360		107068-107277			
	406506	7711374		6843-8077			
	406598	8248514	Plus	56373-56849			
70	TABLE 3	4A: ABOUT	197 GENES UP-R	EGULATED IN KIDNEY	CANCER		
						that are likely to be extracellular or cell-surface proteins. These were select	ed as for
		A and the p			ain that is indicative of extracellula	r localization (e.g. ig, fn3, egf, 7tm domains). Predicted protein domains an	a noted.
	Pkey:			set identifier number			
75	ExAcon; Unigene		Unigene number	on number, Genbank at	cession number		
	Unigene		Unigene gene title				
	PSDom:		Protein Structural				
	R1:		Ratio of tumor to r				
80	DL	ExAcon	Alata aurio	I helenno Title	DCDame'r	01	
50	Pkey 421471	U90545		UnigeneTitle sotute carrier	PSDomain TM,SS	R1 1007.4	
	452401	NM_00		turnor necrosis	TM,SS,XIInk,CUB	336.4	
	421727			kynurenine 3-mo	TM.SS,Monooxygenase	323.6	
					204		

394

	426471	M22440	Hs.170009	transforming gr	TM,SS,EGF	224.6
	441031	AI110684	Hs.7645	fibrinogen, B b	fibrinogen_C	174.0
	411642	NM_014932	Hs.71132	neuroligin 1	TM,SS,COesterase	172.4
5	452838	U65011	Hs.30743	preferentially	TM	161.4
)	425984	AW836277	Hs.165636	hypothetical pr	TM	151.0
	453165	\$74727	Hs.32042	aspartoacylase	TM	134.8
	452431	U88879	Hs.29499	toll-like recep	TM,SS,TIR.LRRCT	130.6
	423508	AW604297	Hs.129711	hepatitis A vir	TM,SS.ig	120.4
10	407975	X89426	Hs.41716	endothelial cel	SS,IGFBP	111.8
10	415076	NM_000857	Hs.77890	guanylate cycla	TM.guarrylate_cyc	97.0
	447046	AA326187	Hs.17170	G protein-coupi	TM,7Im_1	90.2
	423109 422544	M59305	Hs.123655	natriuretic pep	TM,SS,ANF_receptor	78.0
	429352	AB018259	Hs.118140	KIAA0716 gene p	TM	74.8
15	453392	AK001512	Hs.200097	hypothetical pr	TM	73.0
13		U23752	Hs.32964	SRY (sex determ	TM,HMG_box	72.2
	403345 430440	X52599	Hs.2561		TM,alpha-amylase	69.6
	408609	AA330431		nerve growth fa	TM,SS,NGF	69.0
	449101	AA205847	Hs.640 Hs.23016	calcitonin rece	TM,SS,7tm_2	57.4
20	423685	BE350494		G protein-coupl	TM,7tm_1	52.0
20	452891	N75582	Hs.49753 Hs.212875	Homo sapiens mR	TM, Myosin_tail	48.0
	408430	S79876	Hs.44926	ESTs, Weakly si	SS SUCCESSION IN A CONTRACT OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF	44.0
	419287	X91906	Hs.89872	dipeptidylpepti	TM,SS,DPPIV_N_term,Peptidase_S9	42.6
	428822	W28418	Hs.301148	chloride channe potassium volta	TM,CBS,vollage_CLC TM	40.6
25	434208	T92641	Hs.127648	hypothetical pr	TMSS	40.2
	400792	AA635062	Hs.50094	Homo sapiens mR		39.2
	444743	AA045648	Hs.11817	nudix (nucleosi	TM,BIR,CARD,zI-C3HC4 TM,muit	38.6
	406411	7 10 100 10	110.11017	HOUR (HOUSEAS)	TM, wa, FG-GAP	38.4
	423657	AL045128	Hs.1691	glucan (1,4-alp	TM,alpha-amylase	37.6 37.5
30	424871	NM_004525	Hs.153595	low density lip	TM,SS,EGF,IdI_recept_a,IdI_recept_b	37.5 32.8
	449625	NM_014253	Hs.23796	odz (odd Oz/ten	SH2,EGF	30.5
	423020	AA383092	Hs.1608	replication pro	TM	29.6
	422420	U03398	Hs.1524	turnor necrosis	TMITHE	29.6
	414245	BE148072	Hs.75850	WAS protein fam	TM,WH2	28.8
35	410247	AF181721	Hs.61345	RU2S	TM	27.4
	406414				TM, wra, FG-GAP	27.2
	435951	AF269162	Hs.41267	c21orf7 form A	TM	27.2
	419948	AB041035	Hs.93847	NADPH oxidase 4	TM,SS,Ferric_reduct	26.4
40	448595	AB014544	Hs.21572	KIAA0644 gene p	TM,SS,LRRCT,LRR	25.8
40	419569	AJ971651	Hs.91143	jagged 1 (Alagi	TM,SS,DSL,EGF	25.6
	433242	AB040938	Hs.113940	KIAA1505 protei	SS	25.6
	416778	M16505	Hs.79876	steroid suffata	TM,Sulfatase	23.0
	401352				TM	22.6
4.5	404200				SS	19.6
45	446591	H44186	Hs.15456	PDZ domain cont	TM,PDZ	19.2
	431806	AF186114	Hs.270737	turnor necrosis	TMSS	18.0
	423909	AJ223183	Hs.135194	niludolgonummi	TMLSS.ig	17.6
	446364	AB006624	Hs.14912	KIAA0286 protei	TM.	17.4
50	425695	NM_005401	Hs.159238	protein tyrosin	TM,Band_41,Y_phosphatase	17.0
20	410947	AK000305	Hs.67055	hypothetical pr	TM	16.8
	421002	AF116030	Hs.100932	transcription f	TM,KRAB,zf-C2H2	16.5
	421659	NM_014459	Hs.106511	protocadherin 1	TM,SS,cadherin	16.0
	458679	AW975460	Hs.143563	ESTs	SS	14.4
55	406598	EE363333	11- 404660	Annua	SS	13.6
55	428508 423321	BE252383	Hs.184668	SBBI31 protein	TMPX	13.2
	423321	AB013885	Hs.126926	beta-ureidoprop	TM,SS,CN_hydrolase	12.5
	428227	NM_001147 AA321649	Hs.115181 Hs.2248	angiopoletin 2	fibrinogen_C	12.2
	414923	AW445008	Hs.77637	small inducible homeo box A4	IL8	12.0
60	433231	AB040926	Hs.143552	KIAA1493 protei	TM,homeobox	11.9
- 0	443672	AA323362	Hs.9667	butyrobetaine (	SS TM	11.6
	405609	14052005	113.3007	outproceasing (		11.4
	418912	NM_000685	Hs.89472	angiotensin rec	TM,Myosin_tail,myosin_head TM,7tm_1	11.4
	449802	AW901804	Hs.23984	hypothetical pr	TM	11.4
65	404347		10240304	пуровноса р	SS	11.2
	429945	NM_006729	Hs.226483	diaphanous (Oro	TM.FH2	10.8
	435085	AW130284	Hs.192752	ESTs, Moderatel	TM	10.6
	404115			COTO, MODELLA	SS	10.6
	420757	X78592	Hs.99915	androgen recept	TM.Androgen_recep,hormone_rec.zf-C4	10.2 10.2
70	448298	AF187813	Hs.14637	kidney- and fiv	TM.Acetyltransi	10.1
	433703	AA210863	Hs.3532	nemo-like kinas	TM.pkinase	9.2
	417404	NM_007350	Hs.82101	pleckstrin homo	TM	9.2
	451621	AI879148	Hs.26770	fatty acid bind	TM,SS,lipocatin	9.2
~~	402045				TM,SS	9.0
75	403095				SS.PAX.homeobox	8.B
	401439				TM	8.6
	407721	Y12735	Hs.38018	dual-specificit	7M.pkinase	8.4
	402921				TM	8.4
00	419503	AA243642	Hs.137422	ESTs	TM	8.4
80	452259	AA317439	Hs.28707	signal sequence	TM	8.4
	402696			•	TM	8.3
	450001	NM_001044	Hs.406	solute carrier	TM,SS,SNF	8.1
	433190	M26901	Hs.3210	renin	SS,æp	7.8
					•	••••

	449444	AW818436	Hs.23590	solute carrier	TM,MCT	7.7
	444042 452883	NM_004915	Hs.10237	ATP-binding cas	TM,ABC_tran	7.7
	425151	X80031 AA351814	Hs.150318 Hs.298678	EST's	TM,C4,Collagen	7.4
5	455068	AI807B94	Hs.27910	ESTs	TM	7.2
•	406504	70001034	115.27510	centrosomal pro	TM,SS TM	7.2
	410274	AA381807	Hs.61762	hypoxia-inducib	SS	7.2 7.0
	423349	AF010258	Hs.127428	homeo box A9	TM_homeobox	6.8
	408771	AW732573	Hs.47584	polassium volta	TM.K_tetra.ion_trans	6.8
10	445575	Z25368	Hs.172004	titin	TM	6.6
	415138	C18356	Hs.78045	tissue factor p	Kunitz_BPTI,G-gamma	6.3
	443595	AF169312	Hs.9613	PPAR(gamma) ang	TM,SS,fibrinogen_C	6.3
	404939	******			TM	6.3
15	436209 403111	AW850417	Hs.254020	ESTs, Moderatel	TMLSS	6.2
13	405394				TM	6.2
	454392	BE260893		gb:601150677F1	TM TM.SS	6.0
	415910	U20350	Hs.78913	chemokine (C-X3	TM,7m_1	6.0
	402421	01000	14.03.3	ereneere (ove	TM	5.9 5.8
20	425717	X07282	Hs.171495	retinoic acid r	TM.hormone_rec,zf-C4	5.7
	427920	Z11502	Hs.181107	annexin A13	TM annexin	5.6
	407864	AF069291	Hs.40539	chromosome 8 op	TMFHABRCT	5.5
	441006	AW605267	Hs.7627	CGI-60 protein	TM	5.4
25	422232	D43945	Hs.113274	transcription f	TMHLH	5.4
23	425782	U66468	Hs.159525	cell growth reg	SS	5.3
	450236 413841	AW162998	Hs.24684	KIAA1376 protei	TM,SS	5.3
	436032	M34276 AA150797	Hs.75576	plasminogen	SS,trypsin,kringte,PAN	5.3
	447081	Y13896	Hs.109276 Hs.17287	latexin protein	TM	5.1
30	421126	M74587	Hs.102122	potassium inwar insulin-like gr	TM,IRK	5.1
	426651	AU076646	Hs.171683	nuclear recepto	SS,thyroglobulin_1,IGFBP TM,zf-C4,harmone_rec	5.1 5.0
	432328	AI572739	Hs.195471	6-phosphotructo	TM,6PF2K,PGAM	5.0
	409506	NM_006153	Hs.54589	NCK adaptor pro	TM,SH2,SH3	5.0
26	410361	BE391804	Hs.62661	guanytate bindi	TM,SS,GBP	4.8
35	453891	AB037751	Hs.36353	Homo sepiens mR	TM	4.8
	447269	NM_004861	Hs.17958	cerebroside (3*	TM,SS	4.8
	422357	AF016272	Hs.115418	cadherin 16, KS	TM,cadherin ·	4.B
	417355	D13168	Hs.82002	endothelin rece	TM,SS,7tm_1,zf-C3HC4	4.7
40	402739 443486	ARIA 002420	14-0450	-t •	SS	4.6
70	408380	NM_003428 AF123050	Hs.9450 Hs.44532	zinc finger pro	TM,KRAB,zi-C2H2	4.6
	414812	X72755	Hs.77367	diubiquitin monokine induce	TM.ubiquitin,7tm_3.ANF_receptor,sushi,7tm_1	4.6
	424063	NM_002019	Hs.138671	fins-related tyr	SS,IL8 TM,SS,pkinase,ig	4.4
	413384	NM_000401	Hs.75334	exostoses (mult	TM	4.4
45	457030	AJ301740	Hs.173381	dihydropyrimidi	TM,SS,Dihydroorotase	4.4
	410407	X56839	Hs.63287	carbonic anhydr	TM,SS,carb_anhydrase	4.3
	401157				TM,citrate_synt	4.3
	432004	BE018302	Hs.2894	placental growt	SS,POGF	4.3
60	424704	Al263293	Hs.152096	cytochrome P450	SS,p450	4.2
50	407065	Y10141		gb:H.sapiens DA	TM,SS,SNF	4.2
	411213	AA676939	Hs.69285	neuropilin 1	TM,CUB,F5_F8_type_C,MAM	4.2
	430806 414596	S69377	Hs.247978	T-cell acute ly	TM.HLH	4.1
	408830	AF002020 AK001709	Hs.76918 Hs.48403	Niemann-Pick di	TM,SS,Patched	4.1
55	416655	AW968813	H\$.79428	hypothetical pr BCL2/adenovirus	TM,UPF0013 TM	4.1
	412494	AL133900	Hs.792	ADP-ribosylatio	TM,arf,zf-B_box,zf-C3HC4	4.1 4.0
	453195	BE241876	Hs.32352	hypothetical pr	TM	4.0
	428816	AA004986	Hs.193852	ATP-binding cas	TM_ABC_membrane_ABC_tran,COX15-CtaA	3.9
<b>CO</b>	401189			•	TM,SET,PHD,HMG_box	3.8
60	451988	AF263928	Hs.27410	papillomavirus	TM	3.8
	421013	M62397	Hs.1345	mutated in colo	TM	3.7
	420041	AB005142	Hs.94592	klotha	TM, SS, Glyco_hydro_1	3.7
	432579	AF043244	Hs.278439	nucleotar prote	TM	3.6
65	453496 446636	AA442103 AC002563	Hs.33064 Hs.15767	solute carrier	TM.SS.sugar_tr	3.6
0.0	426274	D38122		citron (rho-int	TM,CNH,DAG_PE-bind,PH,pkinase,pkinase_C	3.6
	452355	N54926	Hs.2007 Hs.29202	tumor necrosis G protein-coupt	TM,TNF TM,7tm_1	3.6
	453775	NM_002916	Hs.35120	replication (ac	TM,SS.AAA	3.5
	426559	AB001914	Hs.170414	paired basic am	TM,Peptidase_S8.P	3.4 3.4
70	420737	£08096	Hs.99899	turnor necrosis	TM,TNF	3.4
	448733	NM_005629	Hs.187958		TM.SNF.ABC_tran.isodh.pldnase,Ribosomal_L18ae	3.4
	413719	BE439580	Hs.75498	small inducible	SS,IL8	3.4
	427914	AA417350	Hs.20575	ESTs	TM,GAS2	3.4
75	412642	BE244598	Hs.809	hepatocyte grow	loringle,PAN,trypsin	3.4
75	421893	NM_001078	Hs.109225	vascular cell a	TM,SS,ig	3.3
	417924	AU077231	Hs.82932	cyclin D1 (PRAD	TM.cyclin	3.3
	405257 450396	AU077002	Un 24050	-and determined O	TM	3.3
	416892	L24498	Hs.24950	regulator of G-	TM,RGS	3.3
80	425236	AW067800	Hs.80409 Hs.155223	growth arrest a stanniocalcin 2	TM,Ribosomal_L7Ae	3.3
	430812	L10405	Hs.247992		SS TM,SS	3.3
	431842	NM_005764	Hs.271473		TMSS	3.2 3.2
	424897	D63216	Hs.153684		TMFANTR	3.2
						w. E

	414821	M63835	Hs.77424	Fc fragment of	TM,SS,ig	3.1
	418030	BE207573	Hs.83321	neuromedin B	<b>\$\$</b>	3.1
	421633	AF121860	Hs.106260	sorting nexin 1	TMPX	3.1
_	441285	NM_002374	Hs.167	microtubule-ass	SS, tubulin-binding	3.1
5	418526	BE019020	Hs.85838	solute carrier	TMMCT	3.1
	401260				TMSS	31
	450705	U90304	Hs.25351	iroquois-class	TM.homeobox	3.1
	424415	NM_001975	Hs.146580	enclase 2, (gam	TM,SS,enolase	3.0
	403346	NW_001313	113.146500	encese z, (gen		
10	432757	AP443013	U. 270010	COCCOCC analysis	TM,atpha-amylase	3.0
10		AF113013	Hs.278919	PRO0806 protein	TM	3.0
	434398	AA121098	Hs.3838	serum-inducible	TM.pkinase,POLO_box	3.0
	424539	L02911	Hs.150402	activin A recep	TM_Activin_recp.pkinase	3.0
	406117				SS	3.0
16	408119	W26213		gb:22d10 Human	TM,SS	3.0
15	431984	AL080239	Hs.272284	Human DNA seque	TM	3.0
	403782				TM	3.0
	447922	Z92910	Hs.20019	hemochromatosis	TM,SS,ig,MHC_I,histone,SPRY,zf-B_box,zf-C3HC4	3.0
	428857	AF008192	Hs.194283	putative GR6 pr	SS	3.0
	432596	AJ224741	Hs.278461	matrilin 3	SS	3.0
20	453202	AW085781	Hs.26270	Homo sapiens cD	TM	3.0
~~	405547	A11005701	110.20270	right septens co	TM,SS,ABC_membrane,ABC_tran	3.0
	423496	U91963	U- 420700	Antiald Die 4		
		031303	Hs.129700	tolloid-like 1	TM,SS,EGF,CUB,Astacin	3.0
	401707				SS	3.0
25	403144				TM,ion_trans,K_tetra	3.0
25	418375	NM_003081	Hs.84389	synaptosomal-as	TM,NA	3.0
	422992	AF016833	Hs.122785	maitase-glucoam	TM,Glyco_hydro_31,trefoil	3.0
	406506				TM	3.0
	413472	BE242870	Hs.75379	sotute carrier	TMLSOF	3.0
30	TABLE 34	B:				
	Pkey:		ue Fos ambes	set identifier number		
	CAT numt		e duster numb			
	Accession		bank accessio		,	
	Accession	. 901	DOWN GOCCOSSIO	ii iidiiida		
35	Pkey	CAT number	Accession.			
55						
•	408119	1040172_1		)8055 Z44031 AW954559 R		
	454392	115882_1	BE560883	AA078319 R85057 AW8030	JZ4 H85811 AAQ78293	
		_				
40	TABLE 34					
40	Pkey:	Uniq		rresponding to an Eos prob		
40		Uniq Seq	uence source.	The 7 digit numbers in this	column are Genbank Identifier (GI) numbers. "Dunham,	, et al." refers to the publication entitled "The DNA
40	Pkey:	Uniq Seq	uence source.	The 7 digit numbers in this		, et al." refers to the publication entitled "The DNA
40	Pkey:	Uniq Seq: seq:	uence source. vence of huma	The 7 digit numbers in this on chromosome 22" Dunham	column are Genbank Identifier (GI) numbers. "Ounham, n, et al. (1999) <u>Natura</u> 402:489-495.	, et al." refers to the publication entitled "The DNA
	Pkey: Ref:	Uniq Seq: sequ Indix	uence source. vence of huma cates DNA stra	The 7 digit numbers in this an chromosome 22" Dunham and from which exons were	: column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Natura</u> 402:489-495. predicted.	, et al." refers to the publication entitled "The DNA
40 45	Pkey: Ref: Strand:	Uniq Seq: sequ Indix	uence source. vence of huma cates DNA stra	The 7 digit numbers in this on chromosome 22" Dunham	: column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Natura</u> 402:489-495. predicted.	, et al." refers to the publication entitled "The DNA
	Pikey: Ref: Strand: Nt_positio	Uniq Seq sequ Indix on: tndix	uence source. uence of huma cates DNA stra cates nucleotic	The 7 digit numbers in this an chromosome 22" Dunhan and from which exons were de positions of predicted exo	: column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Natura</u> 402:489-495. predicted.	, et al." refers to the publication entitled "The DNA
	Pkey: Ref: Strand: Nt_position	Uniq Seq: sequ Indix on: Indix Ref	uence source. uence of huma cates DNA stra cates nucleotic Strand	The 7 digit numbers in this an chromosome 22" Dunhard and from which exons were to positions of predicted exo Nt_position	: column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Natura</u> 402:489-495. predicted. ons.	, et al." refers to the publication entitled "The DNA
	Pkey: Ref: Strand: Nt_position Pkey 401157	Uniq Seq: seq: Indix on: tndix Ref 9438289	uence source. uence of hume cates DNA stra cates nucleotic Strand Minus	The 7 digit numbers in this in chromosome 22" Dunham and from which exons were to positions of predicted exo Nt_position 114133-114247,114567-	: column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Natura</u> 402:489-495. predicted. ons.	, et al." refers to the publication entitled "The DNA
	Pkey: Ref: Strand: Nt_position Pkey 401157 401189	Uniq Seq: seq: India on: India Raff 9438289 9690246	uence source. uence of hume cates DNA stra- cates nucleotic Strand Minus Minus	The 7 digit numbers in this an chromosome 22" Dunhan and from which exons were fe positions of predicted exo Nt_position 114133-114247,114567- 90815-90929	: column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Natura</u> 402:489-495. predicted. ons.	, et al." refers to the publication entitled "The DNA
45	Pkey: Ref: Strand: Nt_position Pkey 401157 401189 401260	Uniq Seq: seq: India on: India Ref 9438289 9690246 8076883	uence source. uence of hume cates DNA stra cates nucleotic Strand Minus Minus Minus	The 7 digit numbers in this an chromosome 22" Dunhar and from which exons were to positions of predicted exc Nt_position 114133-114247,114567-90815-90929 85008-86355	: column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Natura</u> 402:489-495. predicted. ons.	, et al." refers to the publication entitled "The DNA
	Pkey: Ref: Strand: Nt_positio Pkey 401157 401189 401260 401352	Uniq Seq: seq: Indix on: Indix Ref 9438289 9690246 8076883 9931258	uence source. uence of huma cates ONA str cates nucleotic Strand Minus Minus Minus Minus Minus	The 7 digit numbers in this in chromosome 22" Dunhain and from which exons were to positions of predicted exo Nt_position 114133-114247,114567- 90815-90929 85008-86355 25064-26208	: column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Natura</u> 402:489-495. predicted. ons.	, et al." refers to the publication entitled "The DNA
45	Pkey: Ref: Strand: Nt_position Pkey 401157 401189 401250 401352 401439	Uniq Seq: seq: Indix on: Indix Ref 9438289 9690246 8076883 9931258 8246737	uence source. uence of huma cates DNA stra cates nucleotic  Strand  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus	The 7 digit numbers in this in chromosome 27 Dunhari and from which exons were fe positions of predicted exo Nt_position 114133-114247,114567- 90815-90929 65008-66355 26064-26208 92993-94026	: column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Natura</u> 402:489-495. predicted. ons.	, et al." refers to the publication entitled "The DNA
45	Pkey: Ref: Strand: NL position Pkey 401157 401189 401250 401352 401439 401707	Uniq Seq sequ India nr: India Ref 9438289 9690246 8075883 9931258 8246737 2951946	uence source, uence of hums cates ONA streates nucleotic Strand Minus Minus Minus Minus Minus Plus Ptus	The 7 digit numbers in this an chromosome 22" Dunhan and from which exons were to positions of predicted exc Nt_position 114133-114247,114567-90815-90929 85008-86355 26064-26208 92993-94026 21972-22104	: column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Natura</u> 402:489-495. predicted. ons.	, et al." refers to the publication entitled "The DNA
45	Pkey: Ref: Strand: NL position Pkey 401157 401189 401250 401352 401439 401707 402045	Uniq Seq: seq: India India Pd38289 9690246 8075883 9931258 8246737 2951946 7923943	uence source. uence of hume cates DNA stre cates nucleotic Strand Minus Minus Minus Minus Plus Plus Plus Plus	The 7 digit numbers in this in chromosome 22 Dunham and from which exons were to positions of predicted exo Nt_position 114133-114247,114567-90815-90929-86008-86355-26064-26208-92933-94026-21972-22104-5964-6128	s column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Natura</u> 402:489-495. predicted. ons.	
45 50	Pkey: Ref: Strand: Ni_position Pkey 401157 401189 401250 401352 401439 401707 402045 402421	Uniq Seq: seq: India India Ref 9438289 9690246 8075883 9931258 8246737 2951946 7923943 9796341	uence source. uence of hume cates DNA stre cates nucleotic Strand Minus Minus Minus Minus Plus Plus Plus Plus Minus Minus	The 7 digit numbers in this in chromosome 27 Dunhari and from which exons were go positions of predicted excluding the position of predicted excluding the position of 114133-114247,114567-90815-90929 86008-86355 26064-26208 92993-94026 21972-22104 5964-6128 46609-46662,46758-466	: column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Natura</u> 402:489-495. predicted. ons.	
45	Pkey: Ref: Strand: NL position Pkey 401157 401189 401260 401352 401439 401707 402045 402421 402696	Uniq Sequesequesequesequesequesequesequeseque	uence source, uence of hume cates DNA sire cates nucleotic Strand Minus Minus Minus Plus Plus Plus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Min	The 7 digit numbers in this an chromosome 22" Dunhan and from which exons were to positions of predicted exc Nt_position 114133-114247,114567-90815-90929 85008-86355 26064-26208 92993-94026 21972-22104 5964-6128 45609-46662,46758-465 23600-23731	s column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Natura</u> 402:489-495. predicted. ons.	
45 50	Pkey: Ref: Strand: Nt_position Pkey 401157 401189 401250 401352 401439 401707 402045 402421 40269 402739	Uniq Sequ India on: India 9438289 9690246 8076883 9931258 8246737 2951946 7923943 9796341 7328818 9212192	uence source, uence of hume zates DNA stra cates nucleotic Strand Minus Minus Minus Minus Plus Plus Plus Minus Minus Plus Minus Plus Minus Plus Minus Plus Minus Minus Plus Plus	The 7 digit numbers in this in chromosome 27 Dunhari and from which exons were go positions of predicted excluding the position of predicted excluding the position of 114133-114247,114567-90815-90929 86008-86355 26064-26208 92993-94026 21972-22104 5964-6128 46609-46662,46758-466	s column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Natura</u> 402:489-495. predicted. ons.	
45 50	Pikey: Ref: Strand: NL_position Pikey 401157 401189 401260 401352 401439 401707 402045 402421 40269 402739 402921	Uniq Sequent sequent indix indix 9438289 9690245 8076883 9931258 8246737 2951945 7923943 9796341 7328818 9212192 7981303	uence source. uence of hume zates DNA stra zates nucleotic Strand Minus Minus Minus Minus Plus Plus Plus Plus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus	The 7 digit numbers in this in chromosome 227 Dunham and from which exons were to positions of predicted exo Nt_positions of predicted exo Nt_positions of predicted exo Nt_position 114133-114247,114567-90815-90929 65008-86355 26064-26208 92993-94025 21972-22104 5964-6128 46609-46662,46758-464 23600-23731 60458-61019	s column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Natura</u> 402:489-495. predicted. ons.	
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Jence of hums  Jenses nucleotic  Strand  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Plus  Minus  Plus  Minus  Plus  Minus  Plus  Plus  Minus  Plus  Plus  Plus  Plus  Plus  Plus  Plus  Plus  Plus  Plus  Plus  Plus  Plus  Plus  Plus  Plus  Plus  Plus  Plus  Plus  Minus  Plus  Plus  Minus  Plus  Plus  Minus  Plus  Minus  Plus  Minus  Plus  Minus  Plus  Minus  Plus  Minus  Plus  Minus  Plus  Minus  Plus  Minus  Plus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus  Minus	The 7 digit numbers in this and thromosome 27 Dunham and from which exons were and from which exons were for positions of predicted exo Nt_positions of pred	is column are Genbank Identifier (GI) numbers. "Dunham, et al. (1999) Natura 402:489-495. predicted. ons114645	72924
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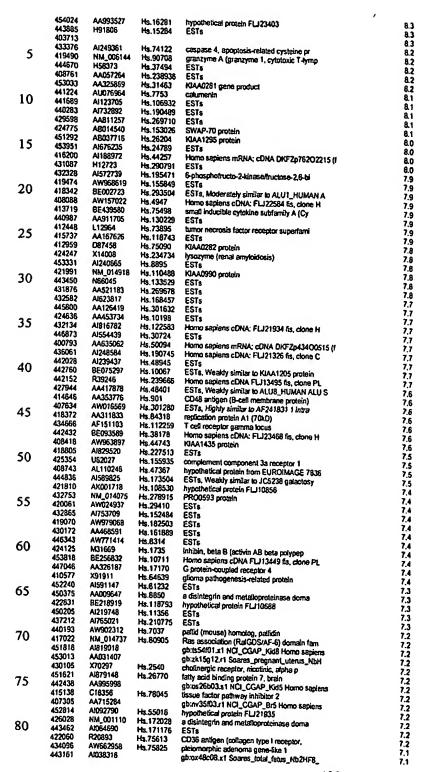
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TABLE 35A: ABOUT 532 GENES UP-REGULATED IN KIDNEY CANCER
Table 35A fasts about 532 genes up-regulated in kidney cancer compared to normal kidney. These were selected as for Table 33A except using an "average" of the 70th pecentile for both the numerator and the denominator and using non-matignant kidney specimens in determining the denominator value.

	Pkay:	Linion	e Eor ambara	t Identifier number	
	ExAcon:	Exem	Plar Accession	number, Genbank accession number	
	Unigenel D:	Unige	ne number		
5	Unigene Ti R1:		ne gene title	- d Carre	
•		Neur	of tumor to no	ma ussua	
	Pkey	ExAcon	UnigenelD	UnigeneTitle	RI
	424704 426559	AI263293 AB001914	Hs.152096 Hs.170414	cytochrome P450, subfamily IU (arachido	40.9
10	458079	AI796870	Hs.54277	paired basic amino acid cleaving system ESTs	35.6 34.6
	433447	U29195	Hs.3281	neuronal pentraxin ()	32.0
	439979 446921	AW600291 AB012113	Hs.6823 Hs.16530	hypothetical protein FLJ 10430	29.3
	435359	T60843	Hs.189679	smaß inducible cytoltine subfamily A (Cy ESTs	25.9 25.4
15	450152	AI138635	Hs.22968	ESTs	25.2
	452401 440304	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	24.8
	414821	BE159984 M63835	Hs.125395 Hs.77424	ESTs Fc fragment of IgG, high affinity Ia, re	24.5 23.4
20	421155	H87879	Hs.102267	lysyl oxidase	22.4
20	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	22.2
	414812 426471	X72755 M22440	Hs.77367 Hs.170009	monokine induced by gamma interferon transforming growth factor, alpha	22.1
	427897	NM_017413	Hs.181060	apelin; peptide ligand for APJ receptor	21,3 21,3
25	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	20.7
23	436961 447499	AW375974 AW262580	Hs.156704 Hs.147674	ESTS	20.5
	438817	AI023799	Hs.163242	KIAA1621 protein ESTs	20.4 20.4
	430630	AW269920	Hs.2621	cystatin A (stefin A)	19.8
30	428227 424086	AA321649 Al351010	Hs.2248	small inducible cytokine subfamily 8 (Cy	19.5
50	425289	AW139342	Hs.102267 Hs.155530	lysyl oxidase interferon, gamma-inducible protein 16	18.7 18.7
	438476	AA326108	Hs.53531	ESTs, Weakly similar to enhancer-of-spli	18.7
	415286	AW249540	Hs.72548	ESTs	18.2
35	428157 456804	A1738719 A1421645	Hs.298668 Hs.139851	ESTs caveolin 2	18.1 17.8
	429490	AJ971131	Hs.293684	ESTs, Weakly similar to alternatively sp	17.5
	429732 433757	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	17.1
	400419	A1949974 AF084545	Hs.152670 Hs.81800	ESTs chondroitin sulfate proteoglycan 2 (vers	16.B 16.4
40	428046	AW812795	Hs.155381	ESTs, Moderately similar to 138022 hypot	16.3
	411642	NM_014932	Hs.71132	neuroligin 1	16.2
	444381 435767	BE387335 H73505	Hs.283713 Hs.117874	ESTs, Weakly similar to CA54_HUMAN COLLA ESTs	18.0 15.7
45	427581	NM_014788	Hs.179703	KIAA0129 gene product	15.6
45	448019	AW947164	Hs.195641	ESTs	15.6
	406671 447835	AA129547 AW591623	Hs.285754 Hs.164129	met proto-oncogene (hepatocyte growth fa ESTs	15.5 15.4
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	14.8
50	417308	H60720	Hs.81892	KIAA0101 gene product	14.8
50	432731 421566	R31178 NM_000399	Hs.287820 Hs.1395	fibronectin 1 early growth response 2 (Krox-20 (Drosop	14.7
	419235	AW470411	Hs.288433	neurotrimin	14.6 14.6
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	14.4
55	421485 422603	AA243499 BE242587	Hs.104800 Hs.118651	hypothetical protein FLJ10134 hematopoletically expressed homeobox	14.4 14.4
	418110	R43523	Hs.217754	Homo sapiens cDNA: FLJ22202 fis, clone H	14.2
	425984 432606	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	14.2
	436772	NM_002104 AW975688	Hs.3066 Hs.250867	granzyme K (serine protease, granzyme 3; zona peliucida glycoprotein 3A (sperm re	14.1 14.0
60	444989	AI203334	Hs.160628	ESTs	13.9
	426890 437330	AA393167 AL353944	Hs.41294	ESTs	13.8
	458809	AW972512	Hs.50115 Hs.20985	Homo sepiens mRNA; cDNA DKFZp761J1112 (f sin3-associated polypeptide, 30kD	13.8 13.7
	446627	AI973016	Hs.15725	hypothetical protein SBB148	13.6
65	452960 417280	AK001335	Hs.31137	Homo sapiens cDNA: FLJ22681 fis, clone H	13.3
	422173	AW173116 8E385828	Hs.262206 Hs.250619	ESTs phorbolin-like protein MDS019	13.1 13.0
	420552	AK000492	Hs.98806	hypothetical protein	13.0
70	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	12.6
, 0	427871 446152	AW992405 AJ292038	Hs.59622 Hs.150028	ESTs, Weakly similar to unknown (H.sapie ESTs	12.6 12.5
	426560	AA381661	Hs.119878	ESTs	12.4
	419034	NM_002110	Hs.89555	hemopoletic cell kinase	12.3
75	456508 452281	AA502764 T93500	Hs.123469 Hs.28792	ESTs, Weakly similar to AF208855 1 BM-01 Homo sapiens cDNA FLJ11041 fis, clone PL	12.3 12.3
	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	12.3
	426075	AW513691	Hs.270149	ESTs	12.2
	434398 450506	AA121098 NM_004460	Hs.3838 Hs.418	serum-inducible kinase fibroblast activation protein, alpha	12.2
80	425782	U56468	Hs.159525	cell growth regulatory with EF-hand doma	12.1 12.0
	426108	AA622037 RB2342	Hs.166468	programmed cell death 5	11.9
	416000 450236	AW162998	Hs.79856 Hs.24684	ESTs KIAA1376 protein	11.8
					11.7

	449679	AI823951	Hs.296668	Homo sapiens cDNA FLJ11846 fis, clone HE	11.6
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	11.4
	442227	AW771958	Hs.175437	EST\$	11.4
5	414004 447056	AA737033	Hs.7155	ESTs. Wealdy similar to 2115357A TYXG pr	11.4
3	444863	N67879 AW384082	Hs.157695 Hs.301323	ESTs · ESTs	11.3 11.3
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	11.2
	426780	BE242284	Hs.172199	adenylate cyclase 7	11.1
10	453160 449539	AI263307	Hs.146228	ESTs	11.1
10	415323	W80363 BE269352	Hs.58446 Hs.949	ESTs neutrophil cytosolic factor 2 (65kD, chr	11.1 11.0
	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	11.0
	408380	AF123050	Hs.44532	diubiquilin	11.0
15	448410 451277	AK000227 AK001123	Hs.21126 Hs.26176	hypothetical protein FLJ20220	11.0
13	453165	S74727	Hs.32042	hypothetical protein FLJ 10261 espartoacytase (aminoacytase 2, Canavan	10.8 10.8
	435380	AA579001	Hs.192221	ESTs	10.7
	447183	AI554733	Hs.173182	ESTs	10.7
20	438330 441392	AW450572	Hs.257316 Hs.222119	ESTS World similar to KICO HIMAN VERAT	10.6
20	418036	AW451831 237976	Hs.83337	ESTs, Weakly similar to K1CQ_HUMAN KERAT latent transforming growth factor beta b	10.5 10.5
	452862	AW378065	Hs.8687	ESTs	10.4
	431512	BE270734	Hs.2795	lactate dehydrogenase A	10.3
25	421478 413879	AI683243 AA132961	Hs.97258 Hs.212533	ESTS	10.3
	411800	N39342	Hs.5184	Homo sapiens cDNA: FLJ22572 fis, clone H TH1 drosophile homolog	10.3 10.3
	433862	D86960	Hs.3610	KIAA0205 gene product	10.3
	440594	AW445167	Hs.126036	ESTs	10.2
30	414504 431211	AW069181 M86849	Hs.293523 Hs.5566	ESTs, Weakly similar to transformation-r gap junction protein, beta 2, 26kD (conn	10.2
20	437682	AA476652	Hs.94952	Homo sapiens cDNA: FLJ23371 fls, clone H	10.2 10.1
	430097	AI523245	Hs.127638	ESTs	10.1
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	10.0
35	434927 424113	H46812 Al743880	Hs.293815 Hs.12876	Homo sapiens HSPC285 mRNA, partial cds ESTs	9.9 9.9
-	439981	Al348408	Hs.124675	ESTs, Wealthy similar to unnamed protein	9.9
	411937	AW876626		gb:RC3-PT0028-120200-013-d08 PT0028 Homo	9.9
	439653	AW021103	Hs.6631	hypothetical protein FLJ20373	9.9
40	428862 424623	NM_000346 AW963062	Hs.2316 Hs.165809	SRY (sex-determining region Y)-box 9 (ca ESTs	9.8 9.8
	410762	AF226053	Hs.66170	HSKM-8 protein	9.8
	433285	AW975944	Hs.237396	ESTs	9.7
	413795	AL040178	Hs.142003	ESTs	9.6
45	434392 435542	AW983709 AA687376	Hs.268051 Hs.269533	ESTs ESTs	9.6 9.6
	430687	N66801	Hs.260287	ESTs, Wealdy similar to ALU7_HUMAN ALU S	9.5
	410339	AI916499	Hs.298258	ESTs	9.5
	452431 405121	U88879 AB028989	Hs.29499 Hs.88500	toll-like receptor 3	9.5
50	408134	AK000184	Hs.42945	milogen-activated protein kinase 8 inter acid sphingomyelinase-like phosphodieste	9.5 9.4
	438966	AW979074		gb:EST391184 MAGE resequences, MAGP Homo	9.4
	449825	NM_014253	Hs.23796	odz (odd Oz/ten-m, Drosophila) homolog 1	9.4
	441024 445900	AW081530 AF070526	Hs.137088 Hs.13429	ESTs Homo sapiens clone 24787 mRNA sequence	9.3
55	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	9.2 9.2
	440074	AA863045	Hs.199057	ESTs, Wealdy similar to T00050 hypothesi	9.2
	421659	NM_014459		protocadherin 17	9.2
	434542 427283	AA769310 AL119796	Hs.61260 Hs.174185	hypothetical protein FLJ13164 ectonucleotide pyrophosphatase/phosphodi	9.1 9.1
60	428820	AA436187	Hs.172631	integrin, alpha M (complement component	9.1
	419441	AW023731	Hs.274368	Homo sapiens mRNA; cDNA DKFZp586I1524 (I	9.0
	407856 431941	AA045281 AK000106	Hs.266175 Hs.272227	phosphoprotein associated with GEMs	9.0
	446460	AW013999	Hs.150164	Homo sepiens cDNA FLJ20099 fis, clone CO ESTs	9.0 8.9
65	452598	AI831594	Hs.68647	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.9
	407975	X89426	Hs.41716	endothetial cell-specific molecule 1 (NO	8.9
	437259 420235	AI377755 AA256756	Hs.120695 Hs.31178	ESTs ESTs	8.7
	436959	AL133076	Hs.5354	hypothetical protein FLJ12716	8.7 8.7
70	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	8.6
	435894	A1076667	Hs.188011	ESTs	8.6
	418693 425770	AJ750878 NM_014363	Hs.87409	thrombospondin 1	8.6
	456249	AI206144	Hs.159492 Hs.82508	spastic ataxia of Charlevoix-Saguenay (s HRIHFB2206 protein	8.6 8.6
75	437672	AW748265	Hs.5741	flavohemoprotein b5-b5R	8.6
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	8.5
	417225 435266	AA815048 AK001942	Hs.24078	Homo sapiens cDNA FLJ12649 fis, clone NT	8.5
	447974	R76886	Hs.4863	Homo saplens cDNA FLJ11080 fis, clone PL gb:yi64b03.s1 Soares placenta Nb2HP Homo	8.4 8.4
80	447850	AB018298	Hs.19822	SEC24 (S. cerevisiae) related gene famil	8.4
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	8.3
	435717 445784	AF227905 AI253155	Hs.105794		8.3
	440104	الرا الحاد	Hs.146065	ESTS	8.3





	458725	AW970192	Hs.171942	ras responsive element binding protein 1	7.1
	426423	NM_012446	Hs.169833	single-stranded-DNA-binding protein	7.1
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	7.1
_	435664	AI032087	Hs.269819	ESTs	7.0
5	431708	AI698136	Hs.108873	ESTs	7.0
	426501	AW043782	Hs.293616	ESTs	7.0
	453548	AL079983	Hs.75442	albumin	
	426595	AW971980	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	7.0
	412490	AW803564	Hs.288850		7.0
10	431556	AF016028	Hs.260039	Homo sapiens cDNA: FLJ22528 fis, clone H	7.0
	420018	U56387	Hs.94376	sarcospan (Kras oncogene-associated gene	6.9
	418986	Al123555		proprotein convertase subtilisin/kexin t	6.9
	430290		Hs.81796	ESTs	6.9
	427472	AI734110	Hs.136355	ESTs	8.9
15	444042	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	6.9
13	414737	NM_004915	Hs.10237	ATP-binding cassetta, sub-family G (WHIT	6.9
		AJ160386	Hs.125087	ESTs	6.9
	420479	AW183695	Hs.186572	ESTs	6.9
	432656	NM_000246	Hs.3076	MHC class II transactivator	6.9
20	414217	Al309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	6.9
20	431870	AW449902	Hs.105500	ESTs .	6.9
	415788	AW628686	Hs.78851	KIAA0217 protein	6.9
	430066	AI929659	Hs.237825	signal recognition particle 72kD	6.9
	437156	AJ916600	Hs.121194	Homo sapiens cDNA: FLJ21569 ffs, clone C	6.8
25	401539				6.8
25	412782	AI189211	Hs.173044	ESTs	6.8
	416058	L08895	Hs.78995	MADS box transcription enhancer factor 2	6.8
	437205	AL110232		gb:Homo sapiens mRNA; cDNA DKFZp554D2071	6.7
	458814	A1498957	Hs.170861	ESTs	6.7
~~	452106	Al141031	Hs.21342	ESTs	6.7
30	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	6.7
	420910	AL049437	Hs.100292	Homo sapiens mRNA; cONA DKFZp586E1120 (f	
	445527	W39694	Hs.83286	ESTs	6.7 6.7
	424063	NM_002019	Hs.138671	firs-related tyrosine kinase 1 (vascular	6.7
	421977	W94197	Hs.110165	ribosomal protein L26 homotog	6.7
35	430280	AA361258	Hs.237868	interleutin 7 receptor	6.7
	415989	AJ267700	Hs.111128	ESTs	6.7
	418026	BE379727	Hs.83213		6.7
	425295	AA431366	Hs.37251	fatty acid binding protein 4, adipocyte	5.6
	438619	AB032773		ESTs	6.6
40	424916	AW867440	Hs.6341 Hs.23096	TU1281-TY protein	6.6
	429697	AW296451	Hs.24605	ESTs	6.6
	408741			ESTs	6.6
	403549	M73720	Hs.646	carboxypeptidase A3 (mast cell)	6.6
		414/570002	11- 00000		6.6
45	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	6.6
73	435798	BE395289	Hs.12720	elF4E-transporter	6.6
	447217	BE465754	Hs.17778	neuropilin 2	6.6
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	6.6
	410276	A1554545	Hs.68301	ESTs .	6.6
50	435391	AA704588	Hs.58934	ESTs	6.6
20	421878	AA299652	Hs.111496	Homo sepiens cDNA FLJ11543 fis, ctone HE	6.6
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	6.5
	448789	BE539108	Hs.22051	Homo sapiens mRNA; cDNA DKFZp434O119 (fr	6.5
	425331	AW962128		gb:EST374201 MAGE resequences, MAGG Homo	6.5
55	431956	AK002032	Hs.272245	Horno sapiens cDNA FLJ11170 fis, clone PL	6.5
J	444880	AW118683	Hs.154150	ESTs	6.5
	434131	AI858275	Hs.143659	ESTs	6.5
	446658	A1440137	Hs.164989	ESTs	6.5
	408150	BE620274	Hs.43112	Homo sepiens mRNA; cDNA DKFZp434B1620 (f	6.5
40	403790				6.5
60	417129	AI381800	Hs.143275	Homo sapiens cDNA FLJ13233 fis, clone OV	6.5
	452119	A1656378	Hs.33461	ESTs	6.4
	437396	BE140396	Hs.21621	hypothetical protein OKFZp7620076	6.4
	458946	AA009716	Hs.42311	ESTs	6.4
15	452110	T47667	Hs.28005	Homo sapiens mRNA; cDNA DKFZp564G2463 (f	6.4
65	449318	AW236021	Hs.108788	ESTs. Weakly similar to zeste [D.melanog	
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	6.4 6.4
	402474			The same beautiful and changes and	5.4 6.4
	430712	AW044647	Hs.196284	ESTs	6.4
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	6.4
70	432683	AW995441	Hs.10475	ESTs	6.4
	423764	AF054589	Hs.132739	ESTs	6.4
	409571	AA504249	Hs.187585	ESTs	6.4
	401600	BE247275	Hs.151787	US snRNP-specific protein, 116 kD	6.4
	415076	NM_000857	Hs.77890	nuondate cuelace 1 colubte hade 2	6.4
75	432925	AA878324		guanylate cyclase 1, soluble, beta 3	6.4
	427528	AU077143	Hs.192734	ESTS	6.4
	453894	AW937825	Hs.179565	minichromosome maintenance deficient (S.	6.4
	430335	D80007	Hs.56847	Homo sepiens cDNA FLJ12874 fis, clone NT	6.4
	453370	AJ470523	Hs.239499	KIAA0185 protein	6.3
80	421327	AA837295	Hs.182356	ESTs, Moderately similar to translation	6.3
-	450654	AJ245587	Hs.188802	ESTs	6.3
	413497	BE177661	Hs.25275	Kruppel-type zinc finger protein	6.3
	445279		14. 00040	gb:RC1-HT0598-020300-011-h02 HT0598 Homo	6.3
		R41900	Hs.22245	ESTs	6.3

	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	6.3
	421252	AA765930	Hs.130878	ESTs	6.3
	432140 434203	AK000404 BE262677	Hs.272688	hypothetical protein FLJ20397	6.3
5	419436		Hs.283558	hypothetical protein PRO1855	6.2
•	430287	AA991639 AW182459	Hs.15036	ESTs, Highly similar to AF161358 1 HSPC0	6.2
	409690	W45393	Hs.125759 Hs.94542	ESTs, Wealthy similar to tumor suppressor	6.2
	420101	AW500529	Hs.95180	ESTs, Highly similar to ATFa [H.sapiens]	6.2
	435889	AJ249107	Hs.269901	Homo sapiens mRNA; cDNA DXFZp434A205 (fr ESTs	6.1
10	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	6.1
	448030	N30714	Hs.20161	HDCME31P protein	6.1 6.1
	442571	C06338	Hs.165464	ESTs	6.1
	421202	AF193339	Hs.102506	eukaryotic translation initiation factor	6.1
16	415558	AA885143	Hs.125719	ESTs	6.1
15	408042	AL049233	Hs.42244	Homo sapiens mRNA; cDNA DKFZp564A023 (fr	6.1
	438086	AA336519	Hs.301167	Homo sapiens cDNA: FLJ21545 fis, clone C	6,1
	427390	AJ432163	Hs.268231	Homo sepiens cDNA: FLJ23111 fis, clone L	6.0
	440749	W22335	Hs.7392	Homo sapiena mRNA; cDNA DKFZp761E0323 (f	6.0
20	448822 424806	BE149845	Hs.289038	Homo sapiens cONA: FLJ20994 fis, clone C	6.0
20	435185	AA382523 AA669490	Hs.105689	ESTs	6.0
	452235	AL039743	Hs.289109 Hs.28514	dimethylarginine dimethylarninohydrolase	6.0
	432415	T16971	Hs.289014	Homo sapiens mRNA; cDNA DKFZp434H092 (fr ESTs	6.0
	436345	AA873008	Hs.121572	ESTs	6.0
25	439451	AF086270	Hs.278554	heterochromatin-like protein 1	6.0
	434674	AA831879	Hs.136985	ESTs .	6.0
	429653	NM_005955	Hs.211581	metal-regulatory transcription factor 1	6.0
	445822	AB037794	Hs. 16229	KIAA1373 protein	6.0 6.0
20	423590	AW952412	Hs.65874	ESTs	6.0
30	424026	A1798295	Hs.123218	ESTs	5.9
	423246	AL119114	Hs.23107	ESTs	5.9
	420982	AW576160	Hs.100729	KIAA0692 protein	5.9
	435008 420092	AF150262	Hs.182898	ESTs	5.9
35	444484	AA814043 AK002126	Hs.88045	ESTs	5.9
	410193	AJ132592	Hs.11260 Hs.59757	hypothetical protein FLJ11264	5.9
	450534	AI570189	Hs.25132	zinc finger protein 281	5.9
	440146	AW014231	Hs.90790	KIAA0470 gene product Homo sepiens cDNA: FLJ22930 ffs, clone K	5.9
	425361	AA355933	Hs.132221	Homo sapiens cond. PLJ22930 ffs, clone K	5.9
40	425174	D87450	Hs.154978	KIAA0261 protein	5.9
	458287	AA987556	Hs.12867	ESTs	5.9 5.9
	433793	AW975959	Hs.107513	ESTs. Moderately similar to KIAA1058 pro	5.8
	443228	W24781	Hs.293798	ESTs	5.8
15	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	5.8
45	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	5.8
	415714	NM_002290	Hs.78672	laminin, aipha 4	5.8
	421689	N87820	Hs.106826	hypothetical protein	5.8
	431176 443837	A1026984	Hs.293662	ESTs	5.8
50	410623	A1984625 AW958932	Hs.9884	spindle pole body protein	5.8
	421298	AW172431	Hs.293833 Hs.13012	ESTs	5.8
	449052	AW029507	Hs.161102	ESTs ESTs	5.8
	433043	W57554	Hs.125019	ESTs, Highly similar to KIAAD886 protein	5.8
	439444	AJ277652	Hs.54578	ESTs	5.8
55	428698	AA852773	Hs.297939	ESTs, Weakly similar to T17344 hypotheti	<b>5</b> .7 <b>5</b> .7
	411928	AA888624	Hs.19121	adaptor-related protein complex 2, sipha	5.7 5.7
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	5.7
	417315	AI080042	Hs.180450	ribosomal protein \$24	5.7
60	422544	AB018259	Hs.118140	KIAA0716 gene product	5.7
00	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	5.7
	433505 410425	AW504027	Hs_15301	Homo sapiens NY-REN-25 antigen mRNA, par	5,7
	457292	BE278367 AI921270	Hs.63510	KIAA0141 gene product	5,7
	457100	AA417878	Hs.214178	Homo sapiens cDNA FLJ14251 fis, clone OV	5.7
65	436995	AJ160015	Hs.48401 Hs.118112	ESTs, Weakly similar to ALUB_HUMAN ALU S	5.7
	426283	NM_003937	Hs.169139	ESTs	5.7
	441518	AW161697	Hs.294150	kynureninase (L-kynurenine hydrotase) ESTs	5.7
	448807	AI571940	Hs.7549	ESTS	5.7
70	449656	AA002008	Hs.188633	ESTs	5.7
70	439211	A1890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	5,7 5,7
	430440	X52599	Hs.2561	nerve growth factor, beta polypeptide	5.7 5.7
	413551	BE242639	Hs.75425	ubiquilin associated protein	5.7
	441633	AW958544	Hs.112242	ESTs	5.7
75	427093	AA398118	Hs.97579	ESTs .	5.6
, ,	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	5.6
	432267 419839	AK000872	Hs. 274227	Homo sapiens CDNA FLJ 10010 fs. chose HF	5.6
	430253	U24577 AK001514	Hs.93304	phospholipase A2, group VII (platetet-ac	5.6
	450447	AF212223	Hs.236844 Hs.25010	hypothetical protein FLJ10652	5.6
80	434623	AB023163	Hs.4014	hypothetical protein P15-2	5.6
	420642	AK001520	Hs.99545	KIAA0946 protein; Huntingtin Interacting	5.6
	414020	NM_002984	Hs.75703	Homo sapiens cDNA FLJ 10558 fis, clone NT small inducible cytokine A4 (homologous	5.6
	420825	AJ656727		gb:fi53f12.x1 NCI_CGAP_GC6 Homo sapiens	5.6
				Come Toro Louis 25/benz	5.6

	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	5.6
	452046	AB018345	Hs.27657	KIAA0802 protein	5.6
	408911	AW294772	Hs.98321	Homo sapiens cDNA FLJ14103 fis, clone MA	5.6
5	414844 416498	AA296874 U33632	Hs.77494	deoxyguanosine kinase	5.6
•	430512	AF182294	Hs.79351 Hs.241578	potassium channel, subfamily K, member 1 U6 snRNA-associated Sm-like protein LSm8	5.6
	430339	W28608	Hs.239625	Integral membrane protein 28	5.6 5.6
	420153	N22120	Hs.75277	hypothetical protein FLJ13910	5.6
	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	5.6
10	441568	A1733322	Hs.127176	ESTs	5.5
	414575	H11257	Hs.295233	ESTs .	5.5
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	5.5
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	5.5
15	453064	R40334	Hs.301395	Homo sapiens cONA: FLJ21204 fs, done C	5.5
13	433409	AJ278802	Hs.25661	ESTs	5.5
	407094 425234	AF000574 AW152225	Hs.22405 Hs.165909	leukocyte immunoglobulin-like receptor. ESTs	5.5
	447644	AW861622	Hs.108648	Homo sapiens cONA FLJ12534 fts, ctone NT	5.5 5.5
	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	5.5 5.5
20	446534	Al307356	Hs.175225	ESTs	5.5
	452355	N54926	Hs.29202	G protein-coupled receptor 34	5.5
	434715	BE005346	Hs.116410	ESTs .	5.5
	440486	BE243513	Hs.7212	hypothetical protein PP1044	5.5
25	444825	AW167613	Hs.248	mitogen-activated protein kinase kinase	\$.5
23	419172 444931	AW338625 AV652066	Hs.22120	ESTs	5.4
	413940	A1633205	Hs.75113 Hs.159914	general transcription factor IIIA ESTs	5.4
	410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	5.4
	447072	D61594	Hs.17279	tyrosytprotein sutfotransferase 1	5.4 5.4
30	434361	AF129755	Hs.117772	ESTs	5.4
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	5.4
	445175	AV652851	Hs.300848	ESTs	5.4
	411213	AA676939	Hs.69285	neuropilin 1	5.4
35	412530	AA766268	Hs.266273	Homo sapiens cDNA FLJ13348 fis, done OV	5.4
33	422667	H25642	Hs.133471	ESTs	5.4
	434064 429688	AL049045 BE245169	Hs.180758	hypothetical protein PRO0082	5.4
	452060	W26980	Hs.211610 Hs.153612	CUG triplet repeat, RNA-binding protein ATP-binding cassette, sub-family F (GCN2	5.4
	419093	AI804054	Hs.112685	ESTs	5,4 5.4
40	436267	AW450938	Hs.180115	ES7s	5.4
	405257				5.4
	431154	AW971228	Hs.290259	ESTs .	5.4
	415511	AJ732617	Hs.182362	ESTs	5.4
15	419175	AW270037	Hs.179507	KIAA0779 protein	5.3
45	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	5.3
	423720 409995	AL044191 AW960597	Hs.23388	Homo sepiens cDNA: FU21310 fis, clone C	5.3
	414911	NM_000107	Hs.30184 Hs.77602	ESTS	5.3
	455716	BE070263	113.77002	damage-specific DNA binding protein 2 (4 gb:QV4-BT0407-280100-090-e07 BT0407 Horno	5.3
50	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.3 5.3
	419985	H66373	Hs.15973	ESTs, Highly similar to bA393J16.3 [H.se	5.3
	428753	AW939252	Hs.192927	hypothetical protein FLJ20251	5.3
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	5.3
55	404176				5.3
22	431475	AI567669	Hs.287316	ESTs .	5.3
	406625 405475	Y13647	Hs.119597	stearoyl-CoA desaturase (delta-9-desatur	5.3
	430180	AA331406	Hs.75456	A kinase (PRKA) anchor protein 10	5.3
	446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761PQ19 (fr	5.3 5.3
60	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	5.3
	433029	NM_014322	Hs.279926	opsin 3 (encephalopsin)	5.3
	442837	AI022082	Hs.50492	ESTs .	5.3
	437140	AA312799	Hs.283689	activator of CREM in testis	5.3
65	408989	AW361666	Hs.49500	KIAA0746 protein	5.3
U.J	417355	D13168 AA744622	Hs.82002	endothelin receptor type B	5.3
	407361 437734	AA693951	Hs.292645 Hs.180284	ESTs, Weskly similar to ALU5_HUMAN ALU S ESTs	5.3
	452234	AW084176	Hs.223296	ESTs	5.3
~-	423057	AW961597	Hs.130816	ESTs	5.3 5.3
70	439593	8E073597	Hs.124863		5.3
	446501	Al302616	Hs.150819		5.3
	416406	086961	Hs.79299	fipoma HMGIC fusion partner-like 2	5.2
	427164	AB037721	Hs.173871	KIAA1300 protein	5.2
75	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	5.2
, ,	448212 412420	A1475858 AL035668	Lie 22002	gb:tc87d07.x1 NCI_CGAP_CLL1 Homo sepiens	5.2
	416975	NM_004131	Hs.73853 Hs.1051	bone morphogenetic protein 2	5.2
	406815	AA833930	Hs.288036	granzyme B (granzyme 2, cytotoxic T-lymp tRNA isopentenytpyrophosphate transferas	5.2 5.2
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	5.2 5.2
80	425322	U63630	Hs.155637		5.2
	451156	A1983569	Hs.232042		5.2
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	5.2
	423024	AA593731	Hs.75613	CO36 antigen (collagen type I receptor,	5.2

	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Droso	5.2
	451149	AL047586	Hs.10283	ESTs .	5.2
	429458	BE161832	Hs.292689	ESTS	5.2
•	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	5.2
5	432383	AK000144	Hs.274449	Homo sapiens cDNA FLJ20137 fis, clone CO	5.2
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	5.2
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	5.2
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	5.2
10	438995	AI277986	Hs.164875	ESTs	5.1
10	438582	AI521310	Hs.283365	ESTs, Wealdy similar to ALUS_HUMAN ALU S	5.1
	424859 445563	U92014	Hs.153527	Homo saplens pTMS mariner-like transposo	5.1
	416852	AW873606 AF283776	Hs.149006 Hs.80285	ESTs Homo sapiens mRNA; cDNA DKFZp586C1723 (I	5.1
	420567	AK000812	Hs.98874	similar to profine-rich protein 48	5.1 5.1
15	420630	AL133101	Hs.99508	Homo sepiens mRNA; cDNA DKFZp43400921 (I	5.1
	455510	AA422029	Hs.143640	ESTs, Weakly similar to hyperpolarizatio	51
	412676	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con	5.1
	438146	Z36842	Hs.57548	ESTs	5.1
	423430	AF112481	Hs.128501	RAD54, S. cerevisiae, homolog of, B	5.1
20	421633	AF121860	Hs.106260	sorting nextin 10	5.1
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	5.1
	436943	AA773838	Hs.5353	caspase 10, apoptosis-related cysteine p	5.1
	456210	N49729	Hs.156875	ESTs	5.1
25	411893	R82845	Hs.273789	ESTs	5.1
25	432331	W37862	Hs.274358	Homo sapiens mRNA; cDNA DKFZp586i1524 (f	5.1
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	5.1
	426822 444269	W78950 AI590348	Hs.220823		5.1
	437204	AL110216	Hs.146220 Hs.12285	ESTS	5.1 5.1
30	443180	R15875	Hs.70945	ESTS	5.1
-	431510	AA580082	Hs.112264		5.0
	446312	BE087853	113.112204	gb:QV1-BT0681-290400-181-h05 BT0681 Homo	5.0
	449870	AJ672487	Hs.15423	hypothetical protein HDCMC04P	5.0
	430462	AJ584156	Hs.105640	EST\$	5.0
35	457452	AW972675		gb:EST384766 MAGE resequences, MAGL Homo	5.0
	420397	NM_007018	Hs.97437	centrosomal protein 1	5.0
	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	5.0
	426874	N67325	Hs.247132		5.0
40	419746	AW867943	Hs.127216	Homo sepiens cDNA FLJ13465 fis, clone PL	5.0
70	434237	AF119908	Hs.235516	hypothetical protein PRO2955	5.0
		AA381807	He 61767	hypovia industria popular 2	
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	5.0
			Hs.61762	hypoxia-inducible protein 2	
	TABLE 35	<b>58</b> :			
45		i8: Uniq		et Idenlifier number	
45	TABLE 35 Pkey:	i8: Uniq ber: Gen	ue Eos probes	et Identifier number er	
45	TABLE 35 Pkey: CAT num Accession	68: Uniq ber: Gen u Gen	ue Eos probes e cluster numb bank accession	et Identifier number er	
45	TABLE 35 Pkey: CAT num Accession Pkey	iB: Uniq ber: Gen u: Gen CAT number	ue Eos probes e duster numb bank accession Accession	iet Identifier number er n numbers	
	TABLE 35 Pkey: CAT num Accession Pkey 411937	iB: Uniq ber: Gen u Gen CAT number 1266219_1	ue Eos probes e cluster numb bank accession Accession AW876626	et Identifier number er n numbers AW876622 AW876624	
45 50	TABLE 35 Pkey: CAT num Accession Pkey 411937 413497	58: Uniq ber: Gen u: Gen CAT number 1266219_1 1373771_1	que Eos probes e cluster numb bank accession Accession AW876626 BE177661 I	et Identifier number er n numbers AW876622 AW876624 406215 BE144709 BE144829	5.0
	TABLE 35 Pkey: CAT num Accession Pkey 411937	iB: Uniq ber: Gen u Gen CAT number 1266219_1	aue Eos probes e duster numb bank accession Accession AW875628 BE1776611 AI656727 A	el Identifier number er n numbers AW876622 AW876624 406215 BE144709 BE144829 1697887 AI802122 AA910877 Z28718 T16711 AA651731 AL04	5.0 7264 BE000621 R68736 AW992695 AI768764 AW271284 AW974553
	TABLE 35 Pkey: CAT num Accession Pkey 411937 413497	58: Uniq ber: Gen u: Gen CAT number 1266219_1 1373771_1	que Eos probes e cluster numb bank accession Accession AW876628 BE177661 I AI656727 A	el kienüfier number er n numbers AW876622 AW876624 406215 BE144709 BE144829 1697887 AB02122 AA910877 Z28718 T16711 AA651731 AL04 W055145 R93609 AW467031 Al096866 Al371871 Al126182 Al	5.0
50	TABLE 35 Pkey: CAT num Accession Pkey 411937 413497	58: Unique de CAT number 1266219_1 1373771_1 196769_1	que Eos probes o duster numb bank accession AW876828 BE177661 AI556727 A AI308951 A	el Idenüfier number er n numbers AW876622 AW876624 106215 BE144709 BE144829 1697887 AI802122 AA910877 Z28718 T16711 AA651731 AL04 W055146 R93609 AW467031 AI096866 AI371871 AI126182 AI AW008695 R68882 AI719136 R97752 AW196262	5.0 7264 BE000621 R68736 AW992695 AI768764 AW271284 AW974553
	TABLE 35 Pkey: CAT numk Accession Pkey 411937 413497 420825 425331 437205	58: Uniq ber: Gen u: Gen CAT number 1266219_1 1373771_1	que Eos probes o duster numb bank accession AW876828 BE177661 AI556727 A AI308951 A	let Identifier number er n numbers AW876622 AW876624 406215 BE 144709 BE 144829 1697887 AI802122 AA910877 Z28718 T16711 AA651731 AL04 W055146 R93609 AW467031 AI096866 AI371871 AI 126182 AI AW008695 R68682 AI719136 R97752 AW196262 AA356353 AA427363	5.0 7264 BE000621 R68736 AW992695 AI768764 AW271284 AW974553
50	TABLE 35 Pkey: CAT num Accession Pkey 411937 413497 420825 425331 437205 438966	58: Uniq ber. Gen tr Gen CAT number 1266219_1 1373771_1 196769_1 250199_1 43463_1 467438_1	ue Eos probes e duster numb bank accession Accession AW876828 BE1776611 AI556727 A A1308951 A AW088970 AL1102321	let Identifier number er n numbers AW876622 AW876624 406215 BE 144709 BE 144829 1697887 AI802122 AA910877 Z28718 T16711 AA651731 AL04 W055146 R93609 AW467031 AI096866 AI371871 AI 126182 AI AW008695 R68682 AI719136 R97752 AW196262 AA356353 AA427363	5.0 7264 BE000621 R68736 AW992695 AI768764 AW271284 AW974553
50	TABLE 35 Pkey: CAT num Accession Pkey 411937 413497 420825 425331 437205 438966 442438	SB: Unique ber. Gen CAT number 1266219_1 1373771_1 196769_1 250199_1 43453_1 467435_1 542469_1	ue Eos probes o duster numb bank accession Avva7666 BE17766 1 Al556727 A Al308951 A AW088970 AW962128 AL110232 I AW979074 AW979074 AW979074	el Identifier number er n numbers AW876622 AW876624 106215 BE 144709 BE 144829 1697687 A1802122 AA910877 Z28718 T16711 AA651731 AL04 W055146 R93609 AW467031 A1096866 A1371871 A1126182 AI AW008695 R68682 A1719136 R97752 AW196262 AA355333 AA427363 194765 AA834841 AA828650 AI916584 R61781 T77332 F07756 F08149 F07647	5.0 7264 BE000621 R68736 AW992695 AI768764 AW271284 AW974553
50	TABLE 33 Pkey: CAT num Accession Pkey 411937 413497 420825 425331 437205 438966 442438 443161	SB: Unique CAT number 1266219_1 1373771_1 196769_1 250199_1 43463_1 467438_1 542469_1 561305_1	Accession AV876828 BE1776611 AU8951 A AV88970 AV98970 AV98970 AV98970 AV962128 AL110232 I AV979074 AA9959974 AA9959974	let Identifier mumber er n numbers AW876622 AW876624 406215 BE144709 BE144829 1697887 AI802122 AA910877 Z28718 T16711 AA651731 AL04: W055146 R93609 AW467031 AI096866 AI371871 AI126182 AI AW008695 R68682 AI719136 R97752 AW196262 AA356353 AA427363 949765 AA834841 AA828650 AN916584 R61781 T77332 F07756 F08149 F07647 J344631 AJ261653	5.0 7264 BE000621 R68736 AW992695 AI768764 AW271284 AW974553
50 55	TABLE 33 Pkey: CAT num Accession Pkey 411937 413497 420825 425331 437205 438966 442438 443161 448312	SB: Unique ber: Gen under Gen 1266219_1 196769_1 196769_1 250199_1 43453_1 542469_1 561305_1 671114_1	Jue Eos probes e duster numb bank accession Accession AW876628 BE177661 I AI556727 A AU088970 AW962128 AL 110232 I AW979074 AA995998 AI033316 A BE087853	let Identifier number er n numbers AWB76622 AWB76624 106215 BE 144709 BE 144829 1697887 AIB02122 AA910877 Z2871B T16711 AA551731 AL04 WU555146 R93609 AW467031 AI096866 AI371871 AI126182 AI AW008695 R68682 AIT19136 R97752 AW196262 AA356353 AA427363 V94765 AA834841 AA828650 AI916584 R61781 T77332 F07756 F08149 F07647 U344631 AI261653 AI286184	5.0 7264 BE000621 R68736 AW992695 AI768764 AW271284 AW974553
50	TABLE 33 Pkey: CAT num Accession Pkey 411937 413497 420825 425331 437205 43295 442438 443161 448312 447197	SB: Unique ber. Gen CAT number 1266219_1 1373771_1 196769_1 250199_1 43463_1 467438_1 561305_1 671114_1 711623_1	que Eos probes o duster numb bank accession Avva76661 BE177661 AI556727 A AI308951 A AWW88970 AL 1102321 AL 1102321 AL 1102321 AL 1023316 A BE087853 BE087853	el Identifier number er n numbers AW876622 AW876624 106215 BE 144709 BE 144829 1697687 AI802122 AA910877 Z28718 T16711 AA651731 AL04 W055146 R93609 AW467031 AI096866 AI371871 AI126182 AI AW008695 R68682 AI719136 R97752 AW196262 AA353353 AA427363 194765 AA348441 AA828650 AI916584 R61781 T77332 F07756 F08149 F07647 1344631 AI261653 AI286184 AI286184 AI286184	5.0 7264 BE000621 R68736 AW992695 AI768764 AW271284 AW974553
50 55	TABLE 33 Pkey: CAT num Accession Pkey 411937 420825 425331 437205 439966 442438 443161 448312 447197 447974	SB: Unique Der: Gen CAT number 1266219_1 1373771_1 196769_1 250199_1 43453_1 467435_1 561305_1 671114_1 711623_1 745643_1	ue Eos probes e duster numb bank accession Accession AW876828 BE177661 I AI506727 A AV088970 AW962128 AW979074 AA9965998 AI038316 A BE087853. R36075 AI	let Identifier mumber er n numbers er n numbers  AW876622 AW876624	5.0 7264 BE000621 R68736 AW992695 AI768764 AW271284 AW974553
50 55	TABLE 33 Pkey: CAT num Accession Pkey 411937 413497 420825 425331 437205 43966 442438 443161 448312 447197 44797 44797 44797 44784	Se: Unique de la CAT number 1266219_1 196769_1 196769_1 250199_1 43453_1 542469_1 561305_1 671114_1 71523_1 745643_1 745643_1 755099_1	jue Eos probes e duster numb bank accession Avv876626 BE177661 I AI556727 A AV088970 AW962128 AL 110232 I AV979074 AA95998 AI033316 A BE087853 R36075 AI R76885 AI AI47588 A	let Identifier number er n numbers.  AWB76622 AWB76624 106215 BE 144709 BE 144829 1697887 AIB02122 AA910877 Z28718 T16711 AA551731 AL04 W055145 R93609 AW467031 AI096866 AI371871 AI126182 AI AW008695 R68682 AI719136 R97752 AW196262 AA356353 AA427363 V94765 AA834841 AA828650 AI916584 R61781 T77332 F07756 F08149 F07647 J344631 AI261653 AI268184 J66546 R36167 153674 R77049 W9959013	5.0 7264 BE000621 R68736 AW992695 AI768764 AW271284 AW974553
50 55	TABLE 33 Pkey. CAT num Accession Pkey 411937 413497 420825 425331 437205 432956 442438 443161 448312 447197 447974 448212 451818	SB: Unique ber. Gen CAT number 1266219_1 1373771_1 196769_1 250199_1 43463_1 467438_1 542469_1 561305_1 671114_1 711623_1 745643_1 755099_1 887271_1	que Eos probes o duster numb bank accession Avva76661 BE177661 Al556727 A Al308951 A AWW88970 AW962128 AL1102321 AW979074 AW879074 AW879074 AW879075 AI R76885 AI AL4175858 AI AL4175858 AI AL4175858 AI	let Identifier number er n numbers  AW876622 AW876624  106215 BE 144709 BE 144829  10697687 A1802122 AA910877 Z28718 T16711 AA651731 AL04  W055146 R93609 AW467031 A1096866 AI371871 A1126182 AI  AW008695 R68682 AI719136 R97752 AW196262  AA355353 AA427363  194765  AA934841 AA828650  AI916584 R61781 T77332 F07756 F08149 F07647  1344631 A1261653  A1266184  86546 R36167  153674 R777049  W959013  805492 W27615	5.0 7264 BE000621 R68736 AW992695 AI768764 AW271284 AW974553
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50 55 60 65 70	TABLE 33 Pkey: CAT num Accession Pkey 411937 420825  425331 437205 438966 442438 443161 448212 447197 448212 451818 453013 455716 457452 407305 TABLE 3 Pkey: Ref: Strand: Nt_posit	98: Unique ber: Gen CAT number 1266219_1 1 1373771_1 196769_1 250199_1 43463_1 457436_1 561305_1 671114_1 715099_1 887271_1 339381_1 332695_1 339381_1 352695_1 339381_1 55C: Unit Section: Indian Ref	jue Eos probes e duster numb bank accession Accession AW876628 BE177661 I AI556727 A AU308951 A AW088970 AW956128 AL 110232 I AW979074 AA995998. AI033316 A BE087853. R36075 AI3 R76888 AI AI475858 A AIB19018 F AA031407 BE070263 AW972675 AA715284  ique number co quence source quence of hums icstes DNA str icates nucleofi Strand	et Identifier number er n numbers  AW876622 AW876624  106215 BE144709 BE144829  1697887 AI802122 AA910877 Z28718 T16711 AA551731 AL04  W055146 R93609 AW467031 AI096866 AI371871 AI126182 AI AW008695 R68882 AI719136 R97752 AW196262  AA356353 AA427363  N94765  AA834841 AA828650  AI916584 R61781 T77332 F07756 F08149 F07647  J344631 AI261653  AI286184  365546 R936187  S35374 R777049  W969013  205492 W27615  N85751 AW974119 AA031408 AA572965  BE070195 BE070265 BE070202 8E070233 BE070399 BE0702  AA541366 AA523039  Deresponding to an Eos probeset  The 7 digit numbers in this column are Genbank Identifier (GI) an chromosome 227 Dunham, et al. (1993) Nature 402:489-495. del positions of predicted exons.  Nt_position	5.0  7.264 BE000621 R68736 AW992695 AJ768764 AW271284 AW974553 564756 AJ381460 AJ358914 AJ419231 AW439733 R87059 AA628064  203  numbers. "Dunham, et al." refers to the publication entitled "The DNA
50 55 60 65 70	TABLE 33 Pkey: CAT num Accession Pkey 411937 413497 420825 425331 437205 439966 442438 443161 446312 447197 448212 447197 448212 451818 453013 4557162 407305 TABLE 3 Pkey: Ref: Strand: Pkoy 401539	SB: Unique ber: Gen CAT number: Gen 1266219_1 1373771_1 196769_1 250199_1 43463_1 467436_1 561305_1 671114_1 711623_1 745643_1 755099_1 339381_1 339381_1 3312657	jue Eos probes e duster numb bank accession ACRESSION AV876828 BE177661 I AI565727 A AI508951 A AW089970 AW9962122 AW979074 AA995998 AI10232 I AW979074 AA995998 AI033316 A BE087853 R35075 AI2 R75888 AI AI475858 AI AI475858 AAI AI475858 AIA91018 F AA031407 BE070263 AW972675 AA715284	el Identifier number er n numbers er n numbers  AWB76622 AWB76624  106215 BE144709 BE144829  1697887 AIB02122 AA910877 228718 T16711 AA551731 AL04  WUS5145 R93609 AW467031 AI096866 AI371871 AI126182 AI AW008695 R68682 AI719136 R97752 AW196262  AA356353 AA427363  N94765  AA834841 AA828650  AI916584 R61781 T77332 F07756 F08149 F07647  U344631 AI261653  AI268184  166546 R36187  153674 R77049  W969013  305492 W27615  N85751 AW974119 AA031408 AA572965  BE070195 BE070265 BE070202 8E070233 BE070399 BE0702  AA541366 AA523039  Deresponding to an Eos probeset  The 7 digit numbers in this column are Genbank Identifier (GI) an chromosome 227 Dunham, et al. (1999) Nature 402:489-495. and from which exons were predicted. de positions of predicted exons.  Nt_position 62028-62608	5.0  7.264 BE000621 R68736 AW992695 AJ768764 AW271284 AW974553 564756 AJ381460 AJ358914 AJ419231 AW439733 R87059 AA628064  203  numbers. "Dunham, et al." refers to the publication entitled "The DNA
50 55 60 65 70	TABLE 33 Pkey: CAT num Accession Pkey 411937 420825  425331 437205 438966 442438 443161 448212 447197 448212 451818 453013 455716 457452 407305 TABLE 3 Pkey: Ref: Strand: Nt_posit	98: Unique ber: Gen Gen Gen 1266219_1 196769_1 196769_1 196769_1 196769_1 196769_1 196769_1 196769_1 196769_1 196769_1 196769_1 1967643_1 715623_1 745643_1 194390_1 194390_1 1352695_1 339381_1 312657	Jue Eos probes o duster numb bank accession AW876826 BE177661 II AI556727 A AI308951 A AW088970 AW962128 AL 110232 II AV979074 AA995998 AI033316 A BE087853 R36075 AI R76886 AII AI475884 AIB19018 F AA031407 BE070263 AW972675 AA715284  Gue number oc quence of hum- icidies DNA str icidies DNA str icidies DNA str icidies DNA str icidies DNA str icidies DNA str icidies DNA str icidies uncleofi	et Identifier number er n numbers  AW876622 AW876624  106215 BE144709 BE144829  1697887 AI802122 AA910877 Z28718 T16711 AA551731 AL04  W055146 R93609 AW467031 AI096866 AI371871 AI126182 AI AW008695 R68882 AI719136 R97752 AW196262  AA356353 AA427363  N94765  AA834841 AA828650  AI916584 R61781 T77332 F07756 F08149 F07647  J344631 AI261653  AI286184  365546 R936187  S35374 R777049  W969013  205492 W27615  N85751 AW974119 AA031408 AA572965  BE070195 BE070265 BE070202 8E070233 BE070399 BE0702  AA541366 AA523039  Deresponding to an Eos probeset  The 7 digit numbers in this column are Genbank Identifier (GI) an chromosome 227 Dunham, et al. (1993) Nature 402:489-495. del positions of predicted exons.  Nt_position	5.0  7.264 BE000621 R68736 AW992695 AJ768764 AW271284 AW974553 564756 AJ381460 AJ358914 AJ419231 AW439733 R87059 AA628064  203  numbers. "Dunham, et al." refers to the publication entitled "The DNA
50 55 60 65 70	TABLE 33 Pkey: CAT num Accession Pkey 411937 413497 420825 425331 437205 439966 442438 443161 446312 447197 448212 447197 448212 407305 TABLE 3 Pkey: Ref: Strand: RNL_posit Pkoy 401539 402474 403594 403713	SB: Unique ber: Gen CAT number: Gen 1266219_1 1373771_1 196769_1 250199_1 43463_1 467438_1 711623_1 715099_1 1325695_1 339381_1 339381_1 339381_1 339381_1 36577 156081591 166788072433 7547175 8081591 6573831	Jue Eos probes o duster numb bank accession AW876828 BE177661 I AI565727 A AI508951 A AW089970 AW952128 AW979074 AA955998 A AI 10232 I AW979074 AA955998 A AI5083316 A BE087853. R36075 AI R76886 AI A4475858 A AB19018 F AA031407 BE070263 AW972675 AA715284  Sque number oc quence of hum icates DNA str icates nucleofi Strand Minus Minus	el Identifier number er n numbers er n numbers  AW876622 AW876624  H06215 BE144709 BE144829  H697887 AH802122 AA910877 Z28718 T16711 AA651731 AL04  W055146 R93609 AW467031 Al096866 Al371871 AL126182 AI AW008695 R68682 AI719136 R97752 AW196262  AA35353 AA427363  H94765  AA83481 AA828650  AH916584 R61781 T77332 F07756 F08149 F07647  H344631 AL261653  AI266184  B66546 R36187  H53674 R77049  W959013  R05492 W27615  N85751 AW974119 AA031408 AA572965  BE070195 BE070265 BE070202 BE070233 BE070399 BE0702  AA541366 AA523039  AM541366 AA523039  AM561364 R61866  The 7 digit numbers in this column are Genbank Identifier (GI) an chromosome 27 Dunham, et al. (1993) Natura 402:483-495. and from which exons were predicted. de positions of predicted exons.  N1_position  62028-62608  53526-53628.55755-55920.57530-57757  137150-137362	5.0  7.264 BE000621 R68736 AW992695 AJ768764 AW271284 AW974553 564756 AJ381460 AJ358914 AJ419231 AW439733 R87059 AA628064  203  numbers. "Dunham, et al." refers to the publication entitled "The DNA
50 55 60 65 70	TABLE 33 Pkey: CAT num Accession Pkey 411937 420825  425331 437205 438966 442438 44318 448312 447197 448212 451818 453013 455716 457452 407305  TABLE 3 Pkey: Ref: Strand: NLpositi	B: Unique ber: Gen CAT number: Gen 1266219_1 1373771_1 196769_1 250199_1 43453_1 467435_1 561305_1 671114_1 711623_1 745643_1 755099_1 332855_1 339381_1 332655_1 561305_1 67114_1 687271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 687271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 687271_1 6887271_1 687271_1 6887271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 67	jue Eos probes e duster numb bank accession Accession AW876628 BE177661 I AI556727 A AU308951 A AW088970 AW962128 AL 110232 I AW979074 AA995998. AI038316 A BE087853. R36075 AI3 R76888 AI AI475858 A AI819018 F AA031407 BE070263 AW972675 AA715284  ique number co quence source quence of hum- icestes DNA str icestes nucleofi Strand Minus Minus Minus	et Identifier number er n numbers  AW876622 AW876624  106215 BE144709 BE144829  1697887 AI802122 AA910877 Z28718 T16711 AA551731 AL04  W055146 R93609 AW467031 AI096866 AI371871 AI126182 AI AW008695 R68882 AI719136 R97752 AW196262  AA356353 AA427363  W94765  AA834841 AA828650  AI916584 R61781 T777332 F07756 F08149 F07847  J344631 AJ261653  AI286184  366546 R36187  S3674 R77049  W969013  305492 W27615  N85751 AW974119 AA031408 AA572965  BE070195 BE070265 BE070202 8E070233 BE070399 BE0702  AA541368 AA523039  AA541368 AA523039  AA541368 AA523039  AIR Column are Genbank Identifier (GI) an chromosome 22° Dunham, et al. (1999) Nature 402:489-495. and from which exons were predicted. de positions of predicted exons.  N1_position  62028-62608  53526-53528,55755-55920,57530-57757  137150-137362	5.0  7.264 BE000621 R68736 AW992695 AJ768764 AW271284 AW974553 564756 AJ381460 AJ358914 AJ419231 AW439733 R87059 AA628064  203  numbers. "Dunham, et al." refers to the publication entitled "The DNA
50 55 60 65 70	TABLE 33 Pkey: CAT num Accession Pkey 411937 420825  425331 437205 439966 442438 443161 448212 451818 453013 455716 457452 407305 TABLE 3 Pkey: Ref: Strand: Nt_oosit Pkoy 401539 40274 403549 403713	98: Unique ber: Gen CAT number 1266219_1 1373771_1 196769_1 250199_1 43463_1 457436_1 561305_1 671114_1 715099_1 887771_1 94390_1 1352695_1 339381_1 312657 Unit Sec Sec Sec Sec Sec Sec Sec Sec Sec Sec	jue Eos probes e duster numb bank accession Accession AW876628 BE177661 I AI556727 A AU308951 A AW088970 AW962128 AL 110232 I AW979074 AA995998. AI038316 A BE087853. R36075 AI3 R76888 AI AI475858 A AI819018 F AA031407 BE070263 AW972675 AA715284  ique number co quence source quence of humn- icestes DNA str icates nucleofi Strand Minus Minus Minus Minus Minus Minus Minus Minus Minus Plus	et Identifier number er n numbers  AW876622 AW876624  106215 BE 144709 BE 144829  1697887 AI802122 AA910877 Z28718 T16711 AA551731 AL04  W055146 R93609 AW467031 AI096866 AI371871 AI126182 AI AW008695 R68882 AI719136 R97752 AW196262  AA356353 AA427363  N94765  AA834841 AA828650  AI916584 R61781 T77332 F07756 F08149 F07647  J344631 AI261653  AI286184  56546 R936187  535674 R777049  W969013  005492 W27615  N85751 AW974119 AA031408 AA572965  BE070195 BE070265 BE070202 8E070233 BE070399 BE0702  AA541366 AA523039  Demosponding to an Eos probeset  The 7 digit numbers in this column are Genbank Identifier (GI) an chromosome 22 Dunham, et al. (1993) Nature 402:489-495. and from which exons were predicted. de position of predicted exons.  Nt_position  62028-62608  53526-53628.55755-55920,57530-57757  137150-137362  152769-153155  87826-87947,89835-90002  52685-52800	5.0  7.264 BE000621 R68736 AW992695 AJ768764 AW271284 AW974553 564756 AJ381460 AJ358914 AJ419231 AW439733 R87059 AA628064  203  numbers. "Dunham, et al." refers to the publication entitled "The DNA
50 55 60 65 70	TABLE 33 Pkey: CAT num Accession Pkey 411937 420825  425331 437205 438966 442438 44318 448312 447197 448212 451818 453013 455716 457452 407305  TABLE 3 Pkey: Ref: Strand: NLpositi	B: Unique ber: Gen CAT number: Gen 1266219_1 1373771_1 196769_1 250199_1 43453_1 467435_1 561305_1 671114_1 711623_1 745643_1 755099_1 332855_1 339381_1 332655_1 561305_1 67114_1 687271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 687271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 6887271_1 687271_1 6887271_1 687271_1 6887271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 67	jue Eos probes e duster numb bank accession AW876828 BE177661 I AI5656727 A AI508951 A AW089970 AW952128 AW979074 AA955998 A AI 10232 I AW979074 AA955998 A AI5089595 A AI50875 AI5 R76885 AI6 AI475858 A AIB19018 F AA031407 BE070263 AW972675 AA715284  ique number oc quence of humi icates DNA str icates nucleofi Strand Minus Minus Minus Minus Minus Minus Minus Minus	el Identifier number er in numbers er in numbers  AW876622 AW876624  406215 BE144709 BE144829  1697887 AI802122 AA910877 Z28718 T16711 AA651731 AL04  W055146 R93609 AW867031 AI096866 AI371871 AI126182 AI AW008695 R68682 AI719136 R97752 AW196262  AA356353 AA427363  949765  AA834841 AA828650  AI95684 R61781 T777332 F07756 F08149 F07647  AI344631 AI261653  AI266184  B66546 R36167  153674 R77049  W969013  R05492 W27615  N85751 AW974119 AA031408 AA572965  BE070195 BE070265 BE070202 BE070233 BE070399 BE0702  AA541366 AA523039  AM541366 AA523039	5.0  7.264 BE000621 R68736 AW992695 AJ768764 AW271284 AW974553 564756 AJ381460 AJ358914 AJ419231 AW439733 R87059 AA628064  203  numbers. "Dunham, et al." refers to the publication entitled "The DNA



405475 1931025 Plus 1548-1702

TABLE 38A: ABOUT 169 GENES UP-REGULATED IN KIDNEY CANCER
Table 36A lists about 169 genes up-regulated in kidney cancer compared to normal kidney that are likely to be extracellular or cell-surface proteins. These were selected as for Table 36A and the predicted protein contained a structural domain that is indicative of surface or extracefular localization (e.g. ig, In3, egi, 7tm domains). Predicted protein domains are 5

10

35A and the pre-noted. Pkey; ExAccn; UnigenetO: Unigene Title: PSOomain; R1: Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Unigena number Unigena gene tide Protein Structural Domain Ratio of turnor to normal tissue

	KI.	70800	Of Children in	MUSI 62206		
15	Pkey	ExAcon	UnigenelD	Unigene Title	PSDomain	04
••	424704	AI263293	Hs.152096	cytochrome P450	SS,p450	R1
	426559	AB001914	Hs. 170414	paired basic am	TM,Peptidase_S8,P	40.9
	458079	AI796870	Hs.54277	ESTs	TM	35.6 34.6
	446921	AB012113	Hs.16530	small inducible	SS,IL8	25.9
20	452401	NM_007115	Hs.29352	tumor necrosis	TM,SS,Xink,CUB	24.8
	414821	M63835	Hs.77424	Fc fragment of	TM,SS.ig	23.4
	414812	X72755	Hs.77367	monokine Induce	SS.U.8	22.1
	426471	M22440	Hs.170009	transforming gr	TM,SS,EGF	21.3
	449523	NM_000579	Hs.54443	chemokine (C-C	TM,7tm_1	20.7
25	428227	AA321649	Hs.2248	small inducible	ILB	19.5
	456804	AJ421645	Hs.139851	caveolin 2	TM, Caveolin	17.8
	411642	NM_014932	Hs.71132	neuroligin 1	TM,SS,COesterase	16.2
	427581	NM_014788	Hs.179703	KIAA0129 gene p	TM	15.6
20	448520	AB002367	Hs.21355	doublecorfin an	TM,pkinase	14.8
30	417308	H60720	Hs.81892	KIAA0101 gene p	TM	14.8
	421566	NW_000399	Hs.1395	early growth re	TM.zf-C2H2	14.6
	422603	BE242587	Hs.118651	hematopoietical	TM,SS,homeobox	14.4
	425984	AW836277	Hs.165636	hypothetical pr	ŤM	14.2
35	432606	NM_002104	Hs.3068	granzyme K (ser	TM,SS,trypsin	14.1
23	458809	AW972512	Hs.20985	sin3-associated	\$\$	13.7
	446627	AI973016	Hs.15725	hypothetical pr	TM	13.6
	452960	AK001335	Hs.31137	Homo sapiens cD	TM,Y_phosphatase	13.3
	420552	AK000492	Hs.98806	hypothetical pr	TM,SS	13.0
40	425188	AK002052	Hs.155071	hypothetical pr	TM	12.6
40	419034	NM_002110	Hs.89555	hemopoletic cel	TM,pkinase,SH2,SH3	12.3
	442932	AA457211	Hs.8858	bromodomain adj	TM, bromodomain, PHD	12.3
	434398	AA121098	Hs.3838	serum-inducible	TM,pkinase,POLO_box	12.2
	450506	NM_004460	Hs.418	fibroblast acti	SS,DPPIV_N_term,Peptidase_S9	12.1
45	425782	U66468	Hs. 159525	cell growth reg	SS	12.0
72	426108 450236	AA622037	Hs.166468	programmed cell	TM,DUF122	11.9
	452838	AW162998	Hs.24684	KIAA1376 protei	TMSS	11.7
	426780	U65011 BE242284	Hs.30743	preferentially	TM	11.2
	415323	BE269352	Hs.172199	adenylate cycla	TM,guanylate_cyc	11.1
50	423508	AW604297	Hs.949 Hs.129711	neutrophil cyto	TM,SH3,TPR	11.0
-	408380	AF123050	Hs.44532	hepatitis A vir	TM,SS,ig	11.0
	448410	AK000227	Hs.21126	diubiquitin hypothetical pr	TM,ubiquitin,7tm_3,ANF_receptor,sushi,7tm_1	11.0
	451277	AK001123	Hs.26176	hypothetical pr	TM TM	.11.0
	453165	\$74727	Hs.32042	aspartoacylase	TM	10.8
55	418036	Z37976	Hs.83337	latent transfor	SS,TB,EGF	10.8 10.5
	431512	BE270734	Hs.2795	factate dehydro	TM,idh	10.3
	433862	D86960	Hs.3610	KIAA0205 gene p	TMSS	10.3
	431211	M86849	Hs.5566	gap junction or	TM.connexin	10.2
	432579	AF043244	Hs.278439	nucleolar prote	TM	10.0
60	439653	AW021103	Hs.6631	hypothetical pr	TM.SS	9.9
	428862	NM_000346	Hs.2316	SRY (sex-determ	TM.HMG_box	9.8
	410762	AF226053	Hs.66170	HSKM-B protein	SS,zf-MYND	9.8
	452431	U88879	Hs.29499	toff-like recep	TM,SS,TIR,LRRCT	9.5
60	405121	AB028989	Hs.88500	mitogen-actival	SS,vwa,vwd,TIL,Cys_knot,vwc	9.5
65	449625	NM_014253	Hs.23796	odz (odd Oz/ten	SH2,EGF	9.4
	421659	NM_014459	Hs.106511	protocadherin 1	TM,SS,cadherin	9.2
	427283	AL119796	Hs.174185	ectonucleotide	TM,SS,Phosphodiest,Somatomedin_B	9.1
	407975	X89426	Hs.41716	endothelial cel	SS,IGFBP	8.9
70	413554	AA319146	Hs.75426	secretogramin I	TM,SS,Granin	8.6
70	418693	A1750878	Hs.87409	thrombospondin	EGF.TSPN.tsp_1,tsp_3,vwc	8.6
	437672	AW748265	Hs.5741	flavohemoprotei	TM,heme_1,oxidored_fad,Cyt_reductase	8.6
	430268	AK000737	Hs.237480	hypothetical pr	TM,SS	8.5
	447850	AB018298	Hs.19822	SEC24 (S. cerev	TM	8.4
75	435717	AF227905	Hs.105794	UDP-glucose:gly	TM,Glyco_transf_8	8.3
13	433376	AI249361	Hs.74122	caspase 4, apop	TM,ICE_p20,ICE_p10,CARD	8.2
	419490	NM_006144	Hs.90708	granzyme A (gra	TM,SS,trypsin	8.2
	453033	AA325869	Hs.31463	KIAA0281 gene p	TM	8.2
	432328	Al572739	Hs.195471	6-phosphotructo	TM6PF2KPGAM	7.9
80	413719	BE439580	Hs.75498	small inducible	SS,ILB	7.9
50	412448 424247	L12964 X14008	Hs.73895	tumor necrosis	TM,SS,TNFR_c6	7.9
	421991	NM_014918	Hs.234734 Hs.110488	lysozyme (renal	SS.tys	7.8
	400793	AA635062	Hs.50094	KIAA0990 protei Homo sapiens mR	SS TM PIP CAPP - CTUP	7.8
	100,00		13.50034	servino patricios mix	TM,BIR,CARD,zf-C3HC4	7.7

	414646	AA353776	Hs.901	CO48 antigen (B	TMig	7.6
	418372	AA311833	Hs.84318	replication pro	TM	7.6
	408418	AW963897	Hs.44743	KIAA1435 protei	TM_WD40,FYVE	7.6
-	425354	U52027	Hs.155935	complement comp	TM,7tm_1	7,5
5	432753	NM_014075	Hs.278915	PRO0593 protein	TM.pkinase	7.4
	447045	AA326187	Hs.17170	G protein-coupt	TM,7tm_1	7.4
	410577	X91911	Hs.64839	glioma pathogen	TM,SCP	7.4
	422631	BE218919	Hs.118793	hypothetical pr	TM	7.3
10	417022	NM_014737	Hs.80905	Ras association	TM,RA	7.2
10	430105	X70297	Hs.2540	cholinergic rec	TM,neur_chan	7.2
	451621	AJ879148	Hs.26770	fatty acid bind	TM, SS, lipocatin	7.2
	415138	C18356	Hs.78045	tissue factor p	Kunitz_BPTI,G-gamma	7.2
	426028 434098	NM_001110	Hs.172028	a disintegrin a	TM, SS, disintegrin, Reprotysin	7.2
15	426423	AW662958	Hs.75825	pleiomorphic ad	TMLzI-CZHZ	7.1
13	412783	NM_012446	Hs.169833	single-stranded	TM	7.1
	431556	BE276738	Hs.74578	DEAD/H (Asp-Glu	TM,dsmn,heficase_C	7.1
	420018	AF016028 U56387	Hs.260039	sarcospan (Kras	TM	6.9
	444042	NM_004915	Hs.94376	proprotein conv	TM,SS,Peptidase_S8,P	6.9
20	432656	NM_000246	Hs.10237 Hs.3076	ATP-binding cas	TM_ABC_tran	6.9
	430066	A1929659	Hs.237825	MHC class II tr	TMLRR	6.9
	401539	14353033	15.231023	signal recognit	TM,TPR	6.9
	416058	L08895	Hs.78995	MADS box transc	TM,SS,zf-8_box,zf-C3HC4,Lysyl_oxidase TM,SRF-TF	6.8
	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu	TM.SAP	6.8
25	424063	NM_002019	Hs.138671	fms-related by	TM,SS,pkinase,ig	6.7
	418026	BE379727	Hs.83213	fatty acid bind	TM,SS,Ripocatin	6.7
	438619	AB032773	Hs.6341	TU12B1-TY prote	TM	6.6
	408741	M73720	Hs.646	carboxypeptidas	SS,Zn_carbOpept,Propep_M14	6.6
	403549		. 4.0		TM.pkinase	6.6 6.6
30	435798	BE395289	Hs.12720	elF4E-transport	TM	6.6
	453070	AK001465	Hs.31575	SEC63, endoptes	TM.SS.DnaJ	6.6
	452092	BE245374	Hs.27842	hypothetical pr	TM,SS,Acyltransferase	6.5
	437396	BE140396	Hs.21621	hypothetical pr	TM	6.4
~-	402474			.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	TM,Peptidase_C1	8.4
35	401600	BE247275	Hs.151787	U5 snRNP-specif	TM,SS,HECT	6.4
	415076	NM_000857	Hs.77890	guanylate cycla	TM,guanylate_cyc	5.4
	430335	D80007	Hs.239499	KIAA0185 protei	TM,S1	6.3
	434203	BE262677	Hs.283558	hypothetical pr	TM	6.2
40	430287	AW182459	Hs.125759	ESTs, Wealtly si	TM.SS	6.2
40	417259	AW903838	Hs.81800	chandraitin sul	TM,Xlink,lectin_c,sushi,EGF,ig	6.1
	421202	AF193339	Hs.102506	eukaryotic tran	TM,SS	6.1
	452235	AL039743	Hs.28514	Homo sapiens mR	TM	6.0
	429653	NM_005955	Hs.211581	metal-regulator	TM,zI-C2H2	6.0
45	444484	AK002126	Hs.11260	hypothetical pr	TM	5.9
42	410193	AJ132592	Hs.59757	zinc finger pro	TM,zf-C2H2	5.9
	425361	AA355933	Hs.132221	Homo sapiens cD	TM	5.9
	410361	BE391804	Hs.62661	guanylate bindi	TM,SS,G8P	5.8
	415714	NM_002290	Hs.78672	laminin, alpha	TM,SS,taminin_G,taminin_EGF	5.8
50	421689 443837	N87820	Hs.106826	hypothetical pr	TM,SS,PHD	5.8
50	422544	AI984625	Hs.9884	spindle pole bo	SS	5.8
	412584	AB018259 X54870	Hs.118140	KIAA0716 gene p	TM	5.7
	410425	BE278367	Hs.74085	DNA segment on	TM,tectin_c	5.7
	426283	NM_003937	Hs.63510 Hs.169139	KIAA0141 gene p	TM	5.7
55	430440	X52599	Hs.2561	kynureninase (L	TM	5.7
	413551	BE242639	Hs.75425	nerve growth fa ubiquitin assoc	TM,SS,NGF	5.7
	418250	U29926	Hs.83918	adenosine monop	TM,SS,UBA	5.7
	419839	U24577	Hs.93304	phospholipase A	TMA_deaminase SS	5.6
	430253	AK001514	Hs.236844	hypothetical pr	TM	5.6
60	450447	AF212223	Hs.25010	hypothetical pr	TM,ANF_receptor,guarrylate_cyc,pkinase	5.6 5.6
	414020	NM_002984	Hs.75703	small inducible	SS,IL8	5.6
	414844	AA296874	Hs.77494	deoxyguanosine	SS,dNK	5.6
	416498	U33632	Hs.79351	potassium chann	TM	5.6
	430512	AF182294	Hs.241578	U6 snRNA-associ	SS	5.6
65	419929	U90268	Hs.93810	cerebral cavern	SS,ank,Band_41	5.5
	407094	AF000574	Hs.22405	leukocyte Immun	TM,SS.ig	
	411653	AF070578	Hs.71168	Homo sapiens d	TM,SS,Aa_trans	5.5 5.5
	452355	N54926	Hs.29202	G protein-count	TM,7tm_1	5.5
70	440486	BE243513	Hs.7212	hypothetical pr	TM	5.5
70	444825	AW167613	Hs.248	mitogen-activat	TM,SS,pkinase	5.5
	447072	D61594	Hs.17279	tyrosylprotein	SS	5.4
	453392	U23752	Hs.32964	SRY (sex determ	TM,HMG_box	5.4
	411213	AA676939	Hs.69285	neuropilin 1	TM,CUB,F5_F8_type_C,MAM	5.4
75	429688	8E245169	Hs.211510	CUG triplet rep	TM.rm	5.4
75	405257				TM	5.4
	414911	NM_000107	Hs.77602	damage-specific	TM,WD40	5.3
	430598	AK001764	Hs.247112	hypothetical pr	TM	5.3
	428753	AW939252	Hs.192927	hypothetical pr	TMSS	5.3
80	406625	Y13647	Hs.119597	stearcyl-CoA de	TM,Desaturase	5.3
80	405475	44004444			TM,sugar_tr	5.3
	430180	AA331406	Hs.75456	A kinase (PRKA)	TM	5.3
	417381	AF164142	Hs.82042	solute certier	TM_xan_ur_permease	5.3
	433029	NM_014322	Hs.279926	opsin 3 (enceph	TM,7tm_1	5.3

	417355	D13168	LL 02002	and the Ferman	THE CO. 71-1 4 COURT		
			Hs.82002	endothelin rece	TM,SS,7tm_1,zI-C3HC4	5.3	
	412420	AL035668	Hs.73853	роче шольноденя	SS,TGFb_propeptide,TGF-beta	5.2	
	416975	NM_004131	Hs.1051	granzyme B (gra	SS, trypsin	5.2	
_	451418	8E387790	Hs.26369	hypothetical pr	TM	5.2	
5	425322	U63630	Hs.155637	protein kinase,	TM,MCM,FAT,FATC,PI3_PI4_kinase	5.2	
	415910	U20350	Hs.78913	chemokine (C-X3	TM,7tm_1	5.2	
	428593	AW207440	Hs.185973				
				degenerative sp	TM	5.2	
	417696	BE241624	Hs.82401	CD69 antigen (p	TM,lectin_c	5.2	
• •	442991	BE281238	Hs.8886	hypothetical pr	TM	5.2	
10	420567	AK000812	Hs.98874	similar to prof	TM	5.1	
	412676	NM_000165	Hs.74471	gap junction pr	TM.connexin	5.1	
	423430	AF112481	Hs.128501	RAD54, S. cerev			
					TM,SNF2_N,helicase_C	5.1	
	421633	AF121860	Hz.106260	sorting nextin 1	TMPX	5.1	
16	436943	AA773838	Hs.5353	caspase 10, apo	20,DEDم_10,ICE و_TM,ICE	5.1	
15	414696	AF002020	Hs.76918	Niemann-Pick di	TM,SS,Patched	5.1	
	446312	BE087853		gb:QV1-BT0681-2	TM	5.0	
	420397	NM_007018	Hs.97437	centrosomal pro	TM	5.0	
	410274	AA381807	Hs.61762		SS		
	710274	A-00 1007	113.01702	hypoxia-inducib	55	5.0	
20	TAN 6 446						
20	TABLE 368						
	Pkey:	Uniq	ue Eos probese	et identifier number			
	CAT numb		duster numbe				
	Accession:		ank accession				
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25	Ohau	C47	A				
23	Pkey	CAT number					
	446312	671114_1	BE087853 A	J286184			
	TABLE 360	C:					
	Pkey:		ue number con	responding to an Eos probe	e cet		
30	Ref:						
30	FVEI.	Octi	ATICE SOUICE.	The Folgit numbers in this	column are Genbank Identitier (GI) numbi	ers. "Dunham, et al." refers to the publication entitled "	The DNA
					et al. (1999) Nature 402:489-495.		
	Strand:			id from which exons were p			
	Nt_position	n: Indic	ates nucleotide	positions of predicted exor	15.		
	_			,			
35	Pkey	Ref	Strand	Att pacifies			
-	401539			Nt_position			
		8072433	Minus	62028-62608			
	402474	7547175	Minus	53528-53628,55755-5592	20,57530-57757		
	403549	8081591	Minus	137150-137362			
	405257	7329310	Plus	73121-73273			
40	405475	1931025	Plus	1548-1702			
	TARIE 37	A- ABOLIT 280	CENES DOW	N DECLII ATED IN VIDUE	CANCED		
	TABLE 37	A: ABOUT 280	GENES DOW	N-REGULATED IN KIDNEY	CANCER		
15	Table 37A	lists about 280	genes significa	N-REGULATED IN KIDNEY andy down-regulated in kidn	CANCER ey cancer opmpared to normal kildney Ti	nese were selected as for Table 35A, except that the r	numerator and
45	Table 37A denominat	A: ABOUT 280 lists about 280 or were switch	genes significa	N-REGULATED IN KIDNEY antly down-regulated in kidn	CANCER ey cancer compared to normal kidney Ti	nese were selected as for Table 35A, except that the r	numerator and
45	Table 37A	lists about 280 or were switch	genes significa ed.	N-REGULATED IN KIDNEY antly down-regulated in kidn et identifier number	CANCER ey cancer compared to normal kidney T	nese were selected as for Table 35A, except that the $lpha$	numerator and
45	Table 37A denominat	lists about 280 for were switch: Unit	genes significa ed. jue Eos probes	ently down-regulated in kidn et identifier number	ey cancer compared to normal kidney Ti	nase ware selected as for Table 35A, except that the r	numerator and
45	Table 37A denominat Pkey: ExAccn:	lists about 280 for were switch Unic Exe	genes significa ed. pue Eos probes mplar Accessio	antly down-regulated in kidn	ey cancer compared to normal kidney Ti	nese were selected as for Table 35A, except that the o	numerator and
45	Table 37A denominat Pkey: ExAccn: Unigenel0	lists about 280 for were switch Unic Exe ): Unic	genes significa ed. que Eos probes mplar Accessio pene number	ently down-regulated in kidn et identifier number	ey cancer compared to normal kidney Ti	nese were selected as for Table 35A, except that the $lpha$	numerator and
	Table 37A denominat Pkey: ExAccn: UnigenelD Unigene T	lists about 280 for were switch Unic Exe b: Unic lite: Unic	genes significa ed. jue Eos probes mplar Accessio jene number jene gene title	antly down-regulated in kidn et identifier number n number, Genbank access	ey cancer compared to normal kidney Ti	nese were selected as for Table 35A, except that the r	numerator and
45 50	Table 37A denominat Pkey: ExAccn: Unigenel0	lists about 280 for were switch Unic Exe b: Unic lite: Unic	genes significa ed. que Eos probes mplar Accessio pene number	antly down-regulated in kidn et identifier number n number, Genbank access	ey cancer compared to normal kidney Ti	nese were selected as for Table 35A, except that the o	numerator and
	Table 37A denominat Pkey: ExAccn: Unigenel0 Unigene T R1:	lists about 280 for were switche Units Exe b: Units itle: Units Rati	genes significa ed. jue Eos probes mplar Accessio jene number jene gene title o of normal to t	antly down-regulated in kidn et identifier number n number, Genbank access	ey cancer compared to normal kidney Ti	nese were selected as for Table 35A, except that the r	numerator and
	Table 37A denominat Pkey: ExAccn: UnigenelD Unigene T	lists about 280 for were switch Unic Exe b: Unic lite: Unic	genes significa ed. jue Eos probes mplar Accessio jene number jene gene title	antly down-regulated in kidn et identifier number n number, Genbank access	ey cancer compared to normal kidney Ti		numerator and
	Table 37A denominat Pkey: ExAccn: Unigenel0 Unigene T R1:	lists about 280 for were switche Units Exe b: Units itle: Units Rati	genes significa ed. jue Eos probes mplar Accessio jene number jene gene title o of normal to t	antly down-regulated in kidn et identifier number n number, Genbank access urmor tissue UnigeneTide	ey cancer compared to normal kidney Ti	RI	numerator and
	Table 37A denominat Pkey: ExAccn: UnigenelD Unigene T R1: Pkey 425260	lists about 280 for were switch Unic Exe b: Uniq itle: Uniq Rati  ExAccn L47726	genes significated.  Jue Eos probes mplar Accessio gene number gene gene title o of normal to t  UnigeneID Hs.1870	antly down-regulated in kidn et identifier number n number, Genbank access urnor tissue UnigeneTide phenytatanine hydroxylae	ey cancer opmpared to normal kildney Ti sion number	R1 50.20	numerator and
50	Table 37A denominat Pkey: ExAccn: UnigenetD Unigene T R1: Pkey 425260 445835	lists about 280 or were switch Unix Exe b: Unix itle: Unix Rati  ExAccn L47726 A1769774	genes significated.  jue Eos probes implar Accessio jene number jene gene title o of normal to t  UnigeneID Hs.1870 Hs.209831	antly down-regulated in kidnet identifier number on number, Genbank access urnor tissue UnigeneTide phenytalanine hydroxytes ESTs, Weakly similar to .	ey cancer opmpared to normal kildney Ti sion number	R1 50.20 48.14	numerator and
	Table 37A denominat Pkey: ExAccn: Unigened Unigene T R1: Pkey 425260 445835 440243	lists about 280 for were switch Unide Exe it: Unig (itle: Unig Rati  ExAcon L47726 A1769774 BE301029	genes significated.  jue Eos probes mplar Accessio gene number gene gene title o of normal to t UnigeneID Hs. 1870 Hs. 209831 Hs. 226422	et Identifier number n number, Genbank access umor tissue UnigeneTitle phenytalanine hydroxylas ESTs, Weakly similar to , ESTs	ey cancer compared to normal kidney Ti sion number se alu1_HUMAN ALU S	R1 50.20 48.14 42.54	numerator and
50	Table 37A denominat Pkey: ExAccn: Unigenel O Unigene T R1: Pkey 425260 445835 440243 431657	lists about 280 or were switch Unite Exe it: Unit ille: Unit Rati  ExAcon L47726 A1769774 BE301029 A1345227	genes significated. Julie Eos probes mplar Accessio jene number jene gene title o of normal to the UnigeneID Hs. 1870 Hs. 209831 Hs. 226422 Hs. 105448	et identifier number n number, Genbank access umor tissue UnigeneTide phenytalanine hydroxytae ESTs, Weakly similar to / ESTs, Weakly similar to / ESTs, Weakly similar to /	ey cancer compared to normal kidney Ti sion number se alu1_HUMAN ALU S	R1 50.20 48.14 42.54 40.14	numerator and
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_	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	15.46
5	436637	AI783629	Hs.26766	ESTs	15.18
	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	14.52
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	453685	AL110309	115,50035	gb:DKFZp564L0278_r1 564 (synonym; hfbr2)	13.48
10	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	13.24
	436624	T64297	Hs.5241	fatty acid binding protein 1, liver	13.05
	428931	AA994979	Hs.98967	ATPase, H(+)-transporting, lysosomal, no	12.97
	424823 431713	NM_006226 AK000388	Hs.153322 Hs.267997	phospholipase C, epsilon EHM2 gene	12.66 12.66
15	436679	AJ127483	Hs. 120451	ESTs, Weakly similar to unnamed protein	12.36
	413859	AW992356	Hs.8364	pyruvate dehydrogenase kinase, isoenzyme	12.32
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	11.92
	440504	AI948966	Hs.130017	ESTs, Weakly similar to VATX_HUMAN VACUO	11.66
20	417275 410929	X63578 H47233	Hs.81849 Hs.30643	parvalbumin ESTs	11.48 11.40
	427167	AI239607	Hs.99196	ESTs	11.34
	445591	AJ471866	Hs.149095	ESTS	11.30
	443622	AI911527	Hs.11805	ESTs .	11.23
25	438935 · 438451	H40665 AW075485	Hs.31564	ESTs	11.16
23	415539	A1733881	Hs.286049 Hs.72472	phosphoserine aminotransferase ESTs	11.00 10.84
	438081	H49546	Hs.298964	ESTs	9.76
	421688	AK000307	Hs.106825	hypothetical protein FLJ20300	9.74
20	407280	AJ241296	Hs.145609	ESTs	9.71
30	427969 442448	NM_001963	Hs.2230	epidermal growth factor (beta-urogastron	9.61
	442308	A1733144 AA989402	Hs.129611 Hs.45194	ESTs ESTs	9.52 9.51
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	9.35
3.5	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating:	9.32
35	418068	AW971155	Hs.293902	ESTs, Weakly similar to prolyl 4-hydroxy	9.31
	459247 423629	N46243 AW021173	Hs.110373 Hs.18612	ESTS	9.20
	410247	AF181721	Hs.61345	Homo saplens cDNA: FLJ21909 fis, clone H RU2S	9.16 9.10
	430573	AA744550	Hs.136345	ESTs	9.08
40	457411	AW085961	Hs.130093	ESTs	8.99
	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chai	8.92
	435024 435058	AI863518 AW023337	Hs.127743 Hs.5422	ESTs, Wealdy similar to V-ATPase G-subun	8.76 8.74
	426451	At908165	Hs.169946	glycoprotein M6B GATA-binding protein 3	8.50
45	450648	AI703366	Hs.26766	ESTs	8.38
	426255	BE262530	Hs.2006	glutathione S-transferase M3 (brain)	8.31
	431820	AW410408	Hs.271167	L-pipecolic acid oxidase	8.28
	451027 435823	AW519204 R07856	Hs.40808 Hs.16355	ESTS	8.10 8.06
50	429269	AA449013	Hs.99203	ESTs	8.02
	438199	AW016531	Hs.122147	ESTs .	7.94
	442176	AA983764	Hs.128910		7.94
	450164 445627	AI239923 AW818475	Hs.30098	ESTs	7.86
55	445779	AJ253104	Hs.7363 Hs.189267	ESTs ESTs	7.85 7.82
•-	407178	AA195651	Hs.104106		7.68
	426966	AM93134	Hs.159125		7.68
	445659	AW300508	Hs. 149229	ESTs	7.50
60	403204 448037	AW195634	Hs.170401	ESTs	7.46 7.30
•	413589	AW452631	Hs.258811		7.26
	446063	AJ720140	Hs.151079		7.26
	424626	AA344308	Hs.128427	ESTs	7.25
65	403381 414807	A1738616	Hs.77348	hudesus assessable leading debudence and 45 Mil	7.16
05	432102	AW015506	Hs.130730	hydroxyprostaglandin dehydrogenase 15-(N ESTs	7.12 7.12
	442315	AA173992	Hs.7956	ESTs	7.10
	453698	AA037615	Hs.42746	ESTS	7.02
70	415003	M11437	Hs.77741	kininogen	6.95
70	426418 452883	M90464 X80031	Hs.169825 Hs.150318		6.92
	408621	A1970672	Hs.46638	chromosome 11 open reading frame 8	6.88 6.76
	410781	AI375672	Hs.165028		6.74
75	424596	AB020639	Hs.151017		6.66
75	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	6.66
	451099 437553	R52795 AI829935	Hs.25954 Hs.130497	interleukin 13 receptor, alpha 2 ESTs, Wealdy similar to MATS_HUMAN CHLOR	6.64 6.63
	445285	U03886	Hs.264	GS2 gene	6.54
00	408427	AW194270	Hs.177236	ESTs .	6.52
80	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	6.46
	457001 420205	J03258 AA256395	Hs.2062 Hs.88156	vitamin D (1,25- dihydroxyvitamin D3) re ESTs	6.46 6.42
	441364	AW450466	Hs. 126830		6.36

	425649	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	6.34
	405373				6.32
	431322 440094	AW970622 AI651558	Hs.270372	gb:EST382704 MAGE resequences, MAGK Homo ESTs	6.32
5	442764	A1762254	Hs.131122	ESTs	6.27 6.21
-	424433	H04607	Hs.9218	ESTs	6.20
	415025	AW207091	Hs.72307	ESTs *	6.16
	428927 439145	AA441837	Hs.90250 Hs.269187	ESTs	6.16
10	424583	H57348 N87519	Hs.27196	ESTs ESTs	6.06 6.04
	415314	N88802	H3.5422	glycoprotein M6B	5.94
	424025	AJ701852	Hs.301296	ESTS	5.90
	445911	AI985987	Hs.145645	ESTs. Moderately similar to ALU1_HUMAN A	5.89
15	417332 440102	AW972717 AI672443	Hs.288462 Hs.131190	Homo sepiens cDNA: FLJ21511 fis, clone C ESTs	5.86 5.84
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	5.82
	411556	AF106564	Hs.71346	neurofilament 3 (150kD medium)	5.82
	445224	AW450551	Hs.13308	ESTs	5.74
20	422305 436802	A1928242 N34486	Hs.293438 Hs.170504	ESTs, Highly similar to AF198488 1 trans ESTs	5.72 5.72
	412452	AA215731	Hs.283446	ESTs, Weakly similar to ALAT_HUMAN ALANI	5.70
	445611	AW41B497	Hs.145583	EST8	5.66
	440038	AA881627	Hs.243989	ESTs	5.66
25	424028 410530	AF055084 M25809	Hs.153692 Hs.64173	KIAA0686 protein ESTs, Highty similar to VAB1_HUMAN VACUO	5.61 5.60
	425907	AA365752	Hs.155965	ESTs	5.60
	428523	AW974540	Hs.98626	ESTs	5.58
	429918 408369	AW873986	Hs.119383 Hs.182575	ESTs	5.58
30	446163	R38438 AA026880	Hs.25252	solute carrier family 15 (H+/peptide tra Homo sapiens cDNA FLJ 13603 fis, clone PL	5.56 5.56
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	5.52
	418504	BE159718	Hs.85335	Homo sapiens mRNA; cDNA DKFZp564D1462 (f	5.51
	440666 432286	AA902650 AW327432	Hs.192742 Hs.255843	Homo sapiens cDNA FLJ12785 fis, clone NT ESTs	5.50
35	451236	A1767406	Hs.207026	ESTs, Weakly similar to B56205 transcrip	5.48 5.46
	422746	NM_004484	Hs.119651	glypican 3	5.43
	416426 414449	AA180256 AA557660	Hs.210473 Hs.76152	ESTs, Weakly similar to GELS_HUMAN GELSO	5.37
	445898	AF070623	Hs.13423	decorin Homo sapiens cione 24468 mRNA sequence	5.36 5.34
40	451835	T63643	Hs.209715	ESTs, Weakly similar to ALU7_HUMAN ALU S	5.32
	424566	M16801	Hs.1790	nuclear receptor subfamily 3, group C, m	5.22
	408604 456576	D51408 AA287443	Hs.21925	ESTs gb:zs52c10.r1 NCI_CGAP_GC81 Homo sapiens	5.18 5.18
4.5	433212	BE218049	Hs.121820	ESTs	5.16
45	452114	N22687	Hs.8236	ESTs	5.14
	458072 443005	AJ890347 AJ027184	Hs.271923 Hs.200918	Homo sepiens cDNA: FLJ22785 fis, clone K ESTs	5.14 5.14
	408554	AA836381	Hs.7323	ESTs	5.12
50	438609	T62870	Hs.291991	ESTs	5.10
50	429343 452223	AK000785 AA425467	Hs.199480	epsin 3 ESTs	5.10
	446925	AW974605	Hs.8035 Hs.176669	ESTS	5.10 5.09
	407664	AW063476	Hs.279080	ESTs	5.08
55	414664	AA587775	Hs.66295	Homo sapiens HSPC311 mRNA, partial cds	5.06
7,7	40797B 435343	AW385129 AW194962	Hs.41717 Hs.199028	phosphodiesterase 1A, calmodulin-depende ESTs	5.04 5.04
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothellal (venous	5.04
	442317	AI915599	Hs.129225	ESTs	5.02
60	404319 433637	AW024214	Hs.135405	ESTs	5.02
O O	440205	T86950	Hs.188465	ESTS	4.92 4.84
	432029	D31628	Hs.2899	4-hydroxyphenylpyruvate dioxygenase	4.83
	453125	AW779544	Hs. 115497	Homo sapiens cDNA: FLJ22655 fis, clone H	4.80
65	407788 439750	BE514982 AL359053	Hs.38991 Hs.57664	S100 calcium-binding protein A2 Homo sapiens mRNA full length insert cDN	4.78
•••	443633	AL031290	Hs.9654	similar to pregnancy-associated plasma p	4.75 4.74
	449050	AW302858	Hs.187333	ESTs	4.69
	422237 442476	M13149 AF069475	Hs.1498	histidine-rich glycoprotein	4.67
70	431130	NM_006103	Hs.2719	gb:AF069475 Homo sapiens astrocytoma lib epididymis-specific, whey-acidic protein	4.64 4.58
	440624	AF017987	Hs.7306	secreted frizzled-related protein 1	4.58
	403046	000044		POT	4.51
	450838 455887	R65841 BE154173	Hs.28653	ESTs gb:PM1-HT0340-201299-004-112 HT0340 Homo	4.48 4.47
75	453500	A1478427	Hs.43125	ESTs	4.40
	405701	419.4 *****			4.37
	426657 451032	NM_015865 W03692	Hs.171731 Hs.25832		4.37
	426200	AA371876	Hs.234786	Homo sapiens mRNA; cDNA OKFZp564P116 (fr KIAA0707 protein	4.37 4.35
80	418836	AI655499	Hs.161712	ESTs	4.34
	447754 438209	AW073310 AL120659	Hs.163533		4.32
	404559	UP 150000	Hs.6111	KIAA0307 gene product	4.23 4.22
					7.66

	413272	AA127923	Hs.293256	ESTs	4.21
	423068	M25629	Hs.123107	kalikrein 1, renal/pancreas/safivary	4.19
	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcom	4.18
5	445512 445177	A1241246 A1215070	Hs.148903 Hs.16135	EST ESTs	4.17
,	448475	BE613134	Hs.247474	Homo sapiens cDNA: FLJ21032 fis, clone C	4.16 4.14
	402072				4.09
	439285	AL133916	Hs.298998	ESTs	4.02
10	429621 450273	AI823386 AW296454	Hs.130874 Hs.24743	Homo sapiens cDNA FLJ14181 fts, clone NT	3.99
10	453511	AL031224	Hs.33102	hypothetical protein FLJ20171 transcription factor AP-2 beta (activati	3.97 3.94
	452620	AA436504	Hs.119286	ESTs	3.92
	425642	X91220	Hs.158462	solute carrier family 12 (sodium/chlorid	3.91
15	435884 416689	AA701443	Hs.192868	ESTs	390
13	419677	AW250318 N77342	Hs.80395 Hs.21851	mal, T-cell differentiation protein Homo sapiens cDNA FLJ12900 fis. clone NT	3.89 3.88
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	3.84
	456844	AJ264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	3.82
20	442306	AI820660	Hs.129205	ESTs	3.82
20	438453 407198	D17056 H91679	Hs.288959	Homo sapiens cDNA: FLJ20920 fis, clone A gb:yv04e07.s1 Soares fetal liver spleen	3.81
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	3.80 3.79
	413841	M34276	Hs.75576	plasminogen	3.77
25	431161	AA493591		gb:nh01a12.s1 NCI_CGAP_Thy1 Homo sepiens	3.76
23	428544 453903	AA430034 AW299606	Hs.191611 Hs.232777	ESTs ESTs	3.74
	434061	AW024973	Hs.283675	NPD009 protein	3.74 3.73
	444805	AB007899	Hs.12017	KIAA0439 protein; hornolog of yeast ubiqu	3.73
20	440080	AW051597	Hs.143707	ESTs	3.71
30	440230 428735	AJ732970 AJ279246	Hs.126246	ESTs	3.70
	421832	NM_016098	Hs.192657 Hs.108725	NPHS2 gene (podocin) HSPC040 protein	3.68 3.66
	430135	NM_000035	Hs.234234	aktolase B, fructose-bisphosphate	3.65
25	453055	AW291436	Hs.31917	ESTs	3.65
35	450696 440232	A1654223	Hs.16026	Homo sapiens cDNA: FLJ23191 fis, clone L	3.59
	432099	A1766925 U20760	Hs.112554 Hs.272429	ESTs calcium-sensing receptor (hypocalcluric	3.57 3.57
	445924	AI264671	Hs.164166	ESTs	3.56
40	411356	H45377		gb:yn99h03.r1 Soares adult brain N2b5HB5	3.56
40	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.55
	413752 416298	BE161807 NM_003891	Hs.1011	gb:MR3-HT0446-300300-203-h01 HT0446 Homo protein Z, vitamin K-dependent plasma gi	3.53
	423603	AB007880	Hs.129883	KIAA0420 gane product	3.53 3.53
46	436610	AW611912	Hs.120414	ESTs	3.50
45	425905	AB032959	Hs.161700	KIAA1133 protein	3.48
	403625 425210	AA054679	Hs.155150	ethanualacea D (14th D)	3.47
	430168	AW968343	Hs.300896	ribonuclease P (14kD) ESTs, Highly similar to AF128113 1 promi	3.45 3.42
50	448877	AI583696	Hs.253313	ESTs	3.40
50	456586	A1554303	Hs.35982	Homo sapiens cDNA FLJ12776 fis, clone NT	3.38
	414725 453574	AA769791 AI767947	Hs.120355 Hs.50841	Homo sapiens cDNA FLJ 13148 fls, ctone NT ESTs, Weakly similar to tuftelin [M.musc	3.37
	438535	L09078	15.50011	gb:Homo sapiens mRNA fregment	3.32 3.31
<i></i>	414040	N58513	Hs.32171	ESTs	3.30
55	451416	AW631469	Hs.203213	EST8	3.30
	444554 408001	AI167877 AA046458	Hs.143716 Hs.95296	ESTs ESTs	3.29
	406666	V00495	Hs.75442	abumin	3.27 3.24
60	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	3.24
60	445337	NM_013280	Hs.12523	fibronectin leucine rich transmembrane p	3.23
	423968 427209	AF098277 H05509	Hs.136529	solute carrier family 23 (nucleobase tra	3.21
	403442	180003	Hs.92423	KIAA1566 protein	3.20 3.20
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	3.19
65	425548	AA890023	Hs.1906	protactin receptor	3.17
	414502	AL133721	Hs.224680	EST ₆	3.16
	427811 436330	M81057 NM_004413	Hs.180884 Hs.109	carboxypeptidase B1 (tissue)- dipeptidase 1 (renal)	3.14
	433942	AW272166	Hs.123465		3.11 3.11
70	408692	AL040127	Hs.34074	dipeptidylpeptidasa VI	3.10
	448819	AI589190	Hs.188372		3.10
	423041 454554	BE170842 AW847505	Hs.123123		3.10
	405664	L34041	Hs.25478	gb:RC0-CT0210-280999-021-c10 CT0210 Homo glycerol-3-phosphate dehydrogenase 1 (so	3.10 3.10
75	449850	AW206292	Hs. 199751	ESTs	3.08
	427450	AB014526	Hs.178121	KIAA0626 gene product	3.08
	454788	AW820691	14- 2044	gb:RC5-ST0300-300100-012-H06 ST0300 Homo	3.06
	444895 457782	AI874383 N54493	Hs.301192		3.06
80	429023	NM_000312	Hs.2351	gb:yv40g05.s1 Soares fetal fiver spteen protein C (inactivator of coagulation (a	3.05 3.05
_	427041	AI693661	Hs.97557	ESTs	3.01
	434788	AF154121	Hs.102867	sodium-dependent high-affinity dicarboxy	3.01
	419003	T78640	Hs.268595	ESTs	3.01

	TABLE 378	Ŀ			
	Pkey:		a Eos probeset	identifier number	
-	CAY number		cluster number		
5	Accession:	Genb	ank accession i	numbers	
	Ok	CAT aumber			
	Pkøy 411356	CAT number 1240273_1	Accession	37 AW838640	
	413752	1386338_1		161584 BE161700 BE161748	
10	431161	328713_1		829120 AA533792	
	431322	331543_1		A503009 AA502998 AA502989 AA502805 T92188	
	438535	45946_1		IS L09094 L09098 L03165 L09102	
	442476	543547_1		069477 AF069476	
15	453685 454554	977734_1		V088119 H22881	
1.5	******	1223842_1	AWR06001 A	MO11732 BEU01942 BEU01433 AYYO473UG AYYOUSSII AYY WRIANRS AWRNEODS BENEIEEG AWRNINNS BEIACEEG AWR	106996 BE061436 BE061430 BE142460 BE146499 AW806994 AW809158 106995 AW807000 AW845743 AW845747 AW847504 BE142458 BE061431
			BE061435 AV	VB47507 RE146650 RE142470 AWR14096 AWR07012 RED	1438 AW807011 AW806993 BE142465 BE142459 BE142462 AW854330
			AW854331 B	E061434 BE061731 BE142464 AW847501 AW807001 BE16	12463 AW811800 BE061437 AW811802 BE061440 AW806997 AW806998
20			BE061745 BE	6061753	
20	454788	12346941	AW820691		
	455887 456578	1380836_1		154098 BE154096	
	457782	201378_1 405265_1		M19385 BE084078 AI478347 19039 N76605	
	407198	403200_1	H91679	3033 11/0003	
25					
	TABLE 37				
	Pkey:			t identifier number	
	Ref: Strand:		ence gi ID d identification		
30	Nt_position		nosomal nucleo	atide position	•
	Pkey	Ref	Strand	Nt_position	
	402072	8117363	Plus	71983-72128	
35	403046 403204	3540153 7622392	Minus	55707-55859,56369-56511	
55	403381	9438267	Plus Minus	16214-16439 26009-26178	
	403442	7210003	Plus	174560-175270	
	403625	8569879	Plus	6551-7111	
40	404319	9211467	Plus	54438-54608	
40	404559 405373	8748893	Minus Plus	73499-73651,89575-89739	
	405701	2076718 4263751	Plus	21294-21575 93243-93364	
15					
45	TABLE 38	A: ABOUT 850	GENES UP-RE	GULATED IN KIDNEY CANCER COMPARED TO NORMAL	ADULT TISSUES
	1 able 38A	that the cutio of	genes up-regul	ated in lidney cancer compared to normal adult tissues. The	ase were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChi
	percentile	emonast variou	s kidney cance	rs. The "average" normal adult tissue level was set to the 70	n or equal to 3.0. The "average" lidiney cancer level was set to the 90th th percentile amongst various non-malignant tissues. In order to remove gene
<b>50</b>	specific ba	ckground levels	s of non-specific	hybridization, the 15th percentile value amongst various no	n-malignant tissues was subtracted from both the numerator and the
50	denomina	tor before the ra	stio was evaluat	ed.	
	Pkey: ExAccn:			at identifier number	
	Unigenel [		TOTAL MODESSIO		
	Unigene 1		tedmus and	n number, Genbank accession number	
55			ene number iene gene tide	n number, Gendank accession number	
	R1:	lide: Unig	ene gene title	n number, Genbank accession number	
	R1;	lite: Unig Rati	ene gene tide o of tumor to no	ormal adult tissues	
	R1: Pkey	litte: Unig Rati ExAccn	ene gene title o of tumor to no UnigenelD		Ri
	R1: Pkey 435013	Title: Unig Rati ExAcca H91923	jene gene title o of tumor to no UnigenelD Hs.110024	ormal adult tissues Unigene Title	15.71
60	R1: Pkey 435013 447768	ExAccn H91923 X88400	jene gene title o of tumor to no UnigenelD Hs.110024 Hs.19520	ormal adult tissues Unigene Title Hs.19520:FXYD domain-containing ion tran	15.71 14.07
60	R1: Pkey 435013	ExAcca H91923 X88400 AJ792241	ene gene title o of turnor to no UnigenelD Hs.110024 Hs.19520 Hs.129614	ormal adult tissues Unigene Title Hs. 19520:FXYD domain-containing ion tran Hs. 129614:kidney-specific membrane prote	15.71 14.07 12.56
60	R1: Pkey 435013 447768 445178 432542 443595	ExAccn H91923 X88400 A1792241 AW083920 AF169312	jene gene title o of tumor to no UnigenelD Hs.110024 Hs.19520	ormal adult tissues Unigene Title Hs.19520:FXYD domain-containing ion tran	15.71 14.07
60	R1: Pkey 435013 447768 445178 432542 443595 413719	ExAcca H91923 X88400 AJ792241 AW083920 AF169312 8E439580	ene gene tite o of tumor to no UnigenelD Hs.110024 Hs.19520 Hs.129614 Hs.16098 Hs.9613 Hs.75498	umal adult tissues Unigene Title Hs. 19520:FXYD domain-containing ion tran Hs. 129614:kidney-specific membrane prote Hs. 16098:claudin 2 NM_0161093:Homo septens anglopoletin-like NM_004591:Homo septens small inducible c	15.71 14.07 12.56 12.41 11.77 10.39
	R1: Pkey 435013 447768 445178 432542 443595 413719 436878	ExAccn H91923 X88400 A1792241 AW083920 AF159312 8E439580 BE465204	lene gene title o of tumor to no UnigeneID Hs.110024 Hs.19520 Hs.129614 Hs.16098 Hs.9613 Hs.75498 Hs.47448	unigene Title  Hs. 19520:FXYO domain-containing ion tran  Hs. 129614:kidney-specific membrane prote  Hs. 16093:ctaudin 2  NM_016103:Homo septens anglopoletin-like  NM_004591:Homo septens small inducible c  Hs. 47448:ESTs	15.71 14.07 12.56 12.41 11.77 10.39 10.18
60	R1: Pkey 435013 447768 445178 432542 443595 413719 436878 440304	ExAccn H91923 X88400 A1792241 AW083920 AF159312 BE439580 BE159984	ene gene tite o of tumor to no UnigenelD Hs.110024 Hs.19520 Hs.129614 Hs.16098 Hs.9613 Hs.75498	umal adult tissues Unigene Title Hs. 19520:FXYD domain-containing ion tran Hs. 129614:kidney-specific membrane prote Hs. 16098:claudin 2 NM_0161093:Homo septens anglopoletin-like NM_004591:Homo septens small inducible c	15.71 14.07 12.56 12.41 11.77 10.39 10.18 9.95
	R1: Pkey 435013 447768 445178 432542 443595 413719 436878 440304 407065	ExAccn H91923 X88400 AJ792241 AW083920 AF169312 BE439580 BE455204 BE159984 Y10141	ene gene tide o of tumor to no UnigenetD Hs.110024 Hs.19520 Hs.129614 Hs.16098 Hs.9613 Hs.75498 Hs.47448 Hs.125395	unigene Title  Hs. 19520:FXYO domain-containing ion tran Hs. 1266 14:kidney-specific membrane prote Hs. 16098:claudin 2 NM_016109:Homo sapiens anglopoletin-like NM_004591:Homo sapiens small inducible c Hs. 47448:ESTs Hs. 125395:ESTs	15.71 14.07 12.56 12.41 11.77 10.39 10.18 9.95 9.58
	R1: Pkey 435013 447768 445178 432542 443595 413719 436878 440304 407065 413049 425983	ExAccn H91923 X88400 A1792241 AW083920 AF159312 BE439580 BE159984	lene gene title o of tumor to no UnigeneID Hs.110024 Hs.19520 Hs.129614 Hs.16098 Hs.9613 Hs.75498 Hs.47448	unigene Title  Hs. 19520:FXYO domain-containing ion tran  Hs. 129614:kidney-specific membrane prote  Hs. 16093:claudin 2  NM_016109:Homo septens anglopoletin-like  NM_004591:Homo septens small inducible c  Hs. 47448:ESTs  Hs. 125395:ESTs  NM_002151:Homo septens hepsin (transmemb	15.71 14.07 12.56 12.41 11.77 10.39 10.18 9.95 9.55 9.51
65	R1: Pkey 435013 447768 445178 432542 443595 413719 436878 440304 407085 413049 425983 423161	ExAccn H91923 X88400 A1792241 AW083920 AF 169312 BE439580 BE455204 BE159984 Y10141 NM_002151 AK000226	unigene gene title of tumor to not UnigenetD Hs.110024 Hs.19520 Hs.129614 Hs.16098 Hs.9613 Hs.75498 Hs.47448 Hs.125395 Hs.823 Hs.165619 Hs.124776	unigene Title  Hs. 19520:FXYO domain-containing ion tran Hs. 1266 14:kidney-specific membrane prote Hs. 16098:claudin 2 NM_016109:Homo sapiens anglopoletin-like NM_004591:Homo sapiens small inducible c Hs. 47448:ESTs Hs. 125395:ESTs	15.71 14.07 12.56 12.41 11.77 10.39 10.18 9.95 9.58
	R1: Pkey 435013 447768 445178 432542 443595 413719 436878 440304 407085 413049 425983 423161 430569	EXACCI Unig Rabi H91923 XB8400 AJ792241 AW083920 AF169312 BE455204 BE155984 Y10141 NM_002151 AK000226 AL049227 AF241254	jene gene tite of furnor to no. UnigenetD Hs.110024 Hs.19520 Hs.19520 Hs.195613 Hs.75498 Hs.47448 Hs.165519 Hs.823 Hs.165619 Hs.124776 Hs.178098	unigene Title  Hs. 19520:FXYD domain-containing ion tran Hs. 129614:kidney-specific membrane prote Hs. 16093:claudin 2 NM_016109:Homo septens anglopoletin-like NM_004591:Homo septens small inducible c Hs. 47448:ESTs Hs. 125395:ESTs  NM_002151:Homo septens hepsin (transmemb Hs. 165619:mucin and cadherin-like Hs. 144776:Homo septens mR: cD DKFZp564N1 Hs. 179089:anglotensin I converting enzym	15.71 14.07 12.56 12.41 11.77 10.39 10.18 9.95 9.59 9.51 8.88 8.77 8.45
65	R1: Pkey 435013 447768 445178 432542 443595 413719 436878 440304 407065 413049 425983 423161 430569 416768	ExAcon H91923 X88400 A1792241 AW083920 AF169312 BE455980 BE455984 Y10141 NM_002151 AK000226 AL049227 AF241254 AA383733	lene gene title of furnor to not UnigenetD Hs.110024 Hs.19520 Hs.129614 Hs.16098 Hs.9613 Hs.75498 Hs.47448 Hs.125395 Hs.823 Hs.165619 Hs.124776 Hs.178098 Hs.1032	unigene Title  Hs. 19520:FXYD domain-containing ion tran Hs. 19520:FXYD domain-containing ion tran Hs. 1956 Hs. Iddney-specific membrane prote Hs. 16098:Caudin 2 NM_016109:Homo sapiens anglopoletin-like NM_004591:Homo sapiens small Inducible c Hs. 47448:ESTs Hs. 125395:ESTs  NM_002151:Homo sapiens hepsin (transmemb Hs. 165619:mucin and cadherin-like Hs. 124776:Homo sapiens mR; cD DKFZp564N1 Hs. 178098:angiotensin I converting enzym NM_00299:Homo sapiens rogenerating iste	15.71 14.07 12.56 12.41 11.77 10.39 10.18 9.95 9.58 9.51 8.88 8.77 8.45 7.94
65	R1:  Pkey 435013 447768 445178 432542 4435563 413719 436878 4407065 413049 42598 425161 430569 416768 422357	ExAccn H91923 X88400 A1792241 AW083920 AF169312 BE439580 BE455204 BE159984 Y10141 NM_002151 AK000226 AA363733 AF016272	unigene gene title of furmor to not UnigenetD Hs.110024 Hs.19520 Hs.129614 Hs.16098 Hs.9613 Hs.75498 Hs.47448 Hs.125395 Hs.823 Hs.165619 Hs.124776 Hs.178098 Hs.1032 Hs.115518	Hs. 19520:FXYD domain-containing ion tran Hs. 19520:FXYD domain-containing ion tran Hs. 19614:kidney-specific membrane prote Hs. 16098:claudin 2 NM_016109:Homo sapiens anglopoletin-like NM_00459:Homo sapiens small inducible c Hs. 47448:ESTs Hs. 125395:ESTs NM_002151:Homo sapiens hepsin (transmemb Hs. 165619:mucin and cadherin-like Hs. 124776:Homo sapiens mR; cD DKFZp564N1 Hs. 178098:angloidensin I converting enzym NM_002909:Homo sapiens regenerating iste NM_004062:Homo sapiens cagherin 16, KSP-	15.71 14.07 12.56 12.41 11.77 10.39 10.18 9.95 9.58 9.51 8.88 8.77 8.45 7.94
65 70	R1: Pkey 435013 447768 445178 432542 443595 413719 436878 440304 407065 413049 425983 423161 430569 416768	ExAcca H91923 X88400 AJ792241 AW083920 AF159312 8E4539590 BE455204 BE159984 Y10141 NM_002151 AK000226 AL049227 AF241254 AA363733 AF015272 L08096	lene gene title of furnor to not UnigenetD Hs.110024 Hs.19520 Hs.129614 Hs.16098 Hs.9613 Hs.75498 Hs.47448 Hs.125395 Hs.823 Hs.165619 Hs.124776 Hs.178098 Hs.1032	unigene Title  Hs. 19520:FXYO domain-containing ion tran Hs. 129614:kidney-specific membrane prote Hs. 16093:ctaudin 2 NM_016109:Homo septens anglopoletin-like NM_004591:Homo septens small inducible c Hs. 1748:ESTs Hs. 125395:ESTs  NM_002151:Homo septens hepsin (transmemb Hs. 165619:mucin and cadherin-like Hs. 124776:Homo septens mR: cD DKFZp564N1 Hs. 178098:angiotensin I converting enzym NM_002909:Homo septens regenerating isle NM_004062:Homo septens cadherin 16, KSP- NM_001252:Homo septens tumor necrosis fa	15.71 14.07 12.56 12.41 11.77 10.39 10.18 9.95 9.59 9.51 8.88 8.77 8.45 7.94 7.78
65	R1:  Pkey 435013 447768 445778 432542 4435543 413719 436878 4407065 413049 425161 430569 41668 422367 420737 409745 413936	ExAccn H91923 X88400 A1792241 AW083920 AF169312 BE439580 BE455204 P10141 NM_002151 AK000226 AL049227 AF241254 AA363733 AF016272 L08096 AA077391 AF113676	unigene gene title of furmor to not UnigenetD Hs.110024 Hs.19520 Hs.129614 Hs.16098 Hs.9613 Hs.75498 Hs.47448 Hs.125395 Hs.823 Hs.165619 Hs.124776 Hs.178098 Hs.1032 Hs.115518	Hs. 19520:FXYD domain-containing ion tran Hs. 19520:FXYD domain-containing ion tran Hs. 19614:kidney-specific membrane prote Hs. 16098:claudin 2 NM_016109:Homo sapiens anglopoletin-like NM_00459:Homo sapiens small inducible c Hs. 47448:ESTs Hs. 125395:ESTs NM_002151:Homo sapiens hepsin (transmemb Hs. 165619:mucin and cadherin-like Hs. 124776:Homo sapiens mR; cD DKFZp564N1 Hs. 178098:angloidensin I converting enzym NM_002909:Homo sapiens regenerating iste NM_004062:Homo sapiens cagherin 16, KSP-	15.71 14.07 12.56 12.41 11.77 10.39 10.18 9.95 9.58 9.51 8.88 8.77 8.45 7.94
65 70	R1:  Pkey 435013 447768 445178 432542 443595 413719 436878 440304 407085 413049 425883 423161 430569 416768 422357 409745 4199745 4156682	ExAcon H91923 X88400 A1792241 AW083920 AF169312 8E4539590 BE465204 BE159984 Y10141 NM_002151 AK000226 AL049227 AF241254 AA363733 AF016272 L08098 AA077391 AF113676 AV660038	jene gene tite of tumor to no Unigenetid Hs. 110024 Hs. 119520 Hs. 129614 Hs. 169613 Hs. 75498 Hs. 47448 Hs. 125395 Hs. 823 Hs. 165619 Hs. 178098 Hs. 1032 Hs. 115418 Hs. 199899 Hs. 297681 Hs. 297681 Hs. 297681 Hs. 297681	Unigene Title  Hs. 19520:FXYD domain-containing ion tran Hs. 129614:kidney-specific membrane prote Hs. 16093:claudin 2 NM_016109:Homo septens anglopoletin-like NM_004591:Homo septens small inducible c Hs. 4748:ESTs Hs. 125395:ESTs  NM_002151:Homo septens hepsin (transmemb Hs. 165619:mucin and cadherin-like Hs. 124776:Homo septens mR: cD DKFZp564N1 Hs. 178098:anglotensin I converting enzym NM_002909:Homo septens regenerating iste NM_004062:Homo septens tumor necrosis fa AA077391:7814E12 Chromosome 7 Fetal Brai NM_000295:Homo septens serine (or cystei Hs. 2056:UDP glycosyturnsferase 1 family	15.71 14.07 12.56 12.41 11.77 10.39 10.18 9.95 9.59 9.51 8.88 8.77 8.45 7.94 7.78 7.78 7.78
65 70	R1:  Pkey 435013 447768 445178 432542 443595 413719 436878 400304 407085 413049 425983 423161 430568 422357 420737 409745 413936 426851	ExAccn H91923 X88400 A1792241 AW083920 AF169312 BE459580 BE455984 Y10141 NM_002151 AK000226 AL049277 AF241274 AA383733 AF016272 L0809 AB097391 AF113676 AV660038 AA609784	unigene gene title of furnor to not unigened D Hs. 110024 Hs. 19520 Hs. 129614 Hs. 16098 Hs. 9613 Hs. 75498 Hs. 47448 Hs. 125395 Hs. 823 Hs. 165619 Hs. 124776 Hs. 178098 Hs. 1032 Hs. 115418 Hs. 99899 Hs. 2056 Hs. 352392	Unigene Title  Hs. 19520:FXYO domain-containing ion tran Hs. 129614:kidney-specific membrane prote Hs. 16098:daudin 2 NM_016109:Homo sapiens anglopoletin-like NM_004591:Homo sapiens small Inducible c Hs. 144746:ESTs Hs. 125395:ESTs  NM_002151:Homo sapiens hepsin (transmemb Hs. 165619:mucin and cadherin-like Hs. 124776:Homo sapiens Rr cD DKFZp564N1 Hs. 178038:angiotensin I converting enzyrn NM_002909:Homo sapiens rogenerating isle NM_004062:Homo sapiens converting enzyrn NM_004062:Homo sapiens converting enzyrn NM_001252:Homo sapiens rogenerating isle NM_004062:Homo sapiens rogenerating isle NM_004062:Homo sapiens converting enzyrn NM_002909:Homo sapiens rogenerating isle NM_004062:Homo sapiens rogenerating isle NM_004062:Homo sapiens serine (or cystei Hs. 2056:UDP glycosyltransferase 1 family Hs. 352392:major histocompatibility compl	15.71 14.07 12.56 12.41 11.77 10.39 10.18 9.95 9.58 9.51 8.88 8.77 8.45 7.79 7.78 7.78 7.78 7.74 7.32
65 70	R1:  Pkey 435013 447768 445178 432542 4435563 413719 436878 4407065 413049 425161 430569 416768 422367 420737 409745 413936 426682 40682 40682	ExAcon H91923 X88400 A1792241 AW083920 AF169312 BE439580 BE455204 P10141 NM_002151 AK000226 AL049227 AF241254 AA363733 AF016272 L08098 AA077391 AF113676 AV660038 AA609784 AW997938	unigene gene title of furmor to not UnigenetD Hs.110024 Hs.19520 Hs.129614 Hs.16098 Hs.9613 Hs.75498 Hs.47448 Hs.125395 Hs.823 Hs.165619 Hs.124776 Hs.178098 Hs.1032 Hs.99899 Hs.297681 Hs.2056 Hs.352392 Hs.90786	Unigene Title  Hs. 19520:FXYO domain-containing ion tran Hs. 129614:kidney-specific membrane prote Hs. 16098:ctaudin 2 NM_016109:Homo sapiens anglopoletin-like NM_004591:Homo sapiens small inducible c Hs. 47448:ESTs Hs. 125395:ESTs  NM_002151:Homo sapiens hepsin (transmemb Hs. 165619:mucin and cadherin-like Hs. 124751-Homo sapiens mR: c0 DKFZp564N1 Hs. 178098:angiotensin I converting enzym NM_002909:Homo sapiens rogenerating iste NM_004062:Homo sapiens tumor necrosis fa AA077391:7814E12 Curvomosome 7 Fetal Brai NM_000295:Homo sapiens serine (or cystei Hs. 2056:UDP ghycosyttransferase 1 family Hs. 352392:major histocompability compl Hs. 90786:ATP-binding cassette, sub-famil	15.71 14.07 12.56 12.41 11.77 10.39 10.18 9.95 9.58 9.51 8.88 8.77 8.45 7.94 7.78 7.78 7.78 7.78 7.70 7.03 6.57
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65 70 75	R1:  Pkey 435013 447768 445178 432542 443595 413719 436878 407085 4130304 407085 4130369 425983 423161 430569 416768 422357 409745 413936 42682 406851 419508 428953 438895 431842 430014	ExAcon H91923 X88400 A1792241 AW083920 AF169312 BE455204 BE159984 Y10141 NM_002151 AK000226 AL049227 AF241254 AA363733 AF016272 L08098 AA077391 AF113676 AV660038 AA609784 AW997938 NA_005764 H59354	lene gene tite of furnor to no Unigenetic Hs. 110024 Hs. 119520 Hs. 129614 Hs. 169613 Hs. 75498 Hs. 75498 Hs. 75498 Hs. 125395 Hs. 823 Hs. 165619 Hs. 124776 Hs. 178098 Hs. 1032 Hs. 115418 Hs. 99899 Hs. 2056 Hs. 352392 Hs. 5338 Hs. 5338 Hs. 5338 Hs. 5338 Hs. 5338 Hs. 53343343	Unigene Title  Hs. 19520:FXYO domain-containing ion tran Hs. 129614:kidney-specific membrane prote Hs. 1698:claudin 2 NM_016109:Homo septens anglopoletin-like NM_00459:Homo septens small inducible c Hs. 1448:ESTs Hs. 125395:ESTs  NM_002151:Homo septens hepsin (transmemb Hs. 165619:mucin and cadherin-like Hs. 124776:Homo septens mR: cD DKFZp564N1 Hs. 178098:amgiotensin I converting enzym NM_002909:Homo septens regenerating iste NM_004062:Homo septens cadherin 16, KSP- NM_001252:Homo septens tumor necrosis fa AA077391:7814E12 Chromosome 7 Fetal Brai NM_000295:Homo septens serine (or cystei Hs. 2056:UDP glycosyltransferase 1 family Hs. 352392:major histocompatibility compl Hs. 90786:ATP-binding cassette, sub-famil NM_003823:Homo septens tumor necrosis fa NM_001218:Homo septens tumor necrosis fa NM_001218:Homo septens tumor necrosis fa NM_001218:Homo septens carbonic anhydras NM_005764:Homo septens epithelial protei Hs. 374303:hypothetical protein MGC20576	15.71 14.07 12.56 12.41 11.77 10.39 10.18 9.95 9.59 9.51 8.88 8.77 8.45 7.94 7.78 7.78 7.78 7.74 7.32 7.20 7.03 6.57 6.36 6.31 6.20 6.20
65 70 75	R1:  Pkey 435013 447768 445178 432542 443593 413719 436878 4407065 413049 425161 430569 416768 422367 420737 409745 413936 426682 40682 40682 40683 438953 438853 438853	EXACCI H91923 XB400 A1792241 AW083920 AF169312 BE45204 BE159984 Y10141 NM_002151 AK000226 AL049227 AF241254 AA363733 AF016272 L08098 AA077391 AF016272 AV660038 AA609784 AW997938 AA306610 AF017335 NM_005764	lene gene tite of furnor to no Unigenetic Hs. 110024 Hs. 119520 Hs. 129614 Hs. 169613 Hs. 75498 Hs. 75498 Hs. 75498 Hs. 125395 Hs. 823 Hs. 165619 Hs. 124776 Hs. 178098 Hs. 1032 Hs. 115418 Hs. 99899 Hs. 2056 Hs. 352392 Hs. 5338 Hs. 5338 Hs. 5338 Hs. 5338 Hs. 5338 Hs. 53343343	Unigene Title  Hs. 19520:FXYO domain-containing ion tran Hs. 129614:kidney-specific membrane prote Hs. 16098:ctaudin 2 NM_016109:Homo sapiens anglopoletin-like NM_004591:Homo sapiens small inducible c Hs. 47448:ESTs Hs. 125395:ESTs  NM_002151:Homo sapiens hepsin (transmemb Hs. 165619:mucin and cadherin-like Hs. 124751-Homo sapiens mR: c0 DKFZp564N1 Hs. 178098:angiotensin I converting enzym NM_00290:Homo sapiens repenating iste NM_004062:Homo sapiens tumor necrosis fa AA077391:7814E12 Curvomosome 7 Fetal Brai NM_000295:Homo sapiens serine (or cystei Hs. 2056:UDP ghycosyttransferase 1 family Hs. 352392:major histocompability compl Hs. 90786:ATP-binding cassette, sub-famil NM_003823:Homo sapiens tumor necrosis fa NM_001218:Horno sapiens tumor necrosis fa NM_001218:Horno sapiens tentonic anhydras NM_001764:Homo sapiens carbonic anhydras NM_001764:Homo sapiens carbonic	15.71 14.07 12.56 12.41 11.77 10.39 10.18 9.95 9.59 9.51 8.88 8.77 8.45 7.78 7.78 7.78 7.78 7.70 7.73 7.20 7.03 6.57 6.36 6.31 8.20

	43.4770			11 58454	
	434779	AF153815	Hs.50151	Hs.50151:potassium inwantly-rectifying c	6.11
	435767	H73505	Hs.117874	Hs.117874:ESTs	6.08
	422664	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	6.02
5	425280	U31519	Hs.1872	Hs.1872.phosphoenolpyruvate carboxykise	5.81
,	426559	AB001914	Hs.170414	NM_002570:Homo sapiens paired basic amin	5.73
	451564	AU076698	Hs.132760	NM_001467:Homo sapiens glucose-6-phospha	5.69
	418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	5.68
	444151	AW972917	Hs.128749	Hs.128749:alpha-methylacyl-CoA racemase	5.66
10	426471	M22440	Hs.170009	NM_003236:Homo sapiens transforming grow	5.48
10	432579	AF043244	Hs.278439	NM_003946:Homo sapiens mucleolar protein	5.45
	448733	NM_005629	Hs.187958	NM_005629:Homo sapiens solute carrier fa	5.42
	446650	AB016625	Hs.15813	NM_003060:Homo sapiens solute carrier fa	5.36
	417089	H52280	Hs.18612	Hs.18512:Homo sapiens cD: FLJ21909 fis,	5.35
16	437848	AI906419	Hs.284380	Hs.284380:gamma-glutamyttransferase 1	5.32
15	423081	AF262992	Hs.123159	Hs.123159:sperm associated antigen 4	5.30
	421893	NM_001078	Hs.109225	NM_001078:Homo sapiens vascular cell adh	5.23
	435886	BE265839	Hs.12126	Hs.12126:hepatocellular carcinoma-associ	5.20
	410276	A1554545	Hs.359201	Hs.359201:ESTa	5.20
20	429451	BE409861	Hs.202833	NM_002133:Homo sapiens heme oxygese (dec	5.14
20	446404	AAD19961	Hs.26216	Hs.26216:Homo saplens cD: FLJ22811 fis,	5.13
	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	5.09
	449444	AW818436	Hs.351306	NM_004696:Homo sapiens solute carrier fa	5.05
	438105	BE245551	Hs.6079	NM_014863:Homo sapiens B cell RAG associ	5.02
26	400419	AF084545		AF084545:Homo sapiens versican Vint isof	5.01
25	453920	Al133148	Hs.36602	NM_000204:Homo sapiens I factor (complem	4.99
	447881	BE620886	Hs.355279	Hs.355279:Homo sapiens cD FLJ23711 fis,	4.97
	422253	W81526	Hs.113882	NM_000815:Homo sapiens gamma-aminobutyri	4.93
	439024	R96696	Hs.35598	Hs.35598:ESTs	4.88
	414799	AJ752416	Hs.77326	NM_000598:Homo sapiens insufin-like grow	4.80
30	426530	U24578	Hs.278625	NM_000592:Homo sapiens complement compon	4.77
	410055	AJ250839	Hs.58241	Hs.58241:gene for serine/threonine prote	4.72
	404240				4.71
	414617	AI339520	Hs.288817	Hs.288817:hypothetical protein FLJ22761	4.68
	448249	AW855331	Hs.337124	Hs.337124:ESTs	4.67
35	447818	W79940	Hs.21906	Hs.21906:Homo saplens clone 24670 mR seq	4.66
	449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	4.68
	422424	AI186431	Hs.296638	NM_004864:Homo sapiens prostate differen	4.62
	417338	R70429	Hs.81988	NM_001343:Homo sepiens disabled homolog	4.62
	425873	NM_013390	Hs.160417	NM_013390:Homo sapiens transmembrane pro	4.58
40	444700	NM_003645	Hs.11729	NM_003645: Homo sapiens fatty-acid-Coenzy	4.58
	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	4.56
	414763	U97276	Hs.77266	NM_002826:Homo sapiens quiescin Q6 (QSCN	4.48
	443358	H65417	Hs.17757	Hs.17757:pleckstrin homology domain-cont	4.45
	440091	A1767388	Hs.37890	Hs.37890:Homo sapiens, clone IMAGE:48275	4.43
45	447131	NM_004585	Hs.17466	NM_004585:Horno sapiens retinoic acid rec	4.43
	406973	M34996	Hs.198253	Hs.198253:major histocompatibility compl	4.42
	427740	BE242604	Hs.180616	NM_005505:Horno sapiens CO36 antigen (col	4.40
	436258	AW867491	Hs.107125	Hs.107125:plasmatemma vesicle associated	4.38
	452884	C05964	Hs.31841	Hs.31841:ESTs	4.37
50	444006	BE395085	Hs.10086	NM_015639:Homo sapiens type I transmembr	4.36
• •	422627		Hs.118787	NM_000358:Homo sapiens transforming grow	4.35
	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-lik	4.34
	419011	H56244	Hs.89552	NM_000846:Homo sapiens glutathione S-tra	
	404277	1100244	16.03002	Harmonia Saberra Antramona 3-09	4.34 4.33
55	435563	AF210317	Hs.95497	Hs.95497:solute carrier family 2 (facili	4.30
	431779	AW971178	Hs.268571	NM_001645:Homo sapiens apolipoprotein C-	
	406645	M57466	Hs.814	Hs.814:major histocompatibility complex.	4.29 4.28
	421485	AA243499	Hs.104800	Hs.104800:hypothetical protein FLJ10134	4.26
	426812	AF105365	Hs.172813	NM_006598:Homo sapiens solute carrier fa	4.25 4.25
60	407910	AA650274	Hs.41298	NM_013281:Homo sapiens fibronectin leuci	4.22
••	438030	X98427	Hs.122634	Hs.122634:ESTs	
	430661	AC005551	Hs.130714	Hs.130714:ESTs, Moderately similar to AF	4.22 4.21
	444381	BE387335	Hs.283713	Hs.283713:hypothetical protein BC014245	
	438203	BE540090	Hs.7345	Hs.7345:MAD1 mitofic arrest deficient-fi	4.20
65	411358	R47479	Hs.94761	Hs.94761:KIAA1691 protein	4.16
0_	418323	NM_002118	Hs.1162	NM_002118:Homo saplens major histocompat	.4.15
	449853	AF006823		NM_002246:Homo sapiens potassium channel	4.12
	415198	AW009480	H5.24040		4.11
	418751	BE389014	Hs.943 Hs.372548	NM_004221:Homo sapiens tural killer cell	4.11
70			Hs.75789	Hs.372548:phosphoinositide-3-kise, regul	4.09
, 0	414166 424125	AW888941 M31669	Hs.1735	NM_006096:Homo sapiens N-myc downstream	4.07
				Hs. 1735 inhibin, beta B (activin AB beta	4.00
	416926	H03109	Hs.263395	Hs.263395:sema domain, transmembrane dom	3.92
	419175	AW270037	Hs.362996	Hs.362996:KIAA0779 protein	3.92
75	424218	AF031824	Hs.143212		3.91
, 5	412870	N22788	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	3.88
	452203	X57522	Hs.352018		3.87
	446872	X97058	Hs.16362	NM_004154:Homo sapiens pyrtmidinergic re	3.87
	449961	AW265634	Hs.133100		3.87
80	424517	AI539443	Hs.137447	Hs.137447:Homo sapiens cD FLJ12169 ffs,	3.86
OU	425262	D87119	Hs.155418		3.83
	443639	BE269042	Hs.9661	NM_002801:Homo sapiens proteasome (proso	3.82
	448133	AA723157	Hs.73769	NM_000802:Homo sapiens folate receptor 1	3.81
	418030	BE207573	Hs.83321	Hs.83321:neuromedin B	3.81

		*****			
	412939	AW411491	Hs.75069	NM_005412:Homo sapiens serine hydroxymet	3.80
	409162 427715	H25530 BE245274	Hs.50868	NM_002555:Homo sapiens solute carrier (a	3.79
	412006	AW451618	Hs.180428 Hs.290216	Hs.180428:KIAA1181 protein Hs.290216:ESTs	3.78
5	430413	AW842182	Hs.241392	NM_002985:Homo saplens small inducible c	3.77 3.76
_	422282	AF019225	Hs.114309	Hs.114309:apolipoprotein L, 1	3.76
	420747	BE294407	Hs.99910	Hs.99910:phosphofructokise, platelet	3.76
	414875	H42679	Hs.77522	NM_006120:Homo septens major histocompat	3.75
• •	418793	AW382987	Hs.88474	Hs.88474:prostaglandin-endoperoxide synt	3.74
10	446291	BE397753	Hs.14623	NM_006332:Homo sapiens interferon, gamma	3.71
	417289	D86962	Hs.81875	Hs.81875:growth factor receptor-bound pr	3.69
	422672	X12784	Hs.119129	NM_001845:Homo sapiens collagen, type IV	3.68
	448569	8E382657	Hs.21486	NM_007315:Homo sapiens sigl transducer a	3.68
15	437270 408452	R18087 AA054683	Hs.323769 Hs.192455	Hs.323769:cisplatin resistance related p	3.67
13	443986	AI381750	Hs.283437	Hs.192455:ESTs, Moderately similar to hy Hs.283437:HTGN29 protein	3.67
	418869	AW516565	113.205431	AW516565:xq01d05.x1 Soares_NHCeC_cervica	3.66 3.65
	425998	AU076629	Hs.165950	NM_002011:Homo sepiens Ebroblast growth	3.62
	428699	AW578252	Hs.190161	NM_014020:Horno sapiens LR8 protein (LR8)	3.62
20	418299	AA279530	Hs.83968	NM_000211:Homo sapiens integrin, beta 2	3.61
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	3.59
	415765	NM_005424	Hs.78824	NM_005424:Homo sapiens tyrosine kise will	3.58
	445985	BE621800	Hs.29444	Hs.29444:putative small membrane protein	3.57
25	424893	AW295112	Hs.153848	Hs.153648:protein tyrosine phosphatase,	3.57
23	426046	AA833655	Hs.206868	Hs.206868:Home sapiens cD FU14056 fis.	3.57
	424415 412612	NM_001975	Hs.146580	NM_001975:Homo sapiens enclase 2, (gamma	3.57
	443834	NM_000047 AI741510	Hs.74131 Hs.173548	NM_000047:Homo sapiens arylsulfatase E (	3.56
	431630	NM_002204	Hs.265829	Hs.173548:ESTs NM_002204:Homo sapiens integrin, alpha 3	3.54 3.53
30	418371	M13560	Hs.84298	Hs.84298:CD74 antigen (invariant polypep	3.52
	444838	AV651680	Hs.208558	Hs.208558:ESTs	3.52
	449378	AW664026	Hs.59892	Hs.59892:ESTs, Wealdy similar to alpha 5	3.52
	411393	AW797437	Hs.69771	NM_001710:Homo saplens B-factor, properd	3.50
25	414311	A1693547	Hs.71746	Hs.71746:aminopeptidase-like 1	3.50
35	415149	X12451	Hs.78056	NM_001912:Homo saplens cathepsin L (CTSL	3.50
	424321	W74048	Hs.1765	Hs.1765:lymphocyte-specific protein tyro	3.49
	414825	X06370	Hs.77432	NM_005228:Homo sapiens epidermal growth	3.48
	408194 410600	AA601038 AW575742	Hs.191797 Hs.351676	Hs.191797:ESTs	3.48
40	416899	BE262645	Hs.80420	Hs.351676:ESTs, Weakly similar to T02670 NM_002996:Homo sapiens small inducible c	3.47
. •	436856	A1469355	Hs.127310	Hs.127310:hypothetical protein BC014917	3.47 3.47
	419660	BE280337	Hs.194693	NM_003982:Homo sapiens solute carrier (a	3.47
	413566	AW604451	Hs.285814	Hs.285814:growth factor receptor-bound p	3.47
	412104	AW205197	Hs.240951	Hs.240951:ked cuticle homolog 2 (Drosoph	3.46
45	444488	AW192879	Hs.355660	Hs.355660:peptide-histidine transporter	3.46
	449475	AI348027	Hs.108557	Hs.108557:hypothetical protein PP1057	3.46
	412276	BE262621	Hs.73798	NM_002415:Homo sapiens macrophage migrat	3.45
	449338	H73444	Hs.394	NM_001124:Homo sapiens adrenomedutiin (A	3.44
50	430304 415388	AL122071	Hs.238927	Hs.238927:Homo sapiens mR; cD DKFZp434H1	3.43
30	432210	AF018081 AI567421	Hs.78409 Hs.273330	(locuslink)NM_030582:Homo sapiens colleg	3.43
	418177	N44967	Hs.351554	Hs.273330:agrin Hs.351554:Homo sapiens cD FLJ32092 fis,	3.43 3.42
	414888	AL039185	Hs.77558	Hs.77558:thyroid hormone receptor intera	3.42
	452445	AB002438	Hs.29596	Hs.29596:Homo sapiens mR from chromosome	3.41
55	414803	X03100	Hs.914	Hs.914:major histocompatibility complex,	3.41
	419201	M22324	Hs.1239	NM_001150:Homo sapiens alanyl (membrane)	3.41
	445139	AB037848	Hs.12365	Hs.12365:syptotagmin XIII	3.41
	435021	AA922192	Hs.73962	Hs.73962:EphA7	3.41
60	417259	AW903838	Hs.81800	Hs.81600:chondroitin suifate proteoglyce	3.40
50	439737 410636	A1751438 AAG88177	Hs.41271 Hs.172870	Hs.41271:Homo sapiens mR full length ins	3.39
	431590	AB037789	Hs.263395	Hs.172870:KIAA1913 protein Hs.263395:sema domain, transmembrane dom	3.39
	415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	3.38 3.36
	416700	AW498958	Hs.343475	NM_001909:Homo sapiens cathepsin D (lyso	3.36
65	440516	S42303	Hs.161	NM_001792:Homo sapiens cadherin 2, type	3.35
	423720	AL044191	Hs.23388	Hs.23388:hypothetical protein DKFZp434F0	3.32
	421902	BE392717		BE392717:601307571F1 NIH_MGC_44 Homo sap	3.32
	409220	BE243323	Hs.51233	Hs.51233:tumor necrosis factor receptor	3.32
70	421502	AF111856	Hs.105039		3.32
70	416729	U46165	Hs.1027	NM_004165:Homo saplens Ras-related assoc	3.30
	430302 445084	AL137502	Hs.238679		3.30
	406825	H38914 Al982529	Hs.250848 Hs.84298		3.29
	446272	BE268912	Hs.14601	Hs.84298:CD74 antigen (invariant polypep NM_005335:Homo sapiens hematopoletic cet	3.29
75	437145	AF007216	Hs.5462	NM_003759:Homo sapiens nematopoietic cer NM_003759:Homo sapiens solute cerrier (a	3.28 3.27
	444071	AI627808	Hs.110524		3.27 3.27
	414662	AL036058	Hs.76807	Hs.76807:major histocompatibility comple	3.27
	436576	A1458213	Hs.77542	Hs.77542:ESTs, Weakly similar to S26650	3.26
00	424675	NM_005512	Hs.151641	NM_005512:Homo sapiens glycoprotein A re	3.25
80	437897	AA770561	Hs.146170	Hs.146170:hypothetical protein FLJ22969	3.25
	449703	H61001	Hs.171802		3.25
	414788	X78342	Hs.77313	NM_003674:Homo sepiens cyclin-dependent	3.25
	414249	A1797994	Hs.279929	Hs.279929:gp25L2 protein	3.24

	430396	D49742	Hs.241363	NM_004132:Homo sapiens hyaturon binding	3.23
	424456	AA341017	Hs.25549	Hs.25549:hypothetical protein FLJ20898	3.23
	452303	R27257	Hs.57734	Hs.57734:G protein-coupled receptor kise	3.22
5	425390	AI092634	Hs.156114	NM_004648:Homo sapiens protein tyrosine	3.21
J	416033 450931	NM_012201 N25156	Hs.78979 Hs.25648	NM_012201:Homo saplens golgi apparatus p Hs.25648:tumor necrosis factor receptor	3.19 3.19
	428065	AI834048	Hs.157313	Hs.157313:ESTs	3.18
	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	3.18
10	439318	AW837046	Hs.6527	Hs.6527:G protein-coupled receptor 56	3.17
10	427640	AF058293	Hs.180015	NM_001355:Homo sapiens D-dopachrome taut	3.17
	409936 436001	AK001691 AW903849	Hs.57655 Hs.173840	Hs.57655:dudulin 2 Hs.173840:similar to endothelial cell-so	3.16 3.16
	451154	AA015879	Hs.33536	Hs.33536:ESTs	3.16
1.5	420256	U84722	Hs.76206	NM_001795:Homo sepiens cadherin 5, type	3.16
15	407584	W25945	Hs.8173	Hs.8173:hypothetical protein FLJ10803	3.15
	428593 410026	AW207440 AI912061	Hs.185973 Hs.55016	NM_003676:Homo sapiens degenerative sper Hs.55016:EPS8-retated protein 2	3.15 3.15
	445333	BE537641	Hs.44278	Hs.44278:RAB17, member RAS oncogene fami	3.14
00	448143	AF039704	Hs.20478	NM_000391:Homo saplens ceroid-lipotuscin	3.14
20	423007	AA320134	Hs.196029	Hs.196029:Homo sapiens mR for KIAA1657 p	3.14
	416511 439237	NM_006762	Hs.79356	NM_006762:Homo sapiens Lysosomal-associa	3.14
	446899	AW408158 NM_005397	Hs.318893 Hs.16426	Hs.318893:ESTs, Weatly similar to Z195_H NM_005397:Homo saptens podocalyzin-like	2.13 3.13
	413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	3.13
25	434398	AA121098	Hs.3838	NM_006622:Homo saplens serum-inducible k	3.12
	441283	AA927670	Hs.131704	Hs.131704:ESTs	3.12
	418945 418458	BE246762 AA332941	Hs.89499 Hs.85226	NM_000698:Homo sapiens arachidote 5-lipo NM_000235:Homo sapiens lipase A, lysosom	3.12 3.12
	408989	AW361666	Hs.49500	Hs.49500:KIAA0746 protein	3.11
30	436905	H95990	Hs.181244	Hs.181244:major histocompatibility compl	3.11
	411089	AA456454	Hs.355702	Hs.355702:ESTs, Weatly similar to AC0048	3.11
	432990 425009	AL036071 X58288	Hs.279899 Hs.154151	NM_003820:Homo saplens tumor necrosis fa NM_002845:Homo saplens protein tyrosine	3.11 3.10
	443601	AI078554	Hs.42658	Hs. 42658:Homo sapiens cD FLJ30167 fis, c	3.10
35	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	3.10
	413672	BE156536	Hs.353632	Hs.353632:ESTs, Moderately similar to hy	3.09
	407786 414586	AA687538 AA306160	Hs.38972 Hs.16488	NM_005727:Homo saplens tetrespan 1 (TSPA NM_002298:Homo saplens lymphocyte cytoso	3.09
	423712	W45802	Hs.81988	Hs.81988:disabled homolog 2, mitogen-res	3.08 3.08
40	438552	AJ245820	Hs.6314	NM_012410:Homo sapiens type I transmembr	3.08
	448364	T08958	Hs.297214	Hs.297214:HSPC141 protein	3.06
	426437 437679	BE076537	Hs.169895	NM_004223:Homo sapiens ubiquitin-conjuga	3.06
	422262	NM_014214 AL022315	Hs.5753 Hs.113987	NM_014214:Homo sapiens inositol(myo)-1(o NM_006498:Homo sapiens lectin, galactosi	3.06 3.06
45	410480	R97457	Hs.63984	NM_001257:Homo sapiens cadherin 13, H-ca	3.05
	435818	AA700553	Hs:368614	Hs.368614:ESTs	3.05
	418883 453613	BE387036 F06838	Hs.1211	NM_001611:Homo sapiens acid phosphatase	3.05
	408051	AI623351	Hs.374476 Hs.172148	Hs.374476:ESTs Hs.172148:ESTs	3.05 3.05
50	432278	AL137506	Hs.274256	Hs.274256:hypothetical protein FLJ23563	3.04
	407949	W21874	Hs.247057	Hs.247057:ESTs, Weakly similar to 210926	3.04
	418090	U57059	Hs.83429	NM_003810:Homo sapiens tumor necrosis fa	3.04
	433165 425809	AA578904 AA370362	Hs.292437 Hs.57958	Hs.292437:ESTs Hs.57958:EGF-TM7-latrophilin-related pro	3.03 3.03
55	443884	N20617	Hs.194397	Hs.194397:ESTs, Moderately similar to 22	3.03
	447831	A1433293	Hs.164115	Hs.164115:ESTs	3.02
	413278	BE563085	Hs.833	NM_005101:Homo saplens Interferon-stimul	3.01
	418870 456376	AF147204 AA663904	Hs.89414 Hs.89862	Hs.89414:chemotine (C-X-C motif), recept Hs.89862:TNFRSF1A-associated via death d	3.00 3.00
60	439738	BE246502	Hs.9598	Hs.9598:sema domain, immunoglobulin doma	3.00
	444416	AW288085	Hs.11156	NM_016494:Homo sepiens hypothetical prot	3.00
	406656	M16714	Hs.89643	Hs.89643:transketolase (Wernicke-Korsako	3.00
	406826 418707	AW516005 U97502	Hs.84298 Hs.87497	Hs.84298:CD74 artigen (invariant polypep Hs.87497:butyrophilin, subfamily 3, memb	2.99 2.99
65	421742	AW970004	Hs.107528		2.99
	406824	AW515961	Hs.84298	Hs.84298:CD74 antigen (invariant polypep	2.99
	435605	AF151815	Hs.4973	NM_015680:Horno sapiens hypothetical prot	2.98
	410491 427648	AA465131	Hs.64001	Hs.64001:Homo saplens clone 25218 mR seq	2.98
70	411125	AI376722 AA151647	Hs.180062 Hs.68877	NM_004159:Homo sapiens proteasome (proso NM_000101:Homo sepiens cytochrome b-245,	2.98 2.98
	435550	A1224456	Hs.324507	Hs.324507:hypothetical protein FLJ20986	2.98
	429373	NM_014694		NM_014694:Homo sapiens KIAA0605 gene pro	2.98
	445701	AF055581	Hs.13131	NM_005475:Homo sapiens lymphocyte adapto	2.97
75	414649 444207	A1672727 A1565004	Hs.76753 Hs.374415	NM_000118:Homo sapiens endoglin (Oster-R Hs.374415:ESTs	2.97 2.97
	423225	AA852604	Hs.125359		2.97
	407792	AI077715	Hs.39384	NM_014344:Homo sapiens four jointed box	2.97
	445707	AJ248720	Hs.114390	Hs.114390:ESTs	2.96
80	452888 418478	AW955454 U38945	Hs.30942 Hs.1174	NM_004093:Homo sapiens ephrin-B2 (EFNB2) Hs.1174:cyclin-dependent kise inhibitor	2.95 2.95
-	411441	AL042355	Hs.70202	Hs.70202:WO repeat domain 10	2.95
	443426	AF098158	Hs.9329	Hs.9329:chromosome 20 open reading frame	2.94
	450876	AF189062	Hs.285976	Hs.285976:LAG1 longevity assurance homol	2.94

	426359	AA376409	No 10053	Ur 10062 Unma coniana eD El 102212 6a	204
	425421	L11669	Hs.10862 Hs.157145	Hs.10862:Homo sapiens cD: FLJ23313 fis, NM_001120:Homo sapiens tetracycline tran	2.94 2.93
	449879	H03573	Hs.287830	Hs.287830:Homo sapiens mR; cD DKFZp434E1	2.93
5	454075	R43826	Hs.16313	Hs. 16313:Kruppel-like zinc finger protei	2.93
,	421595 457949	AB014520 W69171	Hs.301685 Hs.334814	Hs.301685:KIAA0620 protein Hs.334814:hypothetical protein FLJ14868	2.93 2.92
	443987	AW163123	Hs.10071	NM_016551:Homo sapiens seven transmembra	2.92
	430259	BE550182	Hs.375142	Hs.375142:RalGEF-like protein 3, mouse h	2.92
10	415906 429762	A1751357 A1346255	Hs.288741 Hs.216354	Hs.288741:Homo sapiens cD: FLJ22256 ffs,	2.91
10	451527	AF022813	Hs.26518	NM_006913:Homo saplens ring finger prote NM_003271:Homo saplens transmembrane 4 s	291 291
	425356	BE244879	Hs.155939	NM_005541:Homo sapiens inositol polyphos	2.91
	427080	AW068287	Hs.301175	NM_002872:Homo sepiens ras-related C3 bo	2.91
15	426432 431476	AF001601 BE612705	Hs.169857 Hs.256697	NM_000305:Homo sapiens paraoxose 2 (PON2 Hs.256697:histidine triad nucleotide bin	2.90 2.89
	406659	AA663985	Hs.277477	Hs.277477:major histocompatibility compl	2.89
	451144	AW956103	Hs.61712	Hs.61712:Homo sapiens cO FLJ31548 fis, c	2.89
	456362 426440	AW973003 BE382756	Hs.179909 Hs.169902	Hs.179909:nuclear receptor coactivator 6 NM_006516:Homo sapiens solute carrier fa	2.88 2.88
20	456974	M12529	Hs.169401	NM_000041:Homo sapiens apolipoprotein E	2.88
	418174	1.20688	Hs.83656	Hs.83656:Rho GDP dissociation inhibitor	2.88
	446055 423184	AJ815981	Hs.12909	Hs.12909:mucolipin 1	2.88
	427700	NM_004428 AA262294	Hs.1624 Hs.180383	NM_004428:Homo sapiens ephrin-A1 (EF1), NM_001946:Homo sapiens dual specificity	2.87 2.87
25	410668	BE379794	Hs.159651	NM_016629:Homo sapiens hypothetical prot	2.87
	444143	AW747996	Hs.160999	Hs.160999:ESTs, Wealdy similar to 178885	2.87
	407151 449349	H25836 A1825386	Hs.301527 Hs.352579	Hs.301527:ESTs, Moderately similar to un Hs.352579:Homo sapiens, chromosome 20 op	2.86 2.86
	436997	AA741151	Hs.137323	Hs.137323:ESTs	2.86
30	446143	BE245342	Hs.306079	NM_013336:Homo sapiens protein transport	2.88
	417355 431685	D13168 AW296135	Hs.82002 Hs.267659	Hs.82002:endothelin receptor type B NM_006113:Homo sapiens vav 3 oncogene (V	2.86
	408877	AA479033	Hs.130315	Hs.130315:ESTs	2.86 2.85
35	429615	AF258627	Hs.211562	NM_005502:Homo sapiens ATP-binding casse	2.85
33	412014 436749	AI620650 AA584890	Hs.43761 Hs.5302	Hs.43761:gap junction protein, alpha 7, NM_006149:Homo sapiens tectin, galactosi	2.84
	419625	U91616	Hs.182885	NM_004556:Homo sapiens nuclear factor of	2.84 2.84
	439941	Al392640	Hs.18272	Hs. 18272:solute carrier family 38, membe	2.84
40	436496 422100	AA281959 AI096988	Hs.5210 Hs.111554	NM_004877:Homo sapiens glia maturation f	2.84
-10	439730	AF035292	Hs.6654	NM_005737:Homo saplens ADP-ribosylation Hs.6654:KIAA0657 protein	2.83 2.83
	447217	BE465754	Hs.17778	NM_003872:Homo sapiens neuropilin 2 (NRP	2.83
	428343	AL043021	Hs.12705	Hs.12705:similar to HYPOTHETICAL 43.1 KD	2.82
45	440524 415523	R71264 ALD42003	Hs.16798 Hs.296847	Hs.16798:Homo sapiens mR; cD DKFZp564O24 NM_003119:Homo sapiens spastic pareplegi	2.82 2.81
	439668	AJ091277	Hs.302634	Hs.302634:frizzled homolog 8 (Drosophila	2.81
	414570	Y00285	Hs.76473	NM_000876:Homo sapiens insufin-like grow	2.80
	426535 409649	AU077012 AA159216	Hs.288582 Hs.55505	NM_006287;Horno sapiens tissue factor pet Hs.55505;hypothetical protein FLJ20442	2.80 2.80
50	406655	M21533	Hs.277477	Hs.277477:major histocompatibility compl	2.79
	415323	BE269352	Hs.949	NM_000433:Homo sapiens neutrophil cytoso	2.79
	443195 451356	BE148235 AA748418	Hs.193063 Hs.164577	Hs.193063:Homo sapiens cD FLJ14201 fis, Hs.164577:ESTs	2.78 2.78
	450708	AA376654	Hs.350065	Hs.350065:Homo saplens cD FU30634 fis,	2.78
55	433681	AI004377	Hs.200360	Hs.200360:Homo sapiens cD FLJ13027 fis,	2.77
	442599 414509	AF078037 AW161311	Hs.324051 Hs.76294	NM_006663:Homo sapiens RelA-associated I NM_001780:Homo sapiens CD63 antigen (mel	2.76 2.76
	431394	AK000692	Hs.252351	Hs.252351:HERV-H LTR-associating 2	2.76
60	417331	AW411297	Hs.81972	Hs.81972:SHC (Src homology 2 domain cont	2.76
UU	415995 414911	NM_004573 NM_000107	Hs.355888 Hs.77602	NM_004573:Homo sapiens phosphofipase C, NM_000107:Homo sapiens damage-specific D	2.75 2.75
	425976	C75094	Hs.334514		2.75
	407893	BE408359	Hs.43621	Hs.43621:hypothetical protein MBC3205	2.75
65	407903 415052	AI287341 AA724811	Hs.154029 Hs.334791	Hs.154029:bHLH factor Hes4 Hs.334791:similar to neurol tetraspanin	2.75 2.75
	428494	AA233439	Hs.184634	Hs.184634:hypothetical protein FLJ20005	2.75
	421506	BE302796	Hs.105097	NM_003258:Homo sapiens thymidine kise 1,	2.74
	427581 424527	NM_014788 AW138558	Hs.179703 Hs.334873		2.74 2.74
70	439578	AW263124	Hs.350547		2.74
	425188	AK002052	Hs.155071	Hs.155071;chromosome 20 open reading fra	2.74
	428013 439333	AF151020 AW384710	Hs.181444 Hs.132986		2.73
	450935	BE514743	Hs.355753		2.73 2.73
75	421532	AW138207	Hs.146170		2.73
	440502	A1824113	Hs.78281	Hs.78281:regulator of G-protein sighing	2.73
	444981 439219	AW855398 N33883	Hs.12210 Hs.41322	Hs.12210:tumor endothelial marker 6 Hs.41322:ESTs	2.72 2.72
00	416847	L43821	Hs.80261	NM_006403:Homo sapiens enhancer of filam	2.72
80	433179	AW362945	Hs.162459		2.72
	424528 411213	AW073971 AA676939	Hs.238954 Hs.69285	Hs.238954:ESTs, Weakly similar to putati NM_003873:Homo saplens neuropilin 1 (NRP	2.71 2.70
	433012	NM_004045			2.70



	425345	AU077297	Hs.155894	NM_002827:Homo saplens protein tyrosine	2.69
	428923	BE047698	Hs.188785	Hs.188785:ESTs	2.69
	427923	AW274357	Hs.301406	Hs.301406:hypothetical protein PP3501	2.69
5	446644	NM_003272	Hs.15791	NM_003272:Homo sapiens transmembrane 7 s	2.69
3	421743	T35958	Hs.107614	Hs.107614:DKFZP564I1171 protein	2.68
	416207 420372	NM_014745 AW960049	Hs.79077	NM_014745:Horno sapiens KIAA0233 gene pro	2.68
	420542	NM_000505	Hs.293660	Hs.293660:gene overexpressed in astrocyt	2.68
	425069	AA687465	Hs.1321 Hs.298184	NM_000505:Homo sapiens coagulation facto Hs.298184:potassium voltage-gated channe	2.67
10	418558	AW082266	Hs.88131	NM_003824:Homo sapiens Fas (TNFRSF6)-ass	2.67 2.67
	426251	M24283	Hs.168383	NM_000201:Homo sapiens intercellular adh	2.66
	406701	AA780613	Hs.62954	Hs.62954:femilin, heavy polypeptide 1	2.66
	431681	AK000378	Hs.267566	Hs.267566:hypothetical protein FLJ20371	2.66
1.5	412833	AW960547	Hs.298262	Hs.298262:ribosomal protein S19	2.66
15	433101	AW572317	Hs.12082	Hs.12082:TIGA1	2.66
	414774	X02419	Hs.77274	NM_002658:Homo sapiens plasminogen activ	2.66
	427868	AI360119	Hs.181013	NM_002629:Homo sapiens phosphoglycerate	2.66
	413929 424762	BE501689	Hs.75617	Hs.75617:collagen, type IV, alpha 2	2.66
20	422048	AL119442 NM_012445	Hs.183684 Hs.288126	Hs.183684:eukaryotic translation initiat	2.66
-0	431350	Al192528	Hs.164537	NM_012445:Homo saplens spondin 2, extrac Hs.164537:ESTs	2.65 2.65
	450184	W31096	Hs.237617	Hs.237617:dipeptidylpeptidase 9	2.65
	419285	D31887	Hs.89868	Hs.89868:KIAA0062 protein	2.65
	414217	AI309298	Hs.279898	Hs.279898:Homo sapiens cD: FLJ23165 fis,	2.64
25	451253	H48299	Hs.26126	NM_006984:Homo sapiens claudin 10 (CLDN1	2.64
	435905	AW997484	Hs.5003	Hs.5003:SUT-ROBO Rho GTPase-activating	2.64
	432581	AU076465	Hs.278441	NM_014634:Homo sapiens KIAA0015 gene pro	2.63
	415782	AA169345	Hs.123177	Hs.123177:hypothetical protein 8C011406	2.63
30	430223	NM_002514	Hs.235935	NM_002514:Homo saplens nephroblastoma ov	2.63
50	417526 409956	AA568906 AW103364	Hs.82240	NM_004177:Homo sapiens syntexin 3A (STX3	2.63
	449843	R85337	Hs.727 Hs.24030	NM_002192:Homo sapiens inhibin, beta A ( NM_001860:Homo sapiens solute carrier fa	2.63 2.62
	417389	BE260964	Hs.82045	NM_002391:Homo sapiens midkine (neurite	2.62
	446312	BE087853	Hs.171802	Hs. 171802:Homo sepiens, clone IMAGE:3956	2.62
35	435099	AC004770	Hs.4756	Hs.4755:flap structure-specific endonucl	2.62
	417920	\$47833	Hs.82927	NM_004037:Homo sapiens adenosine monopho	2.62
	435702	AI033647	Hs.121001	Hs.121001:Homo saplens, clone MGC:45521	2.62
	422959	AV647015	Hs.349256	Hs.349256:paired immunoglobutin-like rec	2.62
40	419938	AU076772	Hs.1279	NM_001733:Homo sapiens complement compon	2.62
40	450954	A1904740	Hs.25691	NM_005856:Homo sapiens receptor (calcito	2.61
	421753 443577	8E314828	Hs.107911	Hs.107911:ATP-binding cassette, sub-fami	2.61
	453886	AI078033 R66282	Hs.177170 Hs.20247	Hs.177170:ESTs, Weakly similar to ALU8_H	. 2.61
	421883	X55079	Hs.1437	Hs.20247:ESTs NM_000152:Homo sapiens glucosidase, a/ph	2.61 2.60
45	440457	BE387593	Hs.21321	Hs.21321:granule cell differentiation pr	2.60
	410295	AA741357	Hs.356624	Hs.356624:ESTs	2.59
	420679	X57152	Hs.99853	NM_001436:Homo sapiens fibrillarin (FBL)	2.59
	451558	NM_001089	Hs.26630	NM_001089:Homo sapiens ATP-binding casse	2.59
EΛ	444672	Z95636	Hs.11669	Hs.11669:taminin, alpha 5	2.59
50	408669	AJ493591	Hs.78146	Hs.78146:platelet/endothelial cell adhes	2.59
	426194	T50872	Hs.2001	Hs.2001:thromboxane A synthase 1 (platel	2.59
	421814	L12350	Hs.108623	NM_003247:Homo sapiens thrombospondin 2	2.59
	456371 429098	S76825 AF030249	Hs.89695	Hs.89695:insutin receptor	2.59
55	414443	AU077268	Hs.196176 Hs.76144	NM_001398:Homo sapiens encyl Coenzyme A	2.59
	428484	AF104032	Hs.184601	NM_002609:Homo sapiens platetet-derived - NM_003486:Homo sapiens solute carrier ta	2.59 2.59
	453309	AI791809	Hs.32949	NM_005218:Horno sapiens defensin, beta 1	2.59
	412867	AU076861	Hs.74637	NM_003217:Homo sapiens testis enhanced g	2.58
<i>(</i> 0	432827	Z68128	Hs.3109	Hs.3109:Rho GTPase activating protein 4	2.58
60	412669	AW880841	Hs.96908	NM_006034:Homo sapiens p53-induced prote	2.58
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	2.58
	452866	R26969	Hs.268016	Hs.268016:Homo sapiens cD: FLJ21243 fis,	2.58
	435129 424482	AI381659 BE268621	Hs.267086	Hs.267086:ESTs	2.57
65	410494	M36564	Hs.149155	NM_003374:Homo sapiens voltage-dependent	2.57
05	433895	Al287912	Hs.64016 Hs.3628	NM_000313:Homo sapiens protein S (alpha) NM_004834:Homo sapiens mitogen-activated	2.56
	442566	R37337	Hs.12111	Hs.12111:ESTs	2.56 2.56
	417640	D30857	Hs.82353	NM_006404:Homo sapiens protein C recepto	2.56
	442622	NM_000435		NM_000435:Homo sepiens Notch homolog 3 (	2.56
70	430346	AK000331	Hs.297641	Hs.297641:retinoblastoma-associated fact	2.55
	419344	U94905	Hs.277445	Hs.277445:diacylglycerol kise, zeta (104	2.55
	426500	NM_014638		NM_014638:Homo sapiens KIAA0450 gene pro	2.55
	408048	NM_007203		NM_007203:Homo sapiens A kise (PRKA) and	2.55
75	450700	AW732799	Hs.25348	NM_005860:Homo sapiens follistatin-like	2.54
13	417018	M16038	Hs.80887	NM_002350:Homo sapiens v-yes-1 Yamaguchi	2.54
	419378	R24922 AA310753	Hs.90078 Hs.42491	Hs.90078:nucleotide-sugar transporter si	2.54
	422451 435906	AI686379	Hs.110796	Hs.42491:ESTs, Moderately similar to hyp Hs.110796:SAR1 protein	2.53
	400231	middlet a	144.110780	Hacitatanani binday	253 253
80	417849	AW291587	Hs.82733	NM_007351:Homo sapiens nidogen 2 (NID2),	2.53
	427380	NM_005534	Hs.177559	NM_005534:Homo sapiens interferon garrama	2.52
	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	2.52
	438000	AJ825880	Hs.5985	Hs.5985:non-kise Cdc42 effector protein	2.52

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	448719	AA033627	Hs.21858	Hs.21858:serine (or cysteine) proteise i	2.52
	422396 420787	W21872	Hs.7907	Hs.7907:L-fucose kise	2.52
	430590	AA564248 AW383947	Hs.351292 Hs.246381	Hs.351292:Homo sapiens cD FLJ32605 fis,	2.51
5	447026	BE313144	Hs.324844	NM_001251:Homo sapiens CD68 entigen (CD6 Hs.324844:hypothetical protein IMAGE3455	2.51
,	439223	AW238299	Hs.250618	Hs.250618:UL16 binding protein 2	2.51 2.50
	435151	AA348482	Hs.4788	Hs.4788:nicastrin	2.50
	448202	AB002292	Hs.20695	NM_014829:Homo sepiens Rho quanine nucle	2.50
	449943	AF104266	Hs.24212	Hs.24212:tatrophilin	2.50
10	425743	BE396495	Hs.159428	Hs.159428:BCL2-associated X protein	2.50
	444681	AJ243937	Hs.288316	Hs.288315:chromosome 6 open reading fram	2.50
	421643	BE281170	Hs.106357	NM_007126:Homo sepiens valosin-containin	2.50
	426865	D63476	Hs.172813	NM_003899:Homo sepiens Rho guanine nucle	2.50
15	432306	Y18207	Hs.303090	NM_005398:Homo saplens protein phosphata	2.49
13	421846 421905	AA017707 Al660247	Hs.1432	NM_002743:Horno saplens protein kisa C su	2.49
	419493	AF001212	Hs.32699 Hs.90744	Hs.32699:Homo sapiens, Similar to RIKEN	2.49
	422530	AW972300	Hs.118110	NM_002815:Homo sapiens proteasome (proso NM_004335:Homo sapiens bone marrow strom	2.49
	442821	BE391929	Hs.8752	NM_014255:Homo sapiens transmembrane pro	2.48 2.48
20	416919	T97839	Hs.80464	NM_006402:Homo sapiens hepatitis B virus	2.48
	.443105	X96753	Hs.9004	NM_001897:Homo saplens chondraitin suffa	2.48
	430040	AW503115	Hs.227823	NM_014287:Homo sapiens pM5 protein (PM5)	2.48
	428028	U52112	Ha.182018	NM_001569:Homo sapiens interleukin-1 rec	2.47
25	424307	AW293399	Hs.356377	Hs.356377:Homo sapiens, clone IMAGE:3633	2.46
25	434511	R28982	Hs.18106	Hs. 18108:ESTs, Weakly similar to T06291	2.46
	454390	AB020713	Hs.56966	Hs.56966:KIAA0906 protein	2.46
	417785	X59812	Hs.82568	NM_000784:Homo sapiens cytochrome P450,	2.46
	424873 422003	AA345051 AA361760	Hs.294092 Hs.296326	Hs. 294092:Homo sapiens mR full length in	2.46
30	432126	AA865239	Hs.37196	Hs.296326:ESTs, Wealdy similar to A33533	2.46
20	445937	AJ452943	Hs.321231	Hs.37198:putative G protein coupled rece NM_003779:Homo sapiens UDP-Gal:betaGloc	2.46 2.46
	409354	N68188	Hs.159472	Hs.159472:Homo sepiens cD: FLJ22224 fis,	2.46
	401179			THE TOTAL CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF	2.46
	418151	AA864238	Hs.83583	NM_005731:Homo sapiens actin related pro	2.45
35	422648	D86983	Hs.118893	Hs.118893:Melanoma associated gene	2.45
	427759	BE245578	Hs.2200	NM_005041:Homo sapiens perforin 1 (prefo	2.45
	431222	X56777	Hs.273790	NM_007155:Homo sepiens zo pellucida glyc	2.45
	411529	AA430348	Hs.317596	Hs.317596:Homo sapiens cD FLJ12927 fis,	2.45
40	426825	AL133415	Hs.297753	NM_003380:Homo sapiens vimentin (VIM), m	2.45
70	422242 408105	AJ251760 AW152207	Hs.273385 Hs.270977	NM_016592:Homo sapiens GS complex locus	2.45
	426410	BE298446	Hs.305890	Hs.270977:ESTs Hs.305890:BCL2-like 1	2.44
	421064	AJ245432	Hs.101382	NM_006291:Homo sapiens tumor necrosis fa	2.44 2.44
	428157	AI738719	Hs.198427	NM_000189:Homo sapiens hexokise 2 (HK2),	-244
45	424398	8E397787	Hs.146393	NM_014685:Homo sapiens homocysteine-indu	2.44
	424825	AF207069	Hs.153357	NM_001084:Homo sepiens procollagen-lysin	2.44
	426031	AA295251	Hs.166066	Hs.166066:cisplatin resistance associate	2.43
	409817	BE295464	Hs.56607	Hs.56607:Williams-Beuren syndrome chromo	2.43
50	429359	W00482	Hs.2399	NM_004995:Homo sapiens matrix metallopro	2.43
20	426761	AJ015709	Hs.172089	Hs.172089:pro-oncosis receptor inducing	2.43
	429332 425923	AF030403 NM_005028	Hs.199263 Hs.162808	NM_013233:Homo saplens serine threonine	2.43
	432211	BE274530	Hs.273333	NM_005026:Homo sepiens phosphoinositide-	2.43
	433339	AF019226	Hs.8036	Hs.273333:hypothetical protein FLJ10986 Hs.8035:RAB3D, member RAS oncogene famil	2.43 2.42
55	420539	AA282735	Hs.44004	Hs.44004:AD031 protein	2.42
	413243	AA769266	Hs.193657	Hs.193657:ESTs	2.42
	435029	AF167706	Hs.19280	Hs.19280:cysteine-rich motor neuron 1	2.42
	422374	AW732869	Hs.1519	Hs.1519:protein kise, cAMP-dependent, re	2.42
60	444501	AW247624	Hs.11342	NM_004148:Homo saplens ninjurin 1 (NINU1	2.42
60	414919	AW087337	Hs.194461	Hs.194461:ESTs	2.42
	419355	AA428520	Hs.90061	NM_006667:Homo sapiens progesterone rece	2.42
	436042 418245	AF284422 AA088767	Hs.119178	Hs.119178:cation-chloride cotransporter-	2.42
	444215	AB033075	Hs.83883 Hs.10669	Hs.83883:transmembrane, prostate androge	2.42
65	408683	R58665	Hs.46847	Hs.10569:development and differentiation NM_015614:Homo sapiens TRAF and TNF rece	2.41 2.41
	423701	AA329856	Hs.143022	Hs.143022:ESTs	2.41
	441783	BE313412	Hs.7961	Hs.7961:Homo sapiens clone 25012 mR segu	2.41
	428072	BE258602	Hs.182366		2.41
=-	434599	AB002313	Hs.3989	Hs.3989:plexin B2	2.40
70	442351	W52642	Hs.8261	Hs.8261:SPRY domain-containing SOCS box	2.40
	407894	AJ278313	Hs.41143	Hs.41143:phospholipase C, beta 1 (phosph	2.40
	453449	W16752	Hs.32981	Hs.32981:sema domain, immunoglobulin dom	2.40
	408688	A1634522	Hs.152925		240
75	422448	AW372922 AA177138	Hs.116774		2.39
, 5	416269 452679	Z42387	Hs.161671 Hs.83883		2.39
	432981	NM_002733		Hs.83883:transmembrane, prostate androge NM_002733:Homo sapiens protein kise, AMP	2.38 2.38
	419846	NM_015977			2.38
	422110	AL376736	Hs.111779		2.38
80	413092	AA126856	Hs.118665		2.38
	433969	AW207279	Hs.271786		2.37
	451267	AI033894	Hs.117865	Hs.117865:solute carrier family 17 (anio	2.37
	447526	AL048753	Hs.303649	NM_002982:Homo sapiens small inducible c	2.37

	441622	A 42+ CDOC	14- 240240	11 010340-lines	
	441623 420255	AA315805 NM_007289	Hs.348710 Hs.1298	Hs.348710:Homo sapiens, cione IMAGE:4242 NM_007289:Homo sapiens membrane metallo-	2.37
	409274	NM_003930	Hs.52644	NM_003930:Homo sapiens are family associ	2.37 2.36
_	422801	AF125672	Hs.287994	Hs.287994:nuclear receptor co-repressor	2.36
5	407887	AA579668	Hs.41072	Hs.41072:serine (or cysteine) proteise i	2.38
	408212	AA297567	Hs.43728	NM_015696:Homo sepiens weakly similar to	2.36
	430478	NM_014349	Hs.241535	NM_014349:Homo sapiens apolipoprotein L,	2.36
	405102 423583	AL122055	Un 42002C	14- 10002C-VIA 11020	2.35
10	426125	X87241	Hs.129836 Hs.166994	Hs.129836:KIAA1028 protein NM_005245:Homo sapiens FAT tumor suppres	2.35 2.35
10	425204	NM_002436	Hs.1861	NM_002435:Homo sapiens membrane protein,	2.35
	420676	AI434780	Hs.4248	Hs.4248:Homo sapiens PP3781 mR, complete	2.35
	421079	AW404994	Hs.101695	Hs. 101695:NCK adaptor protein 2	2.35
16	410039	AF207989	Hs.58014	Hs.58014:G protein-coupled receptor, fam	2.34
15	412958	BE391579	Hs.75087	NM_006712Home saplens FAST tise (FASTK)	2.34
	430363 425397	M28713 J04088	Hs.274464	NM_000398:Homo sepiens diaphorase (DH) (	2.34
	451035	AU076785	Hs.156346 Hs.430	NM_001067:Homo sapiens topoisomerase (D) NM_002670:Homo sapiens plastin 1 (I isof	2.34 2.34
	449027	AJ271216	Hs.22880	Hs.22880:dipeptidylpeptidase III	234
20	429457	BE243065	Hs.202955	Hs.202955:hypothetical protein FLJ20507	2.34
	417709	D87434	Hs.82426	NM_014734:Homo sapiens KIAA0247 gene pro	2.34
	412805	AW954569	Hs.278675	Hs.278675:bromodomain-containing 4	2.34
	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cD FLJ31360 fis,	2.34
25	430702 456804	U56979 AJ421645	Hs.278568 Hs.139851	NM_000186:Homo sepiens H factor 1 (compl NM_001233:Homo sepiens caveolin 2 (CAV2)	2.33 2.33
20	453648	W21493	Hs.28329	Hs.28329:protein phosphatase 1, regulato	2.33 2.33
	450812	AB002360	Hs.25515	Hs.25515:MCF.2 cell line derived transfo	2.33
	402575				2.33
20	424670	W61215	Hs.116651	NM_005797:Homo sapiens epithelial V-like	2.32
30	452960	AK001335	Hs.31137	NM_006504:Homo sapiens protein tyrosine	2.32
	442968 410639	AK000606 BE269047	Hs.8868 Hs.65234	NM_004871:Homo sapiens golgi SP receptor Hs.65234:DEAD/H (Asp-Glu-Ala-Asp/His) bo	2.32
	415169	W42913	Hs.78089	NM_004231:Homo sapiens ATPase, H+ transp	2.32 2.32
	450160	BE048099	Hs.183738	Hs.183738:FERM, RhoGEF (ARHGEF) and plec	2.32
35	407223	H96850		H96850:yw03b12.s1 Soares melanocyte 2NbH	2.32
	426780	BE242284	Hs.172199	NM_001114:Homo sapiens adenylate cyclase	2.32
	434987	AW975114	Hs.371677	Hs.371677:ESTs	2.32
	416354	NM_000633	Hs.79241	NM_000633:Homo sapiens B-cell CLL/lympho	2.31
40	453107 422963	NM_016113 M79141	Hs.279746 Hs.13234	NM_015113:Homo sapiens transient recepto Hs.13234:ESTs, Wealdy similar to hypothe	2.31 2.31
	433618	AA602539	Hs.345494	Hs.345494:ESTs, Moderately similar to ZN	231
	438584	AAB11347		AA811347:ob81h06.s1 NCI_CGAP_GCB1 Homo s	231
	446126	AW085909	Hs.356618	Hs.356618:ESTs, Weakly similar to PC4259	2.31
45	408716	AI567839	Hs.151714	Hs.151714:peroxisomal proliferator-activ	2.30
43	433230	AW136134	Hs.220277	Hs.220277:ESTs, Weakly similar to expres	2.30
	410168 446342	AW834050 BE298665	Hs.351432 Hs.14846	Hs.351432:tensin Hs.14846:Homo sapiens mR; cD 0XFZp564D01	2.30 2.30
	418452	BE379749	Hs.85201	NM_005127:Homo saplens C-type (catcium d	2.30
	453175	NM_006834	Hs.32217	NM_006834:Homo sapiens RAB32, member RAS	2.29
50	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	2.29
	452848	AJ417193	Hs.288912	Hs.288912:BBP-like protein 2	2.29
	418838	AW385224	Hs.35198	Hs.35198:ectonucleotide pyrophosphatase/	2.29
	422562 432828	AI962060 AB042326	Hs.118397	NM_001129:Homo sapiens AE binding protei	2.28
55	412948	BE243313	Hs.287402 Hs.334851	Hs.287402:chondroi5n 4-sulfotransferase NM_006148:Homo sapiens UM and SH3 prote	2.28 2.28
	426068	AF029778	Hs.166154	NM_002225:Homo saplens jagged 2 (JAG2),	2.28
	456919	NM_003900	Hs.182248	NM_003900:Homo sapiens sequestosome 1 (S	2.28
	452806	AW014549	Hs.58373	Hs.58373:ESTs	2.28
60	453983	H94997	Hs.16450	Hs.16450:ESTs	2.28
00	407736 413211	N41744 AW967107	Hs.349326		2.28
	422051	AW327546	Hs.109274 Hs.111024		2.28 2.27
	438438	AA257992	Hs.50651	Hs.50651:Janus kise 1 (a protein tyrosin	2.27
	436278	BE396290	Hs.5097	NM_004710:Homo sapiens syptogyrin 2 (SYN	2.27
65	454080	Al199711	Hs.576	NM_000147:Homo sapiens fucosidase, alpha	2.27
	426542	AF190746	Hs.170310		2.27
	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	2.27
	402901 412898	Al129903	Hs.74669	NM_006634:Homo sapiens vesicle-associate	2.26 2.26
70	413020	R98736	113.17003	R98736;yr31h09.r1 Soares fetal liver spl	2.26
	413939	AL047051	Hs.199961		2.26
	408581	AW953853	Hs.281462		2.25
	412330	NM_005100		NM_005100:Homo sapiens A kise (PRKA) and	2.25
75	442083	R50192	Hs.165062		2.25
13	418271	NM_000919		NM_000919:Homo sapiens peplidylghycine a	2.25
	433376 438562	AI249361 AI566826	Hs.74122 Hs.25890	NM_001225:Homo sepiens caspase 4, apopto	2.25
	443883	AA114212	Hs.9930	Hs.25890:ESTs, Wealdy similar to transdu NM_001235:Homo sapiens serine (or cystei	2.25 2.25
	416976	BE243985	Hs.80680	Hs.80680:major vauli protein	2.24
80	416914	AA344481	Hs.80426	Hs.80426:brain and reproductive organ-ex	2.24
	400288	X06256	Hs.149609	NM_002205:Homo sapiens integrin, alpha 5	2.24
	407904	W44735	Hs.107260		2.24
	429690	AW956329	Hs.23721	Hs.23721:ESTs	2.24



	443813	AA876372	Hs.93961	Hs.93961:Homo sapiens mR; cD DKFZp667D09	2.24
	427458	BE208364	Hs.29283	Hs.29283:ESTs, Weakly similar to UKHU pr	2.24
	454294	AB000734	Hs.50640	NM_003745:Homo sapiens JAK binding prote	2.24
_	407192	AA609200	Hs.366318	Hs.366318:ESTs	2.23
5	425751	T19239	Hs.1940	NM_001885:Homo sapiens crystallin, alpha	2.23
	456437 413019	A1924228 BE281604	Hs.115185 Hs.75140	Hs.115185:ESTs NM_002337:Homo saplens low density Epop	2.23 2.23
	418862	BE550964	Hs.89399	Hs.89399-ATP synthase, H+ transporting,	223
	435284	AA879470	Hs.96849	Hs.96849:Homo sapiens cD FLJ11492 fis, c	2.23
10	429630	M85289	Hs.211573	NM_005529:Homo sapiens heparan sulfate p	2.23
	427609	AK000436	Hs.179791	Hs.179791:RAB20, member RAS oncogene fam	2.23
	421917 446616	AB028943 R65964	Hs.109445 Hs.334873	Hs.109445:hypermethylated in cancer 2 Hs.334873:carboxypep6dase M	2.23 2.23
	407232	X04526	15.00-015	X04526:Human liver mR for beta-subunit s	223
15	423798	AF047033	Hs.132904	Hs.132904:solute cernier family 4, sodiu	2.23
	446755	AW451473	Hs.16134	NM_005990:Homo sapiens serine/threonine	2.22
	452865 431393	AI924046 AW971493	Hs.119567	Hs. 119567:ESTs, Wealdy similar to ALU1_H	2.22
	431890	X17033	Hs.134269 Hs.271986	Hs.134269:ESTs, Weakly similar to 200439 NM_002203:Homo sapiens integrin, atpha 2	2.22 2.22
20	428782	X12830	Hs.193400	NM_000565:Homo sapiens interleukin 6 rec	2.22
	446006	NM_004403	Hs.13530	NM_004403:Horno sapiens deafness, autosom	2.22
	435418	AJ245874	Hs.4245	Hs.4245:chromosoma 11 hypothetical prote	2.22
	423869 437730	BE409301 AW071087	Hs.134012 Hs.239176	NM_006688:Homo saplens C1q-related facto Hs.239176:insufin-fike growth factor 1 r	2.21 2.21
25	444020	R92962	Hs.35052	Hs.35052:ESTs	2.21
	413882	AA132973	Hs.184492	Hs.184492:Homo sapiens mR; cD DKFZp66780	2.21
	412654	AI093480	Hs.374319	Hs.374319:ESTs	2.21
	448988 426841	Y09763 AI052358	Hs.22785 Hs.131741	NM_004961:Homo sapiera gamma-aminobutyri Hs.131741:ESTs	2.21 2.21
30	408196	AL034548	Hs.43627	NM_006943:Homo saplens SRY (sex determin	221
	451711	AK000461	Hs.26890	Hs 26890:cat eye syndrome chromosome reg	2.20
	414325	AA251929	Hs.355341	Hs.355341:Homo sapiens, clone IMAGE:3536	2.20
	424512 448883	X53002 BE614989	Hs.149846 Hs.7503	NM_002213:Homo sapiens integrin, beta 5 Hs.7503:hypothetical protein FLJ14153	2.20 2.20
35	411296	BE207307	Hs.10114	Hs.10114:growth suppressor 1	2.20
	452268	NM_003512	Hs.28777	NM_003512:Homo saplens H2A histone famili	2.20
	416810	AF035606	Hs.80019	NM_013232:Homo saplens programmed cell d	2.20
	441415 444212	H21497 AW503976	Hs.7471 Hs.10649	Hs.7471:88P-like protein 1 NM_004848:Homo sapiens basement membrene	2.20 2.19
40	428044	AA093322	Hs.301404	NM_006743:Homo sapiens R binding motif p	2.19
	430017	AA263172	Hs.35	NM_002832:Homo saplens protein tyrosine	2.19
	424490 431193	AJ278016 AW749505	Hs.55565 Hs.296770	Hs.55565:ankyrin repeat domain 3 Hs.296770:KIAA1719 protein	2.19
	453686	AL110326	Hs.304679	Hs.304679:ESTs, Weakly similar to Z195_H	2.19 2.19
45	448262	AW880830	Hs.186273	Hs.186273:ESTs	2.19
	416065	BE267931	Hs.78996	NM_002592.Homo sapiens proliferating cel	2.19
	442045 423804	C05768 AW403448	Hs.8078 Hs.1706	Hs.8078:Homo sapiens clone FBD3 Cri-du-c NM_006084:Homo sapiens interferon-stimul	2.19 2.19
	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	2.19
50	424503	NM_002205	Hs.149609	NM_002205:Homo sapiens integrin, alpha 5	2.19
	437696 405204	Z83844	Hs.5790	Hs.5790:hypothetical protein dJ37E16.5	2.18
	426158	NM_001982	Hs.199067	NM_001982:Homo sapiens v-erb-b2 erythrob	2.18 2.18
	417418	NM_002468	Hs.82116	NM_002468:Homo sapiens myelold different	2.18
55	412773	H15785	Hs.74573	NM_012268:Homo saplens similar to vaccin	2.18
	409402 443791	AF208234 N64458	Hs.695 Hs.143345	NM_000100:Homo sapiens cystatin 8 (stefi	2.18
	435049	AL122067	Hs.4746	Ha.143345:ESTs Ha.4746:hypothetical protein FLJ21324	2.18 2.18
<b>CO</b>	418389	AA830613	Hs.293849		2.18
60	450712	A1732130	Hs.270496		2.18
	422007 453676	AI739435 AW853745	Hs.39168 Hs.286035	Hs.39168:ESTs, Weakly similar to T17340	2.18
	415718	F30631	Hs.200237		2.18 2.18
	452688	AA721140	Hs.49930	Hs.49930:ESTs, Weakly similar to B34087	2.18
65	415988	BE407713	Hs.78943	NM_000385:Homo sapiens bleomycin hydrola	2.18
	409453 417512	AI885516 X76534	Hs.95812	Hs.95612ESTs	2.17
	427202	BE272922	Hs.82226 Hs.173936	NM_002510:Homo sapiens glycoprotein (tra NM_000628:Homo sapiens interleukin 10 re	2.17 2.17
70	440983	M20681	Hs.7594	NM_006931:Homo sapiens solute carrier fa	2.17
70	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate	2.17
	429642 427213	X68264 AW007211	Hs.211579 Hs.348389		2.17 2.17
	437763	AA469369	Hs.5831	NM_003254:Homo sapiens tissue inhibitor	2.17
76	454000	AA040620	Hs.5672	Hs.5672:golgi membrane protein \$8140	2.17
75	424247	X14008	Hs.234734	NM_000239:Homo sapiens hysozyme (rel army	2.16
	403857 406648	AA563730	Hs.277477	Hs.277477:major histocompatibility compl	216
	400265		- 100211711	- man control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the	2.15 2.16
80	442379	NM_004613		NM_004613:Homo sapiens transglutamise 2	2.16
90	441892 417446	AB028981 AL118671	Hs.8021 Hs.82163	Hs.8021:KIAA1058 protein	2.16
	418386	AA361739	Hs.84549	NM_000898:Homo sepiens monoamine coldese NM_002494:Homo sepiens DH dehydrogese (u	2.16 2.16
	414053	BE391835	Hs.75725	NM_003564;Homo sapiens transgelin 2 (TAG	2.16

	440906	AW161556	Hs.240170	Hs.240170:hypothetical protein MGC2731	2.16
	447660	AW160386 AF216965	Hs.163667	Hs.163667:ESTs, Weakly similar to CA1H_H	2.16
	408279 426152	BE299190	Hs.44095 Hs.167246	Hs.44095:cyclin M3	2.16
5	437952	D63209	Hs.5944	Hs.167246:P450 (cytochrome) axidoreducta	216
-	415661	AF057307	Hs.78575	NM_014585:Homo sapiens solute carrier ta Hs.78575:prosaposin (variant Gaucher dis	2.16 2.15
	425302	U79115	Hs.155566	NM_003805:Homo sapiens CASP2 and RIPK1 d	2.15
	425996	W67330	Hs.374451	Hs.374451:ESTs	215
	413745	AW247252	Hs.75514	NM_000270:Homo sapiens nucleoside phosph	2.15
10	422070	AF149785	Hs.111126	Hs.111126:pituitary tumor-transforming 1	215
	448424	AW009892	Hs.31924	Hs.31924:ESTs	2.15
	430035	NM_003463	Hs.227777	NM_003463:Homo sapiens protein tyrosine	2.15
	438407	AV457122	Hs.129673	Hs.129673:eukaryotic translation initiat	2.15
16	435551	AF212365	Hs.5470	Hs.5470:interleukin 17B receptor	215
15	437741	BE561610	Hs.5809	Hs.5809:putative transmembrane protein;	215
	441192	AA526626	Hs.7736	NM_016504:Homo sapiens mitochondrial rib	215
	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	2.15
	411165 425252	NM_000169 AW391162	Hs.69089 Hs.349306	NM_000169:Homo sapiens galactosidase, al	2.14
20	427600	AW630918	Hs.179774	Hs.349306:hypothetical protein FLJ31951 NM_002818:Homo sapiens proteasome (proso	214 214
20	426818	AA554827	Hs.292996	Hs.292996:postmeiotic segregation increa	2.14
	442110	AF113008	Hs.8102	NM_001023:Homo saplens ribosomal protein	2.14
	407797	AK000524	Hs.39850	Hs.39850:uridine kise-like 1	2.14
	443044	N28522	Hs.8935	NM_014298:Homo sapiens quinolite phospho	2.14
25	437103	AW139408	Hs.152940	Hs.152940:ESTs	2.14
	442069	AW664144	Hs.297007	Hs.297007:Homo sapiens cD FLJ32174 fis,	2.14
	424954	NM_000545	Hs.1846	NM_000546:Homo sapiens turnor protein p53	2.14
	458097	AW341135	Hs.58104	Hs.58104:Homo sapiens, clone IMAGE:47309	2.14
20	411925	AW014588	Hs.72925	NM_003475:Homo sapiens chromosome 11 ope	2.14
30	449644	AW960707	Hs.148324	Hs.148324:ESTs	2.14
	422675	BE018517	Hs.119140	NM_001970:Homo saplens eukaryotic transl	2.14
	428586 429379	M36712 NM_014840	Hs.2299 Hs.200598	Hs.2299:CD8 antigen, beta polypeptide 1	214
	410290	AA402307	Hs.322844	NM_014840:Homo saplens KIAA0537 gene pro Hs.322844:hypothetical protein DKFZp564A	2.13
35	443895	AW979048	Hs.292566	Hs.292566:YEA4 protein	2.13 2.13
-	428145	BE243327	Hs.182626	NM_012264:Homo sepiens chromosome 22 ope	2.13
	453518	AW503205	Hs.27268	Hs. 27268: Homo sapiens cD: FLJ21933 fis.	213
	456534	X91195	Hs.100623	Hs.100623:protein phosphatase 1, regulat	2.13
	419972	AL041465	Hs.182982	Hs.182982:golgin-67	2.13
40	424950	AA602917	Hs.156974	Hs.156974:ESTs	2.13
	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	2.13
	431449	M55994	Hs.256278	NM_001066:Homo saplens tumor necrosis fa	2.13
	418758	AW959311	Hs.172012	Hs.172012:hypothetical protein DKFZp434J	2.13
45	434202	BE382411	Hs.3764	NM_000858:Homo sapiens guanylate kise 1	2.13
73	433233 452700	AB040927 Al859390	Hs.301804	Hs.301804:KIAA1494 protein	2.12
	438033	T26483	Hs.288940 Hs.6059	Hs.288940:transmembrane protein 8 (five	2.12
	400847	120403	na.0033	NM_016938:Homo saplens EGF-containing fi	2.12 2.12
	447547	NM_007229	Hs.18842	NM_007229:Homo sapiens protein kise C an	2.12
50	417052	NM_000712	Hs.81029	NM_000712:Homo sepiens biliverdin reduct	2.12
-	413284	AU077055	Hs.289107	NM_001166:Homo sepiens bacutoviral IAP r	211
	434558	AW264102	Hs.39168	Hs.39168:ESTs, Weakly similar to T17340	211
	404030				2.11
	410801	BE275469	Hs.66493	Hs.66493:Down syndrome critical region g	211
55	418613	AA744529	Hs.86575	Hs.86575:mitogen-activated protein kise	2.11
	447087	AW403870	Hs.301872	Hs.301872:hypothetical protein MGC4840	2.11
	433026	AW160616	Hs.279921	NM_016127:Homo sapiens hypothetical prot	2.11
	426433	1.38969	Hs.169875	NM_007112:Homo sapiens thrombospondin 3	2.11
60	442439 437379	U09759 AL359575	Hs.246857	NM_002752:Homo sapiens mitogen-activated	2.11
00	400208	ALGUSUIS	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	211 211
	455705	AW161061	Hs.356580	Hs.356580:ESTs, Wealthy similar to zinc f	2.11
	417599	AA204688	Hs.62954	Hs.62954:ferritin, heavy polypeptide 1	2.10
	416728	AB024597	Hs.79658	NM_001894:Homo sapiens casein kise 1, ep	2.10
65	439920	H05430	Hs.288433	Hs.288433:neurotrimin	2.10
	422309	U79745	Hs.114924		2.10
	436114	AA778232	Hs.19515	Hs.19515:ESTs, Highly similar to NRG3_HU	2.10
	405517				2.10
70	421872	AA359753	Hs.22824	Hs.22824:MYB binding protein (P160) 1a	2.10
70	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine klse, rec	2.10
	431214	AA294921	Hs.348024		2.10
	412856	BE388745	Hs.74631	NM_001728:Homo sapiens basigin (BSG), mR	2.10
	442064	AJ422867	Hs.88594	Hs.88594:Homo sapiens, clone IMAGE:43329	2.10
75	434845 426728	BE267057	Hs.325321		2.10
, ,	420720	NM_007118 BE379320	Hs.387689 Hs.91448		2.10
	448913	AA194422	Hs.22564	NM_007026:Homo sapiens dual specificity	2.09 2.09
	414721	X90392	Hs.77091	NM_004999:Homo sapiens myosin VI (MYO6), NM_006730:Homo sapiens deoxyribonuclease	2.09
	424658	NM_002406			2.09
80	432805	X94630	Hs.3107	Hs.3107:C097 antigen	2.09
-	447032	AK000310	Hs.17138	Hs.17138:hypothetical protein FLJ20303	2.09
	447484	AA454839	Hs.292566	Hs.292568:YEA4 protein	2.09
	440188	AK001812	Hs.7036	Hs.7036:N-acetylgtucosarráne kíse	2.09

	445504	AC247610	W- 0300	AL GOOD PROMO	200
	445584 402559			Hs.8360:PTD012 protein	2.09 2.09
	416043			Hs.83341:AXL receptor tyrosine kise	2.09
5	448888	AW196663		Hs.200242:caspase recruitment domain fam	2.09
)	436910 422573	AA926944	Hs.261587	Hs.261587:GCN2 etF2alpha kise	2.09
	416448	AW297985 L13210	Hs.295726 Hs.79339	Hs.295726:integrin, atpha V (vitronectin NM_005587:Homo sapiens tectin, galactosi	2.08 2.08
	428727	AF078847	Hs.191356	NM_001515:Homo sapiens general transcrip	2.08
	410301	AW502935	Hs.740	Hs.740:PTK2 protein tyrosine kise 2	2.08
10	449538	AJ559444	Hs.104679	Hs.104679:Homo sepiens, clone MGC:18216	2.08
	421205	AL137540	Hs.102541	Hs.102541:netrin 4	2.08
	411779	AA292811	Hs.72050	NM_003551:Homo sapiens non-metastatic ce	2.08
	427704	AW971063	Hs.292882	Hs.292882:ESTs	2.07
15	413518 447345	BE149455 BE247767	Hs.75415 Hs.18166	NM_004048:Homo saplens beta-2-microglobu Hs.18168:KIAA0870 protein	2.07 2.07
	407143	C14076	Hs.332329	Hs.332329:EST	2.07
	448431	BE613081	Hs.337772	Hs.337772:hypothetical protein BC009331	2.07
	412760	AW379030	Hs.41324	Hs.41324:EST8	2.07
20	446859	AJ494299	Hs.16297	NM_005694:Homo sapiens COX17 homolog, cy	2.07
20	403966	41000000	11. 50054		2.07
	409115 436823	AI223335 AW749865	Hs.50651 Hs.117077	NM_002227:Homo sapiens Janus kise 1 (a p	2.07 2.07
	414045	NM_002951	Hs.75722	Hs.117077:zinc finger protein 264 NM_002951:Homo sapiens ribophorin II (RP	2.06
	413980	NM_002437	Hs.75659	NM_002437:Homo sapiens MoV17 transgene,	2.06
25	439414	NM_001183	Hs.6551	NM_001183:Homo sapiens ATPase, H+ transp	2.06
	426059	BE292842	Hs.166120	NM_001572:Homo sapiens interferon regula	2.06
	429849	U33053	Hs.2499	NM_002741:Homo sepiens protein kise C-li	2.06
	402424 406626	X04526	Hs.215595	Hs.215595:guanine nucleotide binding pro	2.06 2.06
30	458911	AA373131	Hs.24322	Hs.24322-ATPase, H+ transporting, lysoso	2.05
-	426086	T94907	Hs.188572	Hs.188572:EST8	2.05
	419726	U50330	Hs.1274	NM_006129:Homo saplens bone morphogeneti	2.05
	452344	AI264357	Hs.55405	Hs.55405:hypothetical protein MGC16212	2.05
35	442498	U54617	Hs.8364	NM_002612:Homo saplens pyruvate dehydrog	2.05
33	422114 413420	AW194851 AW410235	Hs.111801 Hs.75348	NM_015908:Homo sapiens arsete resistance NM_006263:Homo sapiens proteasome (proso	2.05 2.05
	409430	R21945	Hs.346735	Hs.346735:Homo sapiens, clone IMAGE:3881	2.05
	409932	AJ376750	Hs.57600	Hs.57600:adaptor-related protein complex	2.05
40	434848	BE256304	Hs.32148	Hs.32148:AD-015 protein	2.04
40	453852	AW961818	Hs.374424	Hs.374424:ESTs	2.04
	427637 400264	AK000816	Hs.179986	NM_005803:Homo sapiens flotillin 1 (FLOT	2.04
	430016	NM_004736	Hs.227656	NM_004736:Homo sapiens xenotropic and po	. 2.04 2.04
	410134	U68140	Hs.58927	Hs.58927:nuclear VCP-like	2.04
45	440975	AW499914	Hs.7579	Hs.7579:importin 9	2.04
	432280	BE440142	Hs.2943	NM_003135:Homo sapiens sigl recognition	2.04
	409504 412146	AA304961	Hs.699	NM_000942:Homo sapians peptidylprolyl is	2.04
	434203	M92444 BE262677	Hs.73722 Hs.283558	NM_001641:Homo sapiens APEX nuclease (mu Hs.283558:hypothetical protein PRO1855	2.04 2.04
50	422754	AA316476	Hs.171811	Hs.171811:adenylate kise 2	2.04
	406729	AA069711		AA069711:zm52b11.s1 Stratagene fibroblas	2.04
	413086	AA126841	Hs.183834	Hs.183834:ESTs	2.03
	424340	AA339036	Hs.7033	Hs.7033:ESTs	2.03
55	450440 424662	AB024334 NM_002870	Hs.25001 Hs.151536	NM_012479:Homo sapiens tyrosine 3-monoox NM_002870:Homo sapiens RAB13, member RAS	2.03 2.03
-	415740	N80486	Hs.39911	Hs.39911:Homo sapiens mR for FLJ00089 pr	2.03
	412749	AA378417	Hs.74564	NM_003145:Homo sapiens sigl sequence rec	2.03
	408393	AW015318	Hs.23165	Hs.23165:ESTs	2.03
60	421295	AW081081	Hs.103180		2.03
ŲΟ	445417 414883	AK001058 AA926960	Hs.12680 Hs.348669	Hs. 12680:Homo sapiens cD FLJ10196 fls, c	2.03
	447298	BE617527	Hs.239818		2.03 2.02
	459580	AA022888	Hs.176065		2.02
	422785	AI824114	Hs.289088		2.02
65	452696	A1826645	Hs.211534	Hs.211534:Homo sapiens cD FLJ31565 fis,	2.02
	452056	AW955065	Hs.101150		2.02
	450690 423527	AA296698 AI206965	Hs.333418 Hs.105861		2.02 2.01
	429545	AIB24164	Hs.356130		2.01
70	439180	A1393742	Hs.199067		2.01
	437193	BE259190	Hs.289721		2.01
	436014	AF281134	Hs.283741		2.01
	453329	T97205	Hs.193400		2.01
75	407347 435370	AA829847 AI964074	Hs.225838	T23514:seq3329 1-NiB Homo sapiens cD do Hs.225838:ESTs	2.01 2.01
,,	430657	AA482910	Hs.370602		2.01
	427157	U51166	Hs.173824		201
	424833	NM_003894	Hs.153405	NM_003894:Homo sapiens period homotog 2	2.01
80	440086	NM_005402		NM_005402Homo sepiens v-ref simian teuk	2.01
60	438543 417426	AA810141 NM_002291	Hs.192182		201
	412790			NM_002291:Homo sapiens laminin, beta 1 ( NM_014767:Homo sapiens KIAA0275 gene pro	2.01 2.01
	445892		Hs.93961	Hs.93961:Homo sapiens mR; cD DKFZp667009	2.01

	TABLE 388	t				
	Pkey:	Uniqu	a Eos probasati	dentifier number		
-	CAT number	r. Gene	cluster number			
5	Accession:	Genb	ank accession n	imbers		
	Pkey	CAT Number	Accession			
	409745	MH1944_5	B1030997 AA9	21874 AW188822 BIQ27882 AI347618 AI3614	3 ALUSS 754 AW207491 /	AA077391 BG012775 BG997382 AA286833 AA150722 Bi007625
10			B102/854 B100	9100 81006275 B1006270 B3031000 B1029854	RI009511 RI001651 RI00	06266 BI006991 BI006990 BI007763 BI007762 BG997377
10	419671	253275_1		33518 BI027818 BG015789 BI033807 AA3414 1866 AA248779 W02010	45	
	437495	65231_1		159908 BE177778 BE177779 AW893733 BF75	2319	
	418869	12789_14	AA229762 AA		0310	
	432648	129028_1		518150 AAS57952		
15	421902	276321_1		079601 BE079534 AA299964 BE392717 BE85	3402 RE079532 RE0181	4R RFRR9427 W00396
	414667	MH1944_5				AA077391 BG012775 BG997382 AA286833 AA150722 BI007625
						06266 B1006991 B1006990 B1007763 B1007762 BG997377
				33518 BI027B18 BG015789 BI033807 AA3414		
••	435185	127115_1		304346 AA669490		
20	411331	1076355_1	AW837178 T7			
	451876	2328579_1		021 BF370092 BF370127 BF370060 T62998		
	400261	23110_1				AI144456 AW628070 AI629032 AI358810 AI880433 A1440472
	430406	04000 4		5365 AW014799 AI767973 AW518041 AA909	398 AW768606	
25	439195 454694	21979_1	AF086037 H8			
23	416913	1065666_1 924456_1		V936544 AW813513 V749664 AW749902 BE162498 BE161005 BE	157400 DE151005 AA10	0440 ANK 19466 DE 189600 DE 181007
	459362	1238130_1	AW974073 TS		102455 DE 101000 AA15	0443 WA1313403 BC 105000 BC 101001
	-00002	,540,00_,	A1131 407 5 10	0307		
	TABLE 38	C:				
30	Pkey:		ue number corre	sponding to an Eos probeset		
	Ref:				Identifier (GI) numbers.	Dunham, et al.* refers to the publication entitled "The DNA
		upea	ence of human	thromosome 22" Dunham, et al. (1999) Nature	402:489-495.	
	Strand:			from which exons were predicted.		
35	Nt_position	n: Indic	ates nucleotide	positions of predicted exons.		
33		n-4	O 4	84 tot		
	Pkey 403346	Ref 8569726	Strand Plus	Nt_position 92752-93015		
	401621	8570184	Minus	193-608		
	403344	8569726	Plus	70823-70990		
40	404240	5002624	Minus	116132-116407,116653-116922		
	401964	3126781	Minus	13510-13725,13847-14015		
	404277	1834458	Minus	91665-91946		
	405121	8102330	Minus	35816-36004,36587-36684		
4.5	402493	9797670	Minus	205146-205240,205428-205542		
45	402121	9188523	Plus	25692-25895		
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757		
	403887	7710553	Minus	69533-69868		
	403328	8469086	Minus	120428-120703		
50	401241 401736	4827300 3219338	Minus	30503-30844,31056-31248		
30	405029	7533975	Plus Minus	1771-1894 37929-38224		
	404171	9930793	Plus	173667-173783,176876-177055		
	401797	6730720	Plus	6973-7118		
	401234	9929642	Plus	120173-120337		
55	404170	9930793	Plus	168836-169248		
	406122	9144087	Minus	30940-31386		
	TABLE 3	9A: 856 GENES	UP-REGULATI	ED IN RENAL CANCER COMPARED TO NOR	MAL ADULT TISSUES A	ND TO NON-MALIGNANT RENAL TISSUES THAT ARE LIKELY TO
60	ENCODE	PROTEINS AN	MENABLE TO M	ODULATION BY SMALL MOLECULES, PEPT	IDES, OR ANTIBODIES	
oo						nant renal fissues that are likely to encode proteins amenable to
	the satio	n by small mox	ocules, pepades,	or antibodies. These were selected from the s	itarting collection of 5968	O probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: "average" renal cancer to "average" non-matignant renal tissues was
						s renal specimens, the "average" normal adult tissue tevel was set to was set to the 50th percentile value amongst various non-malignant
65						intellined a structural domain that is indicative of having an oncogenic
• •						ies (e.g. pkinase, death-domain, 7tm, phosphatase, or
	ion_trans				, p-p,	to the brancost goods agricult said branchismond or
	Pkey:	Uni	ique Eos probes	et identifier number		
=0	ExAcen:	Ex	emplar Accessio	n number, Genbank accession number		
70	Unigenel		igene number			
	Unigene	Tida: Uni	igene gene tite			
	R1:	Ra	tio of turnor to a	rmal adult tissues		
	O	E-4	Hate 1	Hainana Wata		
75	Pkey 435013	ExAcon H91923	UnigeneID	Unigene Title		R1
,,	447768	X88400	Hs.110024 Hs.19520	No 10520 EVVD domain containing in a feet		15.71 14.07
	445178	AI792241	Hs.19920	Hs.19520:FXYD domain-containing ion tran Hs.129614:kidney-specific membrane prote		12.56
	432542	AW083920		Hs.16098:claudin 2		12.41
	443595	AF169312	Hs.9613	NM_016109:Homo sapiens angiopoietin-like		11.77
80	413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible of		10.39
	436878	BE465204	Hs.47448	Hs.47448:ESTs		10.18
	440304	BE159984	Hs.125395	Hs.125395:ESTs		9.95
	407065	Y10141				9.58

	413049	NM_002151	Hs.823	NM_002151:Homo saptens hepsin (transmemb	9.51
	425983 423161	AK000226 AL049227	Hs.165619 Hs.124776	Hs.165619:mucin and cadherin-like	8.88
	430569	AF241254	Hs.178098	Hs.124776:Homo saplens mR; cD DKFZp564N1 Hs.178098:angiotensin1 converting enzym	8.77 8.45
5	416758	AA363733	Hs.1032	NM_002909:Homo saptens regenerating isle	7.94
	422357	AF016272	Hs.115418	NM_004062:Homo sapiens cadherin 16, KSP-	7.78
	420737 409745	L08096 AA077391	Hs.99899	NM_001252:Homo sapiens tumor necrosis fa	7.78 7.74
	413936	AF113676	Hs.297681	AA077391:7814E12 Chromosome 7 Fetal Brai NM_000295:Homo sapiens serine (or cystel	7.74
10	426682	AV660038	Hs.2056	Hs.2056:UDP glycosyltransferase 1 family	7.20
	406851	AA609784	Hs.352392	Hs.352392:major histocompatibility compl	7.03
	419508 428953	AW997938 AA306610	Hs.90786 Hs.348183	Hs.90786:ATP-binding cassette, sub-tamil NM_003823:Homo saplens tumor necrosis fa	6.57 6.36
	436895	AF037335	Hs.5338	NM_001218:Homo sapiens carbonic anhydras	6.31
15	431842	NM_005764	Hs.271473	NM_005764:Homo sapiens epithelial protei	6.20
	430014 423803	H59354	Hs.374303	Hs.374303:hypothetical protein MGC20576	6.20
	434779	NM_005709 AF153815	Hs.132945 Hs.50151	NM_005709:Homo sapiens PDZ-73 protein (P Hs.50151:potassium inwardly-rectifying c	6.19 6.11
20	435767	H73505	Hs.117874	Hs.117874:ESTs	6.08
20	422654	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	6.02
	425280 426559	U31519 AB001914	Hs.1872 Hs.170414	Hs.1872:phosphoenolpyruvate carboxykise	5.81
	451564	AU076698	Hs.132760	NM_002570:Homo sapiens paired basic amin NM_001467:Homo sapiens glucose-6-phospha	5.73 5.69
25	418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	5.68
25	444151	AW972917	Hs.128749	Hs.128749:alpha-methylacyl-CoA racemase	5.66
	426471 432579	· M22440 AF043244	Hs.170009 Hs.278439	NM_003236:Homo sapiens transforming grow NM_003946:Homo sapiens nucleolar protein	5.48 5.45
	448733	NM_005629	Hs.187958	NM_005629:Homo sapiens solute carrier fa	5.42
20	446650	AB016625	Hs.15813	NM_003060:Homo sepiens solute carrier fa	5.36
30	417089 437848	H52280	Hs.18612	Hs.18612:Homo sapiens cD: FLJ21909 fis.	5.35
	423081	AI906419 AF262992	Hs.284380 Hs.123159	Hs.284380:gamma-glutarnyttransferase 1 Hs.123159:sperm associated antigen 4	5.32 5.30
	421893	NM_001078	Hs.109225	NM_001078:Homo sapiens vascular cell adh	5.23
35	435886	BE265839	Hs.12126	Hs.12126:hepatoceltular carcinoma-associ	5.20
33	410276 429451	AI554545 BE409861	Hs.359201 Hs.202833	Hs.359201:ESTs	5.20
	446404	AA019961	Hs.26216	NM_002133:Homo sepiens heme oxygese (dec Hs.26216:Homo sepiens cD: FLJ22811 fls,	5.14 5.13
	423445	NM_014324	Hs.128749	NM_014324:Homo sepiens alpha-methylacyl-	5.09
40	449444	AW818436	Hs.351306	NM_004595:Homo sepiens solute carrier fa	5.05
40	438106 400419	BE245551 AF084545	Hs.6079	NM_014863:Homo sapiens B cell RAG associ AF084545:Homo sapiens versican Vintisof	5.02 5.01
	453920	AI133148	Hs.36602	NM_000204:Homo sapiens I factor (complem	4.99
	447881	BE620886	Hs.355279	Hs.355279:Homo sepiens cD FLJ23711 fis.	4.97
45	422253 439024	W81526	Hs.113882	NM_000815:Homo sapiens gamma-aminobutyri	4.93
45	414799	R96696 AI752416	Hs.35598 Hs.77326	Hs.35598:ESTs NM_000598:Homo sapiens insulin-like grow	4.88 4.80
	426530	U24578	Hs.278625	NM_000592:Homo sapiens complement compon	4.77
	410055	AJ250839	Hs.58241	Hs.58241:gene for serine/threonine prote	4.72
50	404240 414617	Al339520	Hs.288817	Hs.288817:hypothetical protein FLJ22761	4.71 4.68
-	448249	AW855331	Hs.337124	Hs.337124:ESTs	4.67
	447818	W79940	Hs.21906	Hs.21906:Homo sapiens clone 24670 mR seq	4.66
	449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	4.66
55	422424 417336	Al186431 R70429	Hs.296638 Hs.81988	NM_004864:Homo saplens prostate differen NM_001343:Homo saplens disabled homolog	4.62 4.62
	425873	NM_013390	Hs.160417	NM_013390:Homo sapiens transmembrane pro	4.58
	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	4.58
	414998 414763	NM_002543 U97276	Hs.77729	NM_002543:Homo saplens oxidised low dens	4.56
60	443358	H65417	Hs.77266 Hs.17757	NM_002826:Homo sapiens quiescin Q6 (QSCN Hs.17757:pieckstrin homology domain-cont	4.48 4.45
	440091	AJ767388	Hs.37890	Hs.37890:Homo sapiens, clone IMAGE:48275	4,43
	447131	NM_004585		NM_004585:Homo sapiens retinoic acid rec	4.43
	406973 427740	M34996 BE242604	Hs.198253 Hs.180616		4.42 4.40
65	436258	AWB67491	Hs.107125		4.38
	452884	C05964	Hs.31841	Hs.31841:ESTs	4.37
	444006	8E395085	Hs.10086	NM_016639:Homo sapiens type I transmembr	4.38
	422627 418054	BE336857 NM_002318	Hs.118787 Hs.83354	NM_000358:Homo sapiens transforming grow NM_002318:Homo sapiens tysyl oxidase-lik	4.35 4.34
70	419011	H56244	Hs.89552	NM_000846:Homo sapiens glutathione S-tra	4.34
	404277				4.33
	435563 431779	AF210317	Hs.95497	Hs.95497:solute carrier family 2 (facili	4.30
	406645	AW971178 M57466	Hs.268571 Hs.814	NM_001645:Homo saptens apolipoprotein C- Hs.814:major histocompatibility complex,	4.29 4.28
75	421485	AA243499	Hs.104800		4.26
	426812	AF105365	Hs.172613	NM_006598:Homo sapiens solute carrier fa	4.25
	407910 438030	AA650274 X98427	Hs.41296 Hs.122634	NM_013281;Homo sapiens fibronectin teuci Hs.122634;ESTs	4.22
••	430561	AC005551	Hs.130714		4.22 4.21
80	444381	BE387335	Hs.2B3713	Hs.283713:hypothetical protein BC014245	4.20
	438203	BE540090	Hs.7345	Hs.7345:MAD1 mitotic arrest deficient-6	4.16
	411358 418323	R47479 NM_002118	Hs.94761 Hs.1162	Hs.94761:KIAA1691 protein	4.15
	-10000		710.1104	NM_002118:Homo sapiens major histocompat	4.12

	449853	AF006823	Hs.24040	NM_002246:Homo sapiens potassium channel	411
	415198	AW009480	Hs.943	NM_004221:Homo sapiens tural killer cell	4.11
	418751	BE389014	Hs.372548	Hs.372548:phosphotnositide-3-kise, regul	4.09
5	414166 424125	AW888941 M31669	Hs.75789 Hs.1735	NM_006096:Homo sapiens N-myc downstream Hs.1735:inhibin, beta B (activin AB beta	4.07 4.00
	416926	H03109	Hs.263395	Hs.263395:sema domain, transmembrane dom	3.92
	419175	AW270037	Hs.362995	Hs.362996:tQAA0779 protein	3.92
	424218 412870	AF031824	Hs.143212	NM_003650:Homo sapiens cystatin F (leuko	391
10	452203	N22788 X57522	Hs.82407 Hs.352018	Hs.82407:chemokine (C-X-C motif) ligand NM_000593:Homo sapiens transporter 1, AT	3.88 3.87
	446872	X97058	Hs.16362	NM_004154:Homo saplens pyrimidinergic re	3.87
	449961	AW265634	Hs.133100	Hs.133100:ESTs	3.87
	424517 425262	A1539443 D87119	Hs.137447 Hs.155418	Hs.137447:Homo sapiens cD FLJ12169 fis,	3.86
15	443639	BE269042	Hs.9661	Hs.155418:GS3955 protein NM_002801:Homo sapiens proteasome (proso	3.83 3.82
	448133	AA723157	Hs.73769	NM_000802:Homo sapiens folate receptor 1	3.81
	418030	BE207573	Hs.83321	Hs.83321:neuromedin B	3.81
	412939 409162	AW411491 H25530	Hs.75069 Hs.50868	NM_005412:Homo sapiens serine hydroxymet NM_002555:Homo sapiens solute carrier ta	3.80 3.79
20	427715	BE245274	Hs.180428	Hs. 180428:KIAA1181 protein	3.78
	412006	AW451618	Hs.290216	Ha.290216:ESTs	3.77
	430413	AW842182	Hs.241392	NM_002985:Homo sapiens small inducible c	3.76
	422282 420747	AF019225 BE294407	Hs.114309 Hs.99910	Hs.114309:apolipoprotein L, 1 Hs.99910:phosphofructokise, platelet	3.76 3.76
25	414875	H42679	Hs.77522	NM_006120:Homo sapiens major histocompat	3.75
	418793	AW382987	Hs.88474	Hs.88474:prostaglandin-endoperoxide synt	3.74
	446291 417289	BE397753 D86962	Hs.14623 Hs.81875	NM_006332:Homo septens interferon, gamma	3.71
	422672	X12784	Hs.119129	Hs.81875:growth factor receptor-bound pr NM_001845:Homo sapiens collegen, type IV	3.69 3.68
30	448569	BE382657	Hs.21486	NM_007315:Homo sapiens sigl transducer a	3.68
	437270	R18087	Hs.323769	Hs.323769:cisplatin resistance related p	3.67
	408452 443986	AA054683 AI381750	Hs.192455 Hs.283437	Hs.192455:ESTs, Moderately similar to hy Hs.283437:HTGN29 protein	3.67
	418869	AW516565	10400001	AW516565:xq01d05.x1 Soares_NHCeC_cervica	3.66 3.65
35	425998	AU076629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	3.62
	428699	AW578252	Hs.190161	NM_014020:Homo sepiens LR8 protein (LR8)	3.62
	418299 432593	AA279530 AW301003	Hs.83968 Hs.51483	NM_000211:Homo sapiens integrin, beta 2 Hs.51483:Homo sapiens, Similar to RIKEN	· 3.61 3.59
40	415765	NM_005424	Hs.78824	NM_005424:Homo sapiens tyrosine kise wit	3.58
40	445985	BE621800	Hs.29444	Hs.29444:putative small membrane protein	3.57
	424893 426046	AW295112 AA833655	Hs.153648 Hs.206868	Hs.153648:protein tyrosine phosphatase,	3.57
	424415	NM_001975	Hs.146580	Hs.206868:Homo sapiens cO FLJ14056 fis, NM_001975:Homo sapiens enclase 2, (gamma	3.57 3.57
4.0	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens aryisulfatase E (	3.56
45	443834	AI741510	Hs.173548	Hs.173548:ESTs	3.54
	431630 418371	NM_002204 M13560	Hs.265829 Hs.84298	NM_002204:Homo sapiens integrin, alpha 3 Hs.84298:C074 antigen (invariant polypep	3.53 3.52
	444838	AV651680	Hs.208558	Hs.208558:ESTs	3.52
50	449378	AW664026	Hs.59892	Hs.59892:ESTs, Weakly similar to atpha 5	3.52
50	411393 414311	AW797437 AI693547	Hs.69771 Hs.71746	NM_001710:Homo sepiens B-factor, properd	3.50
	415149	X12451	Hs.78056	Hs.71746:aminopeptidase-like 1 NM_001912:Homo saplens cathepsin L (CTSL	3.50 3.50
	424321	W74048	Hs.1765	Hs.1765:lymphocyte-specific protein tyro	3.49
55	414825	X06370	Hs.77432	NM_005228:Homo saplens epidermal growth	3.48
"	408194 410600	AA601038 AW575742	Hs.191797 Hs.351676	Hs.191797:ESTs Hs.351676:ESTs, Wealdy similar to T02670	3.48 3.47
	416899	BE262645	Hs.80420	NM_002996:Homo sapiens small inducible c	3.47
	436856	AJ469355	Hs.127310	Hs.127310:hypothetical protein 8C014917	3.47
60	419660 413566	BE280337 AW604451	Hs.194693	NM_003982:Homo sapiens solute carrier fa	3,47
•	412104	AW205197	Hs.285814 Hs.240951	Hs.285814:growth factor receptor-bound p Hs.240951:ked cuticle homotog 2 (Orosoph	3.47 3.46
	444488	AW192879	Hs.355660	Hs.355660:peptide-histidine transporter	3.46
	449475	AI348027	Hs.108557	Hs.108557:hypothetical protein PP1057	3.46
65	412276 449338	8E262621 H73444	Hs.73798 Hs.394	NM_002415:Homo sapiens macrophage migrat NM_001124:Homo sapiens adrenomedullin (A	3.45 3.44
	430304	AL122071	Hs.238927	Hs.238927:Homo saciens mR: cD DKFZp434H1	3.43
	415388	AF018081	Hs.78409	(locuslink)NM_030582:Homo sapiens collag	3.43
	432210 418177	AI567421 N44967	Hs.273330 Hs.351554	Hs.273330:agrin	3.43
70	414888	AL039185	Hs.77558	Hs.351554:Homo sapiens cD FLJ32092 fis, Hs.77558:thyroid hormone receptor intera	3.42 3.42
	452445	AB002438	Hs.29596	Hs.29596:Homo sapiens mR from chromosome	3.41
	414803	X03100	Hs.914	Hs.914 major histocompatibility complex,	3.41
	419201 445139	M22324 AB037848	Hs.1239 Hs.12365	NM_001150:Homo sapiens alanyi (membrane) Hs.12365:syptotagmin XIII	3.41
75	435021	AA922192	Hs.73962	Hs.73962:EphA7	3.41 3.41
_	417259	AW903838	Hs.81800	Hs.81800:chondroitin sulfate proteoglyca	3.40
	439737	A1751438	Hs.41271	Hs.41271:Homo saplens mR full length ins	3.39
	410636 431590	AA088177 AB037789	Hs.172870 Hs.263395		3.39 3.38
80	415000	AW025529	Hs.239812		3.38 3.36
	416700	AW498958	Hs.343475	NM_001909:Homo sapiens cathepsin D (lyso	3.36
	440516 423720	S42303 AL044191	Hs.161	NM_001792:Homo saplens cadherin 2, type	3.35
	. 423120	VED-44 191	Hs.23388	Hs.23388:hypothetical protein DKFZp434F0	3.32

	421902	BE392717		BE392717:601307571F1 NIH_MGC_44 Homo sap	3.32
	409220	BE243323	Hs.51233	Hs.51233:tumor necrosis factor receptor	3.32
	421502	AF111856	Hs.105039	NM_006424:Homo sapiens solute carrier ta	3.32
5	416729 430302	U46165 AL137502	Hs.1027 Hs.238679	NM_004165:Homo sapiens Ras-related assoc Hs.238679:Rag D protein	3.30 3.30
•	445084	H38914	Hs.250848	Hs.250848:Homo sapiens cD FLJ14761 fis,	3.29
	406825	AI982529	Hs.84298	Hs.84298:CD74 antigen (invariant polypep	3.29
	446272 437145	BE268912	Hs.14501	NM_005335:Homo sapiens hematopoletic cel	3.28
10	444071	AF007216 AI627808	Hs.5462 Hs.110524	NM_003759:Homo saplens solute carrier fa Hs.110524:ESTs	3.27 3.27
	414662	AL036058	Hs.76807	Hs.76807:major histocompatibility comple	3.27
	436576	AJ458213	Hs.77542	Hs.77542:ESTs, Weakly similar to \$26650	3.26
	424675 437897	NM_005512 AA770561	Hs.151641 Hs.146170	NM_005512:Homo sapiens glycoprotein A re Hs.146170:hypothetical protein FLJ22969	3.25 3.25
15	449703	H61001	Hs.171802	Hs.171802:Homo saplens, clone IMAGE:3956	3.25
	414788	X78342	Hs.77313	NM_003674:Homo sapiens cyclin-dependent	3.25
	414249 430396	A1797994 D49742	Hs.279929 Hs.241363	Hs.279929:gp25L2 protein	3.24
	424456	AA341017	Hs.25549	NM_004132:Homo sapiens hyaturon binding Hs.25549:hypothetical protein FLJ20898	3.23 3.23
20	452303	R27257	Hs.57734	Hs.57734:G protein-coupted receptor kise	3.22
	425390	A1092634	Hs.156114	NM_004648:Homo sapiens protein tyrosine	3.21
	416033 450931	NM_012201 N25156	Hs.78979 Hs.25648	NM_012201:Homo sapiens golgi apparatus p Hs.25648:tumor necrosis factor receptor	3.19 3.19
	428065	A1634046	Hs.157313	Hs.157313:ESTs	3.18
25	422616	BE300330	Hs.118725	NM_012248:Homo saplens selenophosphate s	3.18
	439318 427640	AW837046 AF058293	Hs.6527 Hs.180015	Hs.6527:G protein-coupled receptor 56 NM_001355:Homo sapiens D-dopachrome taut	3.17
	409936	AK001691	Hs.57655	Hs.57655:dudulin 2	3.17 3.18
20	435001	AW903849	Hs.173840	Hs.173840:similar to endothellal cell-se	3.16
30	451154 420256	AA015879 U84722	Hs.33536	Hs.33536:ESTs	3.16
	407584	W25945	Hs.76206 Hs.8173	NM_001795:Horno sapiens cadherin 5, type Hs.8173:hypothetical protein FLJ10803	3.16 3.15
	428593	AW207440	Hs.185973	NM_003676:Homo saplens degenerative sper	3.15
35	410026	AJ912061	Hs.55016	Hs.55016:EPS8-related protein 2	3.15
33	445333 448143	BE537641 AF039704	Hs.44278 Hs.20478	Hs.44278:RAB17, member RAS oncogene fami NM_000391:Homo sapiens ceroid-lipofuscin	3.14 3.14
	423007	AA320134	Hs.196029	Hs.196029:Homo sapiens mR for KIAA1657 p	3.14
	416511	NM_006762	Hs.79356	NM_006762:Homo sepiens Lysosomal-associa	3.14
40	439237 446899	AW408158 NM_005397	Hs.318893 Hs.16426	Hs.318893:ESTs, Weakly simitar to Z195_H NM_005397:Homo sapiens podocalyxin-like	3.13
-10	413916	N49813	Hs.75615	NM_000483:Homo sapiens podocaryamiae	3.13 3.13
	434398	AA121098	Hs.3838	NM_006622:Homo sapiens serum-inducible k	3.12
	441283 418945	AA927670	Hs.131704	Hs.131704:ESTs	3.12
45	418458	BE246762 AA332941	Hs.89499 Hs.85226	NM_000698:Homo sepiens arachidote 5-lipo NM_000235:Homo sepiens lipase A, lysosom	3.12 3.12
_	408989	AW361666	Hs.49500	Hs.49500:IQAA0746 protein	3.11
	436906	H95990	Hs.181244	Hs.181244:major histocompatibility compl	3.11
	411089 432990	AA456454 AL036071	Hs.355702 Hs.279899	Hs.355702:ESTs, Wealdy similar to AC0048 NM_003820:Homo septens tumor necrosis fa	3.11 3.11
50	425009	X58288	Hs.154151	NM_002845:Homo sapiens protein tyrosine	3.10
	443601	AI078554	Hs.42658	Hs.42658:Homo sepiens cD FLJ30167 fis, c	3.10
	430603 413672	AA148164 BE156536	Hs.247280 Hs.353632	Hs. 247280:chromosome 20 open reading fra	3.10
	407788	AA687538	Hs.38972	Hs.353632:ESTs, Moderately similar to hy NM_005727:Homo sapiens tetraspan 1 (TSPA	3.09 3.09
55	414586	AA306160	Hs.16488	NM_002298:Homo sapiens lymphocyte cytoso	3.08
•	423712 438552	W46802 AJ245820	Hs.81988	Hs.81988:disabled homolog 2, mitogen-res	3.08
	448364	T08958	Hs.6314 Hs.297214	NM_012410:Homo saplens type I transmembr Hs.297214:HSPC141 protein	3.06 3.06
<b>CO</b>	426437	BE076537	Hs.169895	NM_004223:Homo sapiens ubiquitin-conjuga	3.06
60	437679 422262	NM_014214		NM_014214:Homo sapiens inositot(myo)-1(o	3.06
	410480	AL022315 R97457	Hs.113987 Hs.63984	NM_006498:Homo saplens tectin, gatactosi NM_001257:Homo saplens cadherin 13, H-ca	3.06 3.05
	435818	AA700553	Hs.368614	Hs.368614:ESTs	3.05
65	418883 453613	BE387036	Hs.1211	NM_001611:Homo sapiens acid phosphatase	3.05
05	408051	F06838 A1823351	Hs.374476 Hs.172148	Hs.374476:ESTs Hs.172148:ESTs	3.05 3.05
	432278	AL137506	Hs.274258		3.04
	407949	W21874	Hs.247057		3.04
70	418090 433165	US7059 AA578904	Hs.83429 Hs.292437	NM_003810:Homo sapiens tumor necrosis fa Hs.292437:ESTs	3.04 3.03
	425809	AA370362	Hs.57958	Hs.57958:EGF-TM7-latrophilin-related pro	3.03
	443884	N20617	Hs.194397	Hs.194397:ESTs, Moderately similar to 22	3.03
	447B31 413278	A1433293 BE563085	Hs.164115 Hs.833	Hs.164115:ESTs NM_005101:Homo sapiens interferon-stimut	3.02
75	418870	AF147204	Hs.89414	Hs.89414:chemokine (C-X-C močif), recept	3.01 3.00
	456376	AA663904	Hs.89852	Hs.89862:TNFRSF1A-associated via death d	3.00
	439738 444416	BE248502 AW288085	Hs.9598 Hs.11156	Hs.9598:sema domain, immunoglobulin doma	3.00
	406656	M16714	Hs.89643	NM_016494:Homo sapiens hypothetical prot Hs.89843:transketolase (Wemicke-Korsako	3.00 3.00
80	406826	AW516005	Hs.84298	Hs.84298:CD74 antigen (invariant polypep	2.99
	418707	U97502	Hs.87497	Hs.87497:butyrophilin, subfamily 3, memb	2.99
	421742 406824	AW970004 AW515961	Hs.107528 Hs.84298	NM_016108:Homo sapiens androgen induced Hs.84298:CD74 antigen (invariant polypep	2.99 2.99

	435605	AF151815	Hs.4973	NIA 015690-Hama assistant has the standard assistant	2.00
	410491	AA465131	Ms.4973 Ms.64001	NM_015680:Homo sapiens hypothetical prot Hs.64001:Homo sapiens clone 25218 mR seq	2.98 2.98
	427648	AJ376722	Hs.180062	NM_004159:Homo sapiens protezsome (proso	298
5	411125	AA151647	Hs.68877	NM_000101:Homo sapiens cytochrome b-245,	2.98
2	435550 429373	A1224456 NM_014694	Hs:324507	Hs.324507:hypothetical protein FLJ20986	2.98
	445701	AF055581	Hs.200594 Hs.13131	NM_014694:Homo sapiens KIAA0605 gene pro NM_005475:Homo sapiens lymphocyte adapto	2.98 2.97
	414649	AI672727	Hs.76753	NM_00011B:Homo sapiens endoglin (Osler-R	2.97
10	444207	A1565004	Hs.374415	Hs.374415:ESTs	2.97
10	423225	AA852604	Hs.125359	NM_006288:Homo sapiens Thy-1 cell surfac	2.97
	407792 445707	AJ077715 AJ248720	Hs.39384 Hs.114390	NM_014344:Homo sapiens four jointed box Hs.114390:ESTs	2.97 2.96
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	2.96
1.5	418478	U38945	Hs.1174	Hs.1174xyclin-dependent kise inhibitor	2.95
15	411441	AL042355	Hs.70202	Hs.70202:WD repeat domain 10	2.95
	443426 450876	AF098158 AF189062	Hs.9329 Hs.285976	Hs.9329:chromosome 20 open reading frame Hs.285976:LAG1 longevity assurance homol	2.94 2.94
	426359	AA376409	Hs.10862	Hs.10862:Homo sapiens cD: FLJ23313 fis.	2.94
20	425421	L11669	Hs.157145	NM_001120:Homo sapiens tetracycline tran	2.93
20	449879	H03573	Hs.287830	Hs.287830:Homo sapiens mR; cD DKFZp434E1	2.93
	454075 421595	R43826 AB014520	Hs.16313 Hs.301685	Hs.16313:Kruppel-like zinc finger protei Hs.301685:KIAA0620 protein	2.93
	457949	W69171	Hs.334814	Hs.334814;hypothetical protein FLJ14868	2.93 2.92
25	443987	AW163123	Hs.10071	NM_016551:Homo sepiens seven transmembra	2.92
25	430259	BE550182	Hs.375142	Hs.375142:RalGEF-like protein 3, mouse h	2.92
	415906 429762	A1751357 AI346255	Hs.288741 Hs.216354	Hs.288741:Homo sapiens cD: FLJ22256 fis, NM_006913:Homo sapiens ring finger prote	291
	451527	AF022813	Hs.26518	NM_003271:Homo sapiens transmembrane 4 s	2.91 2.91
20	425356	BE244879	Hs.155939	NM_005541:Homo saplens inositol polyphos	2.91
30	427080	AW068287	Hs.301175	NM_002872:Homo sapiens ras-related C3 bo	2.91
	426432	AF001601	Hs.169857	NM_000305:Homo sapiens paraoxose 2 (PON2	2.90
	431476 406659	BE612705 AA663985	Hs.256697 Hs.277477	Hs.256697:histidinė triad nucleotide bin Hs.277477:major histocompatibility compl	2.89 2.89
	451144	AW956103	Hs.61712	Hs.61712 Homo sapiens cD FLJ31548 fis. c	2.89
35	456362	AW973003	Hs.179909	Hs.179909:nuclear receptor coactivator 6	2.88
	426440	8E382756	Hs.169902	NM_006516:Homo sapiens solute carrier fa	2.88
	456974 418174	M12529 L20688	Hs. 169401 Hs. 83656	NM_000041:Homo sapiens apolipoprotein E	2.68
	446055	AI815981	Hs.12909	Hs.83656:Rho GDP dissociation inhibitor Hs.12909:mucolipin 1	2.88 2.88
40	423184	NM_004428	Hs.1624	NM_004428:Homo sapiens ephrin-A1 (EF1),	2.87
	427700	AA252294	Hs.180383	NM_001946:Homo sapiens dual specificity	2.87
	410668	BE379794	Hs. 159651	NM_016629:Homo sepiens hypothetical prot	2.87
	444143 407151	AW747996 H25836	Hs.160999 Hs.301527	Hs.160999:ESTs, Weakly similar to 178885 Hs.301527:ESTs, Moderately similar to un	2.87
45	449349	AI825386	Hs.352579	Hs.352579:Homo sapiens, chromosome 20 op	2.86 2.86
	436997	AA741151	Hs.137323	Hs.137323:ESTs	2.86
	446143	BE245342	Hs.306079	NM_013336:Homo sapiens protein transport	2.86
	417355 431685	D13168 AW296135	Hs.82002 Hs.267659	Hs.82002:endothelin receptor type B NM_006113:Homo saplens vav 3 oncogene (V	2.88 2.85
50	408877	AA479033	Hs.130315	Hs. 130315:ESTs	2.85
	429615	AF258627	Hs.211562	NM_005502:Homo sapiens ATP-binding casse	2.85
	412014	AI620650	Hs.43761	Hs.43761:gap junction protein, alpha 7,	2.84
	438749 419825	AA584890 U91616	Hs.5302 Hs.182885	NM_006149:Homo saplens factin, galactosi NM_004556:Homo sapiens nuclear factor of	2.84 2.84
55	439941	AJ392640	Hs. 18272	Hs.18272:solute carrier family 38, membe	2.84
	435496	AA281959	Hs.5210	NM_004877:Homo sapiens glia maturation f	2.84
	422100	A1096988	Hs.111554	NM_005737:Homo sapiens ADP-ribosylation	2.83
	439730 447217	AF035292 BE465754	Hs.6654 Hs.17778	Hs.6654:KIAA0657 protein	2.83
60	428343	AL043021	Hs.12705	NM_003872:Homo sapiens neuropilln 2 (NRP Hs.12705:similar to HYPOTHETICAL 43,1 KD	2.83 2.82
-	440524	R71264	Hs.16798	Hs.16798:Homo sapiens mR; cD DKFZp564O24	2.82
	415523	AL042003	Hs.296847	NM_003119:Homo sapiens spastic paraplegi	2.81
	439668 414570	AI091277 Y00285	Hs.302634 Hs.76473	Hs.302634:frizzled homolog 8 (Drosophila	2.81
65	426535	AU077012	Hs.288582	NM_000876:Homo sapiens insufin-like grow NM_006287:Homo sapiens tissue factor pat	2.80 2.80
	409649	AA159216	Hs.55505	Hs.55505:hypothetical protein FLJ20442	2.80
	406655	M21533	Hs.277477	Hs.277477:major histocompatibility compl	2.79
	415323 443195	BE269352	Hs.949	NM_000433:Homo sapiens neutrophil cytoso	2.79
70	451356	BE148235 AA748418	Hs.193063 Hs.164577		2.78
	450708	AA376654	Hs.350065		2.78 2.78
	433681	Al004377	Hs.200360	Hs.200360:Homo sapiens cD FLJ13027 fis,	2.77
	442599	AF078037	Hs.324051		2.76
75	414509 431394	AW161311 AK000692	Hs.76294 Hs.252351	NM_001780:Homo sapiens CD63 antigen (met	2.76
, 5	417331	AW411297	Hs.81972	Hs.252351:HERV-H LTR-associating 2 Hs.81972:SHC (Src homology 2 domain cont	2.76 2.78
	415995	NM_004573			2.75
	414911	NM_000107	Hs.77602	NM_000107:Homo sapiens damage-specific D	2.75
80	425976	C75094	Hs.334514		2.75
ou.	407893 407903	BE408359 AI287341	Hs.43621 Hs.154029	Hs.43621:hypothetical protein MBC3205 Hs.154029:bHLH factor Hes4	2.75
	416062	AA724811	Hs.334791		2.75 2.75
	428494	AA233439	Hs.184634		2.75

	424500	00303300	11- 10000	ANA 002250.11	
	421506 427581	BE302796 NM_014788	Hs.105097 Hs.179703	NM_003258:Homo sapiens thymidine kise 1, NM_014788:Homo sapiens tripartite motif-	2.74
	424527	AW138558	Hs.334873	Hs.334873:carboxypeptidase M	2.74 2.74
_	439578	AW263124	Hs.350547	Hs.350547:nuclear receptor co-repressor/	2.74
5	425188	AK002052	Hs.155071	Hs.155071:chromosome 20 open reading fra	2.74
	428013	AF151020	Hs.181444	NM_016456:Homo sepiens hypothetical prot	2.73 .
	439333	AW384710	Hs.132986	Hs. 132986:Homo sapiens cO FLJ31588 fis,	2.73
	450935 421532	BE514743 AW138207	Hs.355753	NM_005851:Homo sapiens tumor suppressor	2.73
10	440502	AI824113	Hs.146170 Hs.78281	Hs.145170:hypothetical protein FLJ22969 Hs.78281:regulator of G-protein sigiling	2.73 2.73
- 0	444981	AW855398	Hs.12210	Hs. 12210:tumor endothelial marker 6	272
	439219	N33883	Hs.41322	Hs.41322:ESTs	2.72
	416847	L43821	Hs.80261	NM_006403:Homo sapiens enhancer of filam	2.72
15	433179	AW362945	Hs.162459	Hs.162459:ESTs	2.72
15	424528	AW073971	Hs.238954	Hs.238954:ESTs, Wealthy similar to putati	2.71
	411213 433012	AA676939 NM_004045	Hs.69285 Hs.279910	NM_003873:Homo sapiens neuropilin 1 (NRP NM_004045:Homo sapiens ATX1 antioxidant	2.70
	425345	AU077297	Hs.155894	NM_002827:Homo sapiens protein tyrosine	2.70 2.69
	428923	BE047698	Hs.188785	Hs.188785:ESTs	269
20	427923	AW274357	Hs.301406	Hs.301406:hypothetical protein PP3501	2.69
	446644	NM_003272	Hs.15791	NM_003272:Homo sepiens transmembrane 7 s	2.69
	421743	T35958	Hs.107614	Hs.107614:DXFZP564I1171 protein	2.68
	416207 420372	NM_014745 AW960049	Hs.79077 Hs.293660	NM_014745:Homo sepiens KIAA0233 gene pro	2.68
25	420542	NM_000505	Hs.1321	Hs.293660:gene overexpressed in astrocyt NM_000505:Homo sapiens coagulation facto	2.68 2.67
	425069	AA687465	Hs.298184	Hs.298184:potassium voltage-gated channe	2.67
	418558	AW082266	Hs.86131	NM_003824:Homo sapiens Fas (TNFRSF6)-ass	2.67
	426251	M24283	Hs. 168383	NM_000201:Homo saplens intercellular adh	2.66
30	406701	AA780613	Hs.62954	Hs.62954:territin, heavy polypeptide 1	2.66
50	431681 412833	AK000378 AW950547	Hs.267566 Hs.298262	Hs.267566:hypothetical protein FLJ20371	2.66
	433101	AW572317	Hs.12082	Hs.298262:ribosomal protein S19 Hs.12082:TIGA1	2.66 2.66
	414774	X02419	Hs.77274	NM_002658:Homo saplens plasminogen activ	2.66
25	427868	Al360119.com	npHs.181013	NM_002629:Homo sepiens phosphoglycerate	2.66
35	413929	BE501689	Hs.75617	Hs.75617:collagen, type IV, atpha 2	2.66
	424762	AL119442	Hs.183684	Hs.183684:eukaryotic translation initiat	2.66
	422048 431350	NM_012445 AJ192528	Hs.288126 Hs.164537	NM_012445:Homo sapiens spondin 2, extrac	2.65
	450184	W31096	Hs.237617	Hs.164537:ESTs Hs.237617:dipeptidytpeptidase 9	2.65 2.65
40	419285	D31887	Hs.89868	Hs.89868:KIAA0062 protein	2.65
	414217	Al309298	Hs.279898	Hs.279898:Homo sapiens cD: FLJ23165 fis,	2.64
	451253	H48299	Hs.26126	NM_006984:Homo sapiens claudin 10 (CLDN1	2.64
	435905	AW997484	Hs.5003	Hs.5003:SUT-ROBO Rho GTPase-activating	2.64
45	432581 415782	AU076465 AA169345	Hs.278441	NM_014634:Homo sapiens KIAA0015 gene pro	2.63
43	430223	NM_002514	Hs.123177 Hs.235935	Hs.123177:hypothetical protein BC011406 NM_002514:Homo sapiens nephroblastoma ov	2.63 2.63
	417526	AA568906	Hs.82240	NM_004177:Homo sapiens syntaxin 3A (STX3	2.63
	409956	AW103364	Hs.727	NM_002192:Homo sapiens Inhibin, beta A (	2.63
50	449843	R85337	Hs.24030	NM_001860:Horno sapiens solute carrier fa	2.62
50	417389	BE260964	Hs.82045	NM_002391:Homo sapiens midkine (neurite	2.62
	446312 435099	BE087853	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	2.62
	417920	AC004770 S47833	Hs.4756 Hs.82927	Hs.4756:flap structure-specific endoruci NM_004037:Homo sapiens adenosina monopho	2.62 2.62
	435702	AI033647	Hs.121001	Hs.121001:Horno sapiens, clone MGC:45521	2.62
55	422959	AV647015	Hs.349256	Hs.349256:paired immunoglobulin-like rec	2.62
	419938	AU076772	Hs.1279	NM_001733:Homo sapiens complement compon	2.62
	450954	A1904740	Hs.25691	NM_005856:Homo sepiens receptor (catcito	2.61
	421753 443577	8E314828 AI078033	Hs.107911	Hs.107911:ATP-binding cassette, sub-fami	2.61
60	453886	R66282	Hs.177170 Hs.20247	Hs.177170:ESTs, Weakly similar to ALU8_H Hs.20247:ESTs	2.61
•	421883	X55079	Hs.1437	NM_000152:Homo sapiens glucosidase, alph	2.61 2.60
	440457	BE387593	Hs.21321	Hs.21321:gramule cell differentiation pr	2.60
	410295	AA741357	Hs.356624		2.59
65	420879	X57152	Hs.99853	NM_001435:Homo sapiens fibrillarin (FBL)	2.59
05	451558 444672	NM_001089	Hs.26630	NM_001089:Homo sapiens ATP-binding casse	2.59
	408669	Z95636 Al493591	Hs.11669 Hs.78146	Hs.11669:laminin, alpha 5 Hs.78146:platelet/endothelial cell adhes	2.59
	426194	T50872	Hs.2001	Hs.2001:thromboxane A synthase 1 (platel	2.59 2.59
	421814	L12350	Hs.108523		2.59
70	456371	S76825	Hs.89695	Hs.89695:insufin receptor	2.59
	429098	AF030249	Hs.196176		2.59
	414443	AU077268	Hs.76144	NM_002609:Homo saplens platelet-derived	2.59
	428484 453309	AF 104032 A1791809	Hs.184601 Hs.32949		2.59
75	412867	AU076861	Hs.74637	NM_005218:Homo sapiens defansin, beta 1 NM_003217:Homo sapiens testis enhanced g	2.59 2.58
	432827	Z68128	Hs.3109	Hs.3109:Rho GTPase activating protein 4	2.58
	412669	AW880841	Hs.96908	NM_006034:Homo saplens p53-induced prote	2.58
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	2.58
80	452866	R26969	Hs.268016		2.58
G <b>U</b>	435129 424482	AI381659 BE268621	Hs.267086 Hs.149156		2.57
	410494	M36564	Hs.64016	i NM_003374:Homo saplens voltage-dependent NM_000313:Homo saplens protein S (alpha)	2.57 2.58
	433895	AI287912	Hs.3628	NM_004834:Homo sapiens mitogen-activated	2.56
				_ · -	

	442566	R37337	Un 12111	U- 12111-FOT-	
	417640	D30857	Hs.12111 Hs.82353	Hs.12111:ESTs NM_006404:Homo sapiens protein C recepto	2.56 2.56
	442622	NM_000435	Hs.8546	NM_000435:Homo sapiens Notch homolog 3 (	2.56
6	430345	AK000331	Hs.297641	Hs.297641:retinoblastoma-associated fact	2.55
5	419344 426500	U94905	Hs.277445	Hs.277445:diacytglycerol kise, zeta (104	2.55
	408048	NM_014538 NM_007203	Hs.170156 Hs.42322	NM_014538:Homo sapiens KIAA0450 gene pro NM_007203:Homo sapiens A kise (PRKA) and	2.55 2.55
	450700	AW732799	Hs.25348	NM_005860:Homo sapiens follistatin-Eke	2.54
10	417018	M16038	Hs.80887	NM_002350:Homo sapiens v-yes-1 Yamaguchi	2.54
10	419378	R24922	Hs.90078	Hs.9007R:nucleotide-sugar transporter si	2.54
	422451 435906	AA310753 AI686379	Hs.42491 Hs.110796	Hs.42491:ESTs, Moderately similar to hyp Hs.110796:SAR1 protein	2.53 2.53
	400231	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	1-0.110.00	16.110730.0001 potent	253
1.5	417849	AW291587	Hs.82733	NM_007361:Homo sapiens nidogen 2 (NIO2),	2.53
15	427380 428385	NM_005534	Hs.177559	NM_005534:Homo sapiens interferon gamma	2.52
	438000	AF112213 AIB25880	Hs.184062 Hs.5985	Hs.184062:chromosome 20 open reading fra Hs.5985:non-kise Cdc42 effector protein	2.52 2.52
	448719	AA033627	Hs.21858	Hs.21858:serine (or cysteine) proteise i	2.52
20	422396	W21872	Hs.7907	Hs.7907:L-hicose kise	2.52
20	420787 430590	AA564248	Hs.351292	Hs.351292:Homo sapiens cD FLI32605 fis,	2.51
	447026	AW383947 BE313144	Hs.246381 Hs.324844	NM_001251:Homo sapiens CD68 antigen (CD6 Hs.324844:hypothetical protein IMAGE3455	2.51 2.51
	439223	AW238299	Hs.250618	Hs.250618:UL16 binding protein 2	2.50
25	435151	AA348482	Hs.4788	Hs.4788:nicestrin	2.50
25	448202 449943	AB002292 AF104266	Hs.20695	NM_014829:Homo sapiens Rho guanine nucle	2.50
	425743	BE396495	Hs.24212 Hs.159428	Hs.24212:latrophilin Hs.159428:BCL2-associated X protein	2.50 2.50
	444681	AJ243937	Hs.288316	Hs.288315:chromosome 6 open reading fram	2.50
20	421643	BE281170	Hs.106357	NM_007126:Homo sapiens valosin-containin	2.50
30	426865 432306	D63476 Y18207	Hs.172813	NM_003899:Homo saplens Rho guanine nucle	2.50
	421846	AA017707	Hs.303090 Hs.1432	NM_005398:Homo sapiens protein phosphata NM_002743:Homo sapiens protein kise C su	2.49 2.49
	421905	A1660247	Hs.32699	Hs.32699:Homo sapiens, Similar to RIKEN	2.49
25	419493	AF001212	Hs.90744	NM_002815:Homo sapiens proteasome (proso	2.49
35	422530 442821	AW972300 BE391929	Hs.118110	NM_004335:Homo sapiens bone marrow strom	2.48
	416919	T97839	Hs.8752 Hs.80464	NM_014255:Homo sapiens transmembrane pro NM_006402:Homo sapiens hepatitis 8 virus	2.48 2.48
	443105	X96753	Hs.9004	NM_001897:Homo sepiens chondroitin sulfa	2.48
40	430040	AW503115	Hs.227823	NM_014287:Homo sapiens pM5 protein (PM5)	2.48
40	428028 424307	U52112 AW293399	Hs.182018	NM_001569:Homo sapiens interteukin-1 rec	2.47
	434511	R28982	Hs.356377 Hs.18106	Hs.356377:Homo sapiens, clone IMAGE:3633 Hs.18106:ESTs, Wealdy similar to T06291	2.46 2.46
	454390	AB020713	Hs.56966	Hs.56966:KIAA0906 protein	2.46
45	417785	X59812	Hs.82568	NM_000784:Homo saplens cytochrome P450,	2.46
43	424673 422003	AA345051 AA361760	Hs.294092	Hs.294092:Homo sapiens mR full tength in	2.46
	432126	AA865239	Hs.296326 Hs.37196	Hs.296326:ESTs, Wealdy similar to A33533 Hs.37196:putative G protein coupled rece	2.46 2.46
	445937	AI452943	Hs.321231	NM_003779:Homo sapiens UDP-Gal:betaGlcc	2.46
50	409354	N58188	Hs.159472	Hs.159472:Homo sapiens cD: FLJ22224 fis,	2.46
30	401179 418151	AARSA23R A	omp Hs.83583	NIA MEZZI-Hama applicate series soluted a-	2.46
	422648	D86983	Hs.118893	NM_005731:Homo sapiens actin related pro Hs.118893:Melanoma associated gene	2.45 2.45
	427759	BE245578	Hs.2200	NM_005041:Homo sapiens perforin 1 (prefo	2.45
55	431222	X56777	Hs.273790	NM_007155:Homo sapiens zo pellucida glyc	2.45
23	411529 426825	AA430348 AL133415	Hs.317596 Hs.297753		2.45 2.45
	422242	AJ251760	Hs.273385		2.45
	408105	AW152207	Hs.270977	Hs.270977:ESTs	2.44
60	426410 421084	BE298446	Hs.305890		2.44
00	428157	Al245432 Al738719	Hs.101382 Hs.198427		2.44 2.44
	424398	BE397787	Hs.146393		244
	424825	AF207069	Hs.153357	NM_001084:Homo sapiens procellagen-lysin	2.44
65	426031 409817	AA295251 BE295464	Hs.166068		2.43
05	429359	W00482	Hs.56507 Hs.2399	Hs.56607;Williams-Beuren syndrome chromo NM_004995;Homo sapiens matrix metallopro	2.43 2.43
	426761	AI015709	Hs.172089		2.43
	429332	AF030403	Hs.199263	NM_013233:Homo sapiens serine threonine	2.43
70	425923 432211	NM_005026 BE274530	Hs.162808 Hs.273333		2.43
, ,	433339	AF019226	Hs.8036	Hs.273333:hypothetical protein FLJ10986 Hs.8036:RAB3D, member RAS oncogene famili	2.43 2.42
	420539	AA282735	Hs.44004	Hs.44004:AD031 protein	2.42
	413243	AA769266	Hs.193657	Hs.193657:ESTs	2.42
75	435029 422374	AF187706 AW732869	Hs.19280	Hs.19280:cysteine-rich motor neuron 1	2.42
, ,	444501	AW247624	Hs.1519 Hs.11342	Hs.1519:protein kise, cAMP-dependent, re NM_004148:Homo sepiens ninjurin 1 (NINJ1	2.42 2.42
	414919	AW087337	Hs.194461	Hs.194461:ESTs	2.42
	419355	AA428520	Hs.90061	NM_006667:Homo sapiens progesterone rece	2.42
80	436042	AF284422	Hs.119178	Hs.119178:cation-chloride cotransporter-	2.42
30	418245 444215	AA088767 AB033075	Hs.83883 Hs.10669	Hs.83883:transmembrane, prostate androge Hs.10569:development and differentiation	2.42 2.41
	408683	R58665	Hs.46847	NM_016614:Homo saplens TRAF and TNF rece	2.41
	423701	AA329856	Hs.143022	Hs.143022:EST8	2.41



	441783	BE313412	Hs.7961	Lie 7051:Home a reines alone 25012 at D com-	241
	428072	BE258602	Hs.182366	Hs.7961:Homo sapiens clone 25012 mR sequ NM_016292:Homo sapiens heat shock protei	2.41 2.41
	434599	AB002313	Hs.3989	Hs.3989:plexin B2	2.40
•	442351	W52642	Hs.8261	Hs.8261:SPRY domain-containing SOCS box	2.40
5	407894	AJ278313	Hs.41143	Hs.41143:phospholipase C, beta 1 (phosph	2.40
	453449 408688	W16752 Al634522	Hs.32981 Hs.152925	Hs.32981:sema domain, immunoglobulin dom	2.40
	422448	AW372922	Hs.116774	Hs.152925:KIAA1268 protein Hs.116774:integrin, alpha 1	2.40 2.39
	416269	AA177138	Hs.161671	Hs.161671:ESTs	2.39
10	452679	Z42387	Hs 83883	Hs.83883:transmembrane, prostate androge	2.38
	432981	NM_002733	Hs.3136	NM_002733:Homo sapiens protein kise, AMP	2.38
	419846 422110	NM_015977 AJ376738	Hs.285681 Hs.111779	Hs.285681:Williams Beuren syndrome chrom Hs.111779:secreted protein, acidic, cyst	2.38
	413092	AA126856	Hs.118665	Hs.118665:ESTs	2.38 2.38
15	433969	AW207279	Hs.271786	Hs.271786:ESTs, Wealthy similar to PC4395	2.37
	451267	AI033894	Hs.117865	Hs.117865:solute carrier family 17 (anio	2.37
	447526	AL048753	Hs.303849	NM_002982:Homo sapiens small inducible c	2.37
	441623 420255	AA315805 NM_007289	Hs.348710 Hs.1298	Hs.348710:Homo sapiens, clone IMAGE:4242 NM_007289:Homo sapiens membrane metallo-	2.37
20	409274	NM_003930	Hs.52644	NM_003930:Homo sapiens are family associ	2.37 2.36
	422801	AF125672	Hs.287994	Hs.287994:nuclear receptor co-repressor	2.35
	407887	AA579668	Hs.41072	Hs.41072:serine (or cystelne) proteise i	2.36
	408212 430478	AA297567	Hs.43728	NM_015696:Homo saplens wealdy similar to	2.36
25	405102	NM_014349	Hs.241535	NM_014349:Homo sapiens apolipoprotein L	2.38 2.35
	423583	AL122055	Hs.129838	Hs. 129838:KIAA1028 protein	2.35
	426125	X87241	Hs.166994	NM_005245:Homo sapiens FAT tumor suppres	2.35
	425204	NM_002436	Hs.1861	NM_002436:Homo sapiens membrane protein,	2.35
30	420676 421079	Al434780 AW404994	Hs.4248 Hs.101695	Hs.4248:Homo sapiens PP3781 mR, complete	2.35
50	410039	AF207989	Hs.58014	Hs.101695:NCK adaptor protein 2 Hs.58014:G protein-coupled receptor, fam	2.35 2.34
	412958	BE391579	Hs.75087	NM_006712:Homo sapiens FAST kise (FASTK)	2.34
	430363	M28713	Hs.274464	NM_000398:Homo sepiens diaphorase (DH) (	2.34
35	425397	J04088	Hs.156346	NM_001067:Homo sapiens topolsomerase (D)	2.34
33	451035 449027	AU076785 AJ271216	Hs.430 Hs.22880	NM_002670:Homo sapiens plastin 1 (I isof	2.34
	429457	BE243065	Hs.202955	Hs.22880:dipeptidylpeptidase III Hs.202955:hypothetical protein FLJ20507	2.34
	417709	D87434	Hs.82426	NM_014734:Homo sapiens KIAA0247 gene pro	2.34
40	412805	AW954569	Hs.278675	Hs.278675:bromodomain-containing 4	2.34
40	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cD FLJ31360 fis.	2.34
	430702 456804	U56979 AI421645	Hs.278568 Hs.139851	NM_000186:Homo sapiens H factor 1 (compl NM_001233:Homo sapiens caveotin 2 (CAV2)	2.33
	453648	W21493	Hs.28329	Hs.28329:protein phosphatase 1, regulato	2.33 2.33
4.5	450812	AB002360	Hs.25515	Hs.25515:MCF.2 cell line derived transfo	2.33
45	402575				2.33
	424670 452960	W61215 AK001335	Hs.116651 Hs.31137	NM_005797:Homo sapiens epithelial V-like	2.32
	442968	AK000606	Hs.8868	NM_005504:Homo sapiens protein tyrosine NM_004871:Homo sapiens golgi SP receptor	2.32 2.32
	410639	BE269047	Hs.65234	Hs.65234:DEAD/H (Asp-Gtu-Ala-Asp/His) bo	2.32
50	415169	W42913	Hs.78089	NM_004231:Homo sapiens ATPase, H+ transp	2.32
	450160	BE048099	Hs.183738	Hs.183738:FERM, RhoGEF (ARHGEF) and plac	2.32
	407223 426780	H96850 BE242284	Hs.172199	H96850;yw03b12.s1 Soares melanocyte 2NbH	2.32
	434987	AW975114	Hs.371677	NM_001114:Homo sapiens adenylate cyclase Hs.371677:ESTs	2.32 2.32
55	416354	NM_000633	Hs.79241	NM_000633:Homo sapiens B-cell CLL/lympho	2.31
	453107	NM_016113	Hs.279746	NM_016113:Homo sapiens transient recepto	2.31
	422963 433618	M79141 AA602539	Hs.13234 Hs.345494	Hs.13234:ESTs, Weakly similar to hypothe Hs.345494:ESTs, Moderately similar to ZN	2.31
	438584	AA811347	113.04.04.04	AA811347:ob81h06.s1 NCI_CGAP_GCB1 Homo s	2.31 2.31
60	446126	AW085909	Hs.356618	Hs.356618:ESTs, Wealty similar to PC4259	2.31
	408716	AI567839	Hs.151714	Hs.151714:peroxisomal proliferator-activ	2.30
	433230 410168	AW136134 AW834050	Hs.220277 Hs.351432	Hs.220277:ESTs, Wealdy similar to expres	2.30
	446342	BE298665	Hs.14846	Hs.351432:tensin Hs.14846:Homo saplens mR; cD DKFZp564D01	2.30 2.30
65	418452	8E379749	Hs.85201	NM_005127:Homo saplens C-type (calcium d	2.30
	453175	NM_006834	Hs.32217	NM_006834:Homo sapiens RAB32, member RAS	2.29
	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	2.29
	452848 418838	Al417193 AW385224	Hs.288912 Hs.35198		2.29
70	422562	AI962060	Hs.118397	Hs.35198:ectonucleolida pyrophosphatase/ NM_001129:Homo sapiens AE binding protei	2.29 2.28
	432828	AB042326	Hs.287402	Hs.287402:chondroltin 4-sulfotransferase	2.28
	412948	BE243313	Hs.334851		2.28
	426068 456919	AF029778 NM_003900	Hs.166154 Hs.182248		2.28
75	452806	AW014549	Hs.58373	NM_003900:Homo sepiens sequestosome 1 (S Hs.58373:ESTs	2.28 2.28
-	453983	H94997	Hs.16450	Hs.16450:ESTs	2.28
	407736	N41744	Hs.349326	Hs.349326:Homo sapiens cD FLJ30677 ffs,	2.28
	413211	AW967107	Hs.109274		2.28
80	422051 438438	AW327548 AA257992	Hs.111024 Hs.50651		2.27
-	436278	BE396290	Hs.5097	Hs.50651:Janus kise 1 (a protein tyrosin NM_004710:Homo sapiens syptogyrin 2 (SYN	2.27 2.27
	454080	Al199711	Hs.576	NM_000147:Homo sapiens fucosidase, alpha	2.27
	426542	AF190746	Hs.170310	NM_017424:Homo sapiens cat eye syndrome	2.27

	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	2.27
	402901 412898	A1129903	U- 74000	Alla COCC34-Morro e ratione survivia Georgiata	2.26
	413020	R98736	Hs.74669	NM_006634:Homo sapiens vesicle-associate R98736:yr31h09.r1 Soares fetal fiver spl	2.26 2.26
5	413939	AL047051	Hs.199961	Hs.199961:ESTs, Weakly similar to hypoth	2.26
	408681	AW953853	Hs.281462	Hs.281462:hypothetical protein FLJ14251	2.25
	412330	NM_005100	Hs.788	NM_005100:Homo sapiens A kise (PRKA) and	2.25
	442083	R50192	Hs.165062	Hs.165062:ESTa	2.25
10	418271 433376	NM_000919 AI249361	Hs.83920 Hs.74122	NM_000919:Homo sapiens peptidylglycine a	2.25
10	438562	AI566826	Hs.25890	NM_001225:Homo saplens caspase 4, apopto Hs.25890:ESTs, Wealdy similar to transdu	2.25 2.25
	443883	AA114212	Hs.9930	NM_001235:Homo sapiens serine (or cystei	2.25
	416976	BE243985	Hs.80680	Hs.80680:major vautt protein	2.24
15	416914	AA344481	Hs.80426	Hs.80426:brain and reproductive organ-ex	2.24
15	400288 407904	X06256 W44735	Hs.149609	NM_002205:Homo sapiens integrin, alpha 5	2.24
	429690	AW956329	Hs.107260 Hs.23721	Hs.107260:putative UDP-Galc:polypeptide Hs.23721:ESTs	2.24 2.24
	443813	AA876372	Hs.93961	Hs.93961:Homo sapiens mR; cO DKFZp667009	2.24
~~	427458	BE208364	Hs.29283	Hs.29283:ESTs, Weakly similar to UCHU pr	2.24
20	454294	AB000734	Hs.50640	NM_003745:Homo sapiens JAK binding prote	2.24
	407192	AA609200	Hs.366318	Hs.366318:ESTs	2.23
	425751 456437	T19239 AJ924228	Hs.1940 Hs.115185	NM_001885:Homo sapiens crystallin, alpha Hs.115185:ESTs	2.23 2.23
	413019	BE281604	Hs.75140	NM_002337:Homo sapiens low density tipop	2.23
25	418862	8E550964	Hs.89399	Hs.89399:ATP synthase, H+ transporting,	2.23
	435284	AA879470	Hs.96849	Hs.96849:Homo sapiens cD FLJ11492 fis, c	2.23
	429630 427609	M85289	Hs.211573	NM_005529:Homo sapiens heparan sulfate p	2.23
	421917	AK000438 AB028943	Hs.179791 Hs.109445	Hs.179791:RAB20, member RAS encogene fam Hs.109445:hypermethylated in cancer 2	2.23 2.23
30	445616	R65964	Hs.334873	Hs.334873:carboxypeptidase M	2.23
	407232	X04526		X04526:Human liver mR for beta-subunit s	2.23
	423798	AF047033	Hs.132904	Hs. 132904:solute carrier family 4, sodiu	2.23
	446755 452865	AW451473	Hs.16134	NM_005990:Homo sapiens serine/threonine	2.22
35	431393	AI924046 AW971493	Hs.119587 Hs.134269	Hs.119567:ESTs, Weakly similar to ALU1_H Hs.134269:ESTs, Weakly similar to 200439	2.22 2.22
-	431890	X17033	Hs.271986	NM_002203:Homo sapiens integrin, alpha 2	2.22
	428782	X12830	Hs.193400	NM_000565:Homo sapiens interteukin 6 rec	2.22
	446006	NM_004403	Hs.13530	NM_004403:Homo sapiens deafness, autosom	2.22
40	435418 423869	AJ245874 BE409301	Hs.4245	Hs.4245:chromosome 11 hypothetical prote	2.22
40	437730	AW071087	Hs.134012 Hs.239176	NM_006688:Homo sapiens C1g-related facto Hs.239176:insulin-like growth factor 1 r	2.21 2.21
	444020	R92952	Hs.35052	Hs.35052:ESTs	2.21
	413882	AA132973	Hs.184492	Hs.184492:Homo sapiens mR; cD OKFZp667B0	2.21
AC	412654	AI093480	Hs.374319	Hs.374319:ESTs	2.21
45	448988 426841	Y09763 AI052358	Hs.22785	NM_004961:Homo sapiens gamma-aminobutyri	2.21
	408196	AL034548	Hs.131741 Hs.43627	Hs.131741:ESTs NM_005943:Homo septens SRY (sex determin	2.21 2.21
	451711	AK000461	Hs. 26890	Hs.26890:cat eye syndrome chromosome reg	2.20
50	414325	AA251929	Hs.355341	Hs.355341:Homo sapiens, clone IMAGE:3536	2.20
50	424512	X53002	Hs.149846	NM_002213:Homo sapiens integrin, beta 5	2.20
	448883 411296	BE614989 BE207307	Hs.7503 Hs.10114	Hs.7503:hypothetical protein FLJ14153	2.20
	452268	NM_003512	Hs.28777	Hs.10114:growth suppressor 1 NM_003512:Horno sapiens H2A histone famil	2.20 2.20
	415810	AF035606	Hs.80019	NM_013232:Homo sapiens programmed cell d	2.20
55	441415	H21497	Hs.7471	Hs.7471:BBP-like protein 1	2.20
	444212	AW503976	Hs.10649	NM_004848:Homo sepiens basement membrane	2.19
	428044 430017	AA093322 AA263172	Hs.301404 Hs.35	NM_006743:Homo sapiens R binding motif p	2.19
	424490	AJ278016	Hs.55565	NM_002832:Homo sapiens protein tyrosine Hs.55565;ankyrin repeat domain 3	2.19 2.19
60	431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	2.19
	453686	AL110326	Hs.304679	Hs.304679:ESTs, Weakly similar to Z195_H	2.19
	448262 416065	AW880830	Hs.186273	Hs.186273:ESTs	2.19
	442045	BE267931 C05768	Hs.78996 Hs.8078	NM_002592:Horno sapiens profiferating cel Hs.8078:Horno sapiens clone FBD3 Cri-du-c	2.19 2.19
65	423804	AW403448	Hs.1706	NM_006084:Homo sapiens interferon-stimut	2.19
	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	2.19
	424503	NM_002205	Hs.149609		2.19
	437698 405204	Z83844	Hs.5790	Hs.5790:hypothetical protein dJ37E16.5	2.18
70	426158	NM 001982	Hs.199067	NM_001982:Homo sapiens v-erb-b2 erythrob	2.18
. •	417418	NM_002458		NM_002468:Homo sapiens myeloid different	2.18 2.18
	412773	H15785	Hs.74573	NM_012268:Homo sapiens similar to vaccin	218
	409402	AF208234	Hs.695	NM_000100:Homo sapiens cystatin 8 (stefi	2.18
75	443791	N64458	Hs.143345		2.18
, ,	435049 418389	AL122087 AA830613	Hs.4748 Hs.293849	Hs.4746:hypothetical protein FLJ21324 Hs.293849:ESTs	2.18 2.18
	450712	AI732130	Hs.270496		218
	422007	AI739435	Hs.3916B	Hs.39168:ESTs, Wealthy similar to T17340	218
80	453676	AW853745	Hs.286035	Hs.286035:hypothetical protein FLJ22686	2.18
οU	415718 452688	F30631 AA721140	Hs.200237		218
	415988	BE407713	Hs.49930 Hs.78943	Hs.49930:ESTs, Weakly similar to 834087 NM_000386:Homo sapiers bloomycin hydrola	218 218
	409453	AJ885516	Hs.95612	Hs.95612:ESTs	2.17



	*****				
	417512 427202	X76534 BE272922	Hs.82226 Hs.173936	NM_002510:Homo sapiens glycoprotein (tra	2.17
	440983	M20681	Hs.7594	NM_000628:Homo sapiens interleukin 10 re NM_006931:Homo sapiens solute carrier fa	2.17 2.17
•	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate	2.17
5	429642	X68264	Hs.211579	NM_006500:Homo saplens melanoma adhesion	2.17
	427213 437763	AW007211 AA469369	Hs.348389 Hs.5831	Hs.348389:hypothetical protein FLJ12876	2.17 2.17
	454000	AA040620	Hs.5672	NM_003254:Homo sapiens tissue inhibitor Hs.5672:golgl membrane protein S8140	2.17
10	424247	X14008	Hs.234734	NM_000239:Homo sapiens lysozyme (rel amy	2.16
10	403857	4.4.5557700			2.16
	406648 400265	AA563730	Hs.277477	Hs.277477:major histocompatibility compl	2.16 2.16
	442379	NM_004813	Hs.8265	NM_004613:Homo sapiens transglutamise 2	216
16	441892	AB028981	Hs.8021	Hs.8021:KIAA1058 protein	2.16
15	417446 418386	AL118671 AA361739	Hs.82163	NM_000898:Homo saptens monoamine oxidase	216
	414053	BE391635	Hs.84549 Hs.75725	NM_002494:Homo sapiens DH dehydrogese (u NM_003564:Homo sapiens transgelin 2 (TAG	2.16 2.16
	440906	AW161556	Hs.240170	Hs.240170:hypothetical protein MGC2731	2.16
20	447660	AW160386	Hs.163667	Hs.163667:ESTs, Weakly similar to CA1H_H	2.16
20	408279 426152	AF216965 BE299190	Hs.44095 Hs.167246	Hs.44095:cyclin M3	216
	437952	D63209	Hs.5944	Hs.167246:P450 (cytochrome) oxidoreducta NM_014585:Homo sapiens solute carrier fa	2.16 2.16
	415661	AF057307	Hs.78575	Hs.78575:prosaposin (variant Gaucher dis	2.15
25	425302	U79115	Hs.155566	NM_003805:Homo saplens CASP2 and RIPK1 d	2.15
23	425996 413745	W67330 AW247252	Hs.374451 Hs.75514	Hs.374451:ESTs NM_000270:Homo septens nucleoside phosph	2.15
	422070	AF149785	Hs.111126	Hs.111126:pituitary tumor-transforming 1	2.15 2.15
	448424	AW009892	Hs.31924	Hs.31924:ESTs	2.15
30	430035 438407	NM_003463	Hs.227777	NM_003463:Homo sapiens protein tyrosine	2.15
50	435551	AJ457122 AF212365	Hs.129673 Hs.5470	Hs.129673:eukaryotic translation Initiat Hs.5470:Interleukin 17B receptor	215
	437741	BE561610	Hs.5809	Hs.5809: putative transmembrane protein;	2.15 2.15
	441192	AA526626	Hs.7736	NM_016504:Homo sapiens mitochondrial rib	2.15
35	435750 411165	AB029012 NM_000169	Hs.4990 Hs.69089	Hs.4990:KIAA1089 protein	2.15
55	425252	AW391162	Hs.349306	NM_000169:Homo sapiens galactosidase, al Hs.349306:hypothetical protein FLJ31951	2.14 2.14
	427600	AW630918	Hs.179774	NM_002818:Homo sapiens proteasome (proso	2.14
	426818	AA554827	Hs.292996	Hs.292996:postmeiotic segregation increa	2.14
40	442110 407797	AF113008 AK000524	Hs.8102 Hs.39850	NM_001023:Homo sapiens ribosomal protein	2.14
	443044	N28522	Hs.8935	Hs.39850:uridine kise-like 1 NM_014298:Homo sapiens quinolite phospho	2.14 2.14
	437103	AW139408	Hs.152940	Hs.152940:ESTs	2.14
	442069	AW684144	Hs.297007	Hs.297007:Homo sapiens cD FLJ32174 fis,	2.14
45	424954 458097	NM_000546 AW341135	Hs.1846 Hs.58104	NM_000546:Homo sapiens tumor protein p53 Hs.58104:Homo sapiens, clone IMAGE:47309	2.14
	411925	AW014588	Hs.72925	NM_003475:Homo sepiens chromosome 11 ope	2.14 2.14
	449644	AW960707	Hs.148324	Hs.148324:ESTs	2.14
	422675 428585	BE018517 M36712	Hs.119140 Hs.2299	NM_001970:Homo sapiens eukaryotic transl	2.14
50	429379	NM_014840	Hs.200598	Hs.2299:CD8 antigen, beta polypeptide 1 NM_014840:Homo saptens KJAA0537 gene pro	2.14 2.13
	410290	AA402307	Hs.322844	Hs.322844:hypothetical protein DKFZp564A	2.13
	443895	AW979048	Hs.292566	Hs.292568:YEA4 protein	2.13
	428145 453518	BE243327 AW503205	Hs.182626 Hs.27268	NM_012264;Homo sapiens chromosome 22 ope Hs.27268;Homo sapiens cD; FLJ21933 fis,	213
55	456534	X91195	Hs.100623	Hs.100623:protein phosphatase 1, regulat	2.13 2.13
	419972	AL041465	Hs.182982	Hs.182982:golgin-67	2.13
	424950 427557	AA602917 NM_002659	Hs.156974	Hs.156974:ESTs	2.13
	431449	M55994	Hs.179657 Hs.256278	NM_002659:Homo sapiens plasminogen activ NM_001066:Homo sapiens tumor necrosis ta	2.13 2.13
60	418758	AW959311	Hs.172012	Hs. 172012:hypothetical protein DKFZp434J	2.13
	434202	BE382411	Hs.3764	NM_000858:Homo sapiens guanylate kise 1	2.13
	433233 452700	AB040927 AI859390	Hs.301804 Hs.288940	Hs.301804:KIAA1494 protein Hs.288940:transmembrane protein 8 (five	2.12
	438033	T26483	Hs.6059	NM_016938:Homo sapiens EGF-containing 6	2.12 2.12
65	400847				2.12
	447547	NM_007229	Hs.18842	NM_007229:Homo saplens protein kise C an	2.12
	417052 413284	NM_000712 AU077055	Hs.81029 Hs.289107	NM_000712:Homo sapiens biliverdin reduct NM_001166:Homo sapiens baculoviral IAP r	2.12
	434558	AW264102	Hs.39168	Hs.39168:ESTs, Weakly similar to T17340	2.11 2.11
70	404030				2.11
	410801 418613	BE275469 AA744529	Hs.66493	Hs.66493:Down syndrome critical region g	2.11
	447087	AW403870	Hs.86575 Hs.301872	Hs.86575:mitogen-activated protein kise Hs.301872:hypothetical protein MGC4840	2.11 2.11
7-	433026	AW160616	Hs.279921	NM_016127:Homo sapiens hypothetical prot	211
75	426433	L38969	Hs.169875	NM_007112:Homo sapiens thrombospondin 3	2.11
	442439 437379	U09759 AL359575	Hs.246857 Hs.23765		211
	400208		110.20103	Hs.23765:membrane metallo-endopeptidase-	211 211
00	455705	AW151051	Hs.356580		211
80	417599 416728	AA204688	Hs.62954	Hs.62954:ferritin, heavy polypeptide 1	2.10
	439920	AB024597 H05430	Hs.79658 Hs.288433	NM_001894:Homo sapians casein kise 1, ep Hs.288433:neurotrimin	2.10
	422309	U79745	Hs.114924		2.10 2.10

	436114	AA778232	Hs.19515	Hs.19515:ESTs, Highly similar to NRG3_HU	2.10
	405517				2.10
	421872	AA359753	Hs.22824	Hs.22824:MYB binding protein (P160) 1a	210
5	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kise, rec	2.10
,	431214	AA294921	Hs.348024	NM_002881:Homo sapiens v-ral simian leuk	210
	412856 442064	BE386745 AJ422867	Hs.74631	NM_001728:Homo sapiens basigin (BSG), mR	2.10
	434845	BE267057	Hs.88594 Hs.325321	Hs.88594:Homo sapiens, clone IMAGE:43329 Hs.325321:WD repeat domain 18	2.10
	426728	NM_007118	Hs.367689	NM_007118:Homo sapiens triple functiol d	210 210
10	419596	BE379320	Hs.91448	NM_007026:Homo sapiens dual specificity	2.09
	448913	AA194422	Hs.22564	NM_004999:Homo sapiens myosin VI (MYO6),	2.09
	414721	X90392	Hs.77091	NM_006730:Homo sapiens deoxyribonuclease	2.09
	424658	NM_002406	Hs.151513	NM_002406:Homo saplens mannosyl (alpha-1	2.09
1.5	432805	X94630	Hs.3107	Hs.3107:CO97 entigen	2.09
15	447032	AK000310	Hs.17138	Hs.17138:hypothetical protein FLJ20303	2.09
	447484	AA464839	Hs.292566	Hs.292566:YEA4 protein	2.09
	440188	AK001812	Hs.7036	Hs.7036:N-acetylglucosamine kise	2.09
	445584 402559	AF217518	Hs.8360	Hs.8360:PTD012 protein	2.09
20	418043	AW377752	Hs.83341	Hs.83341:AXL receptor tyrosine kise	2.09 2.09
	448888	AW196663	Hs.200242	Hs.200242:caspase recruitment domain fam	2.09
	436910	AA926944	Hs.261587	Hs.261587:GCN2 elF2alpha kise	2.09
	422573	AW297985	Hs.295728	Hs.295726:integrin, alpha V (vitronectin	2.08
0.5	416448	L13210	Hs.79339	NM_005567:Homo sapiens lectin, galactosi	2.08
25	428727	AF078847	Hs.191356	NM_001515:Homo sapiens general transcrip	2.08
	410301	AW502935	Hs.740	Hs.740:PTK2 protein tyrosine kise 2	2.08
	449538	A1559444	Hs.104579	Hs.104579:Homo sapiens, clone MGC:18216	2.08
	421205	AL137540	Hs.102541	Hs.102541:netrin 4	2.08
30	411779 427704	AA292811 AW971063	Hs.72050 Hs.292882	NM_003551:Homo sapiens non-metastatic ce	2.08
50	413518	BE149455	Hs.75415	Hs.292882:ESTs NM_004048:Homo sapiens beta-2-microglobu	2.07 2.07
	447345	BE247767	Hs.18166	Hs.18166:KIAA0870 protein	2.07
	407143	C14076	Hs.332329	Hs.332329:EST	2.07
	448431	BE613061	Hs.337772	Hs.337772:hypothetical protein 8C009331	2.07
35	412760	AW379030	Hs.41324	Hs.41324:ESTs	2.07
	446859	AI494299	Hs.16297	NM_005694:Homo sapiens COX17 homolog, cy	2.07
	403966				2.07
	409115	AJ223335	Hs.50651	NM_002227:Homo sapiens Janus kise 1 (a p	2.07
40	436823	AW749865	Hs.117077	Hs.117077:zinc finger protein 264	2.07
70	414045 413980	NM_002951	Hs.75722	NM_002951:Homo saplens ribophorin II (RP	2.06
	439414	NM_002437 NM_001183	Hs.75659 Hs.6551	NM_002437:Homo sapiens MpV17 transgene, NM_001183:Homo sapiens ATPase, H+ transp	2.06
	426059	BE292842	Hs.166120	NM_001572:Homo sapiens interferon regula	2.06 2.06
	429849	U33053	Hs.2499	NM_002741:Homo sapiens protein kise C-8	2.06
45	402424			The Capacitation of the Capacitation of a	2.06
	406626	X04526	Hs.215595	Hs.215595:guanine nucleotide binding pro	2.06
	458911	AA373131	Hs.24322	Hs.24322:ATPase, H+ transporting, lysoso	2.05
	426086	T94907	Hs.188572	Hs.188572:ESTs	2.05
50	419726	U50330	Hs.1274	NM_006129:Homo sapiens bone morphogeneti	2.05
20	452344	AJ264357	Hs.55405	Hs.55405:hypothetical protein MGC16212	2.05
	442498 422114	U54617	Hs.8364	NM_002612:Homo sapiens pyruvate deliydrog	2.05
	413420	AW194851 AW410235	Hs.111801	NM_015908:Homo sapiens arsete resistance	2.05
	409430	R21945	Hs.75348 Hs.346735	NM_006263:Homo sapiens proteasome (proso Hs.346735:Homo sapiens, clone IMAGE:3881	2.05 2.05
55	409932	AJ376750	Hs.57600	Hs.57600:adaptor-related protein complex	2.05
	434848	BE256304	Hs.32148	Hs.32148:AD-015 protein	2.04
	453852	AW961818	Hs.374424	Hs.374424:ESTs	2.04
	427637	AK000816	Hs.179986	NM_005803:Homo sapiens flotillin 1 (FLOT	2.04
60	400264				2.04
00	430018	NM_004736	Hs.227656	NM_004736:Homo sapiens xenotropic and po	2.04
	410134 440975	U68140	Hs.58927	Hs.58927:nuclear VCP-like	2.04
	432280	AW499914 BE440142	Hs.7579 Hs.2943	Hs.7579:importin 9	2.04
	409504	AA304961	Hs.699	NM_003135:Homo sapiens sigl recognition NM_000942:Homo sapiens peptidytprolyl is	2.04 2.04
65	412145	M92444	Hs.73722	NM_001641:Homo sapiens APEX nuclease (mu	2.04
•••	434203	BE262677	Hs.283558	Hs.283558:hypothetical protein PRO1855	2.04
	422754	AA316478	Hs.171811	Hs.171811:adenylate kise 2	2.04
	406729	AA069711		AA069711:zm52b11.s1 Stratagene fibroblas	2.04
20	413085	AA126841	Hs. 183834		2.03
70	424340	AA339036	Hs.7033	Hs.7033:EST6	2.03
	450440	AB024334	Hs.25001	NM_012479:Homo sapiens tyrosine 3-monoox	2.03
	424662	NM_002870			2.03
	415740 412749	N80486 AA378417	Hs.39911	Hs.39911:Homo saplens mR for FU00089 pr	2.03
75	408393	AW015318	Hs.74564 Hs.23165	NM_003145:Homo sapiens sigl sequence rec Hs.23165:ESTs	2.03
, 5	421295	AW081061	Hs.103180		2.03 2.03
	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cD FLJ10196 fis, c	203
	414883	AA926960	Hs.348669	NM_001826:Homo sapiens CDC28 protein kis	2.03
00	447298	BE617527	Hs.239818		2.02
80	459580	AA022888	Hs.176065	Hs.176065:ESTs	2.02
	422785	AI824114	Hs.289088	Hs.289088:heat shock 90kD protein 1, atp	2.02
	452696	AI826845	Hs.211534	Hs.211534:Homo saplens cD FLJ31665 fis,	2.02
	452056	AW955065	Hs.101150	Hs.101150:KIAA1949 protein	2.02
				400	

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	450690 423527	AA296696 AI206965	Hs.333418 Hs.105861	NM_014164:Homo sapiens FXYD domain-conta Hs.105861:engulfment and cell motility 3	2.02 2.01
	429545 439180	AI824164 AI393742	Hs.356130 Hs.199067	Hs.356130:ESTs Hs.199067:v-erb-b2 erythroblastic leukem	2.01 2.01
5	437193	BE259190	Hs.289721	Hs.289721:growth arrest-specific 5	201
	436014 453329	AF281134 T97205	Hs.283741 Hs.193400	Hs.283741:exosome component Rrp48 Hs.193400:interleukin 6 receptor	201 201
	407347	AAB29847		T23514:seq3329 1-NIB Homo sapiens cD do	201
10	435370	AI964074	Hs.225838	Hs.225838:ESTs	2.01
10	430657 427157	AA482910 U51166	Hs.370602 Hs.173824	Hs.370602:ESTs, Wealdy similar to hypoth NM_003211:Homo sapiens thymine-D glycosy	201 201
	424833	NM_00389	4 Hs.153405	NM_003894:Homo sepiens period homolog 2	2.01
	440086 438543	NM_00540 AA810141		NM_005402:Horno saplens v-ral simian leuk Hs.192182:ESTs	201 201
15	417426	NM_00229	1 Hs.82124	NM_002291:Horno sapiens laminin, beta 1 (	201
	412790 445892	NM_01476 AV655500		NM_014767:Homo sapiens KIAA0275 gene pro Hs.93961:Homo sapiens mR; cD DKFZp667D09	201 201
			10.50001	The second state of the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second	241
20	TABLE 391 Pkey:		nique Fos probes	et identifier number	
	CAT numb	er: G	iene cluster numb	er	
	Accession	: G	ienbank accessio	numbers	
25	Pkey	CAT Num			
25	409745	MH1944_			AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377
			AA150780	31033518 81027818 BG015789 B1033807 AA34144	
	418869 421902	12789_14 276321_1		AA230035 BE079601 BE079534 AA299964 BE392717 BE883	102 DE070632 DE018148 DERS0427 WIN1706
30	400231	MH494_5	BC013310	AF261085 BC004109 AY007133 BC009081 BC001	501 NM_002046 M33197 BC020308 J02642 M36164 BE794233 AV721080 BE255459
					2 AA989106 AV728576 BI091380 AA402499 AI200513 AI284734 AI223995 AI289749 BEB90952 AA401181 BG939668 F35525 BI088182 F34674 F33506 BM471326 F34677
			AW276712	AA187508 F34866 AA114245 AA522581 N23935 A	J076923 AJ018505 BE879774 BM465637 AJ753078 BG222159 AA595947 BF970917
35					71 BF339134 BE409272 BE266456 BE796770 BE745957 BG755835 BE266758 7637 BM452667 BM479516 BM452420 BE273297 BM466364 BM450640 BM478743
-					0379 BM459071 BM450106 BM467584 BM464548 BM465044 BM450176 BF569359
	438584	1241536_	BM462924	BM455329 BM471815 BI862301 BG331736 H0490 AA811347 D79715	3 AA374894 BE902964
40	413020	1485885_		R98736 242904	
40	400265	1145_1	X58141 NN	_001119 Al246786 BE645243 Al685698 Al208590	BE222576 Al191715 Al423108 BF064068 BG057819 Al208589 Al880535 Al262890
					AI160385 AJ335983 BF440017 BG231884 AI343699 AJ280745 AI871338 AI123739 AJ306663 AW571658 BF109839 AW273280 AJ888380 AJ571860 AJ357126 AW194105
					1674 BF509394 AI891077 BF221538 AI651874 F25731 AW881176 AI685962 D44936
45					I1 AI908017 AI378261 AA975416 R16732 H47612 H45402 AA668719 AA722441 H40630 NM_014190 BM469282 AL524786 AL527067 BF313768 AL042441 AL037806
			BI1950131	BE219292 BF055534 T95785 BE833037 AV648052	AA382588 W67987 H46049 R92289 H47699 AA380016 AL532433 BG958742 Al292151
					9407 BI044500 H18771 H22071 R09985 R75803 H42172 BE770251 AL529310 F03180 93369 AA617840 H14351 Al866242 Al915028 AA780787 AAS06995 AA827496 AA634305
50					0 AA421274 AA903521 AA411402 AA044448 AA983449 AA076114 AA633470 AA581793
30					M2340 AA976636 AA360268 AA976223 T95788 AA527774 AI620298 AA180888 1994 AA299572 AI092819 AI291438 AA459586 AA136373 R50213 BE622752 AA401414
	400000	10040 1	AA180973	AA766800 W98432 BI550308 H52236 AA491029 E	G420468 BG827522
	400208	16640_1			1 AW487767 AI910663 BF905778 BG251264 AL562106 AI890538 AW769258 AI590391 125 BE456589 AW002786 AW591760 AI968816 AW006268 AW593787 BG236814
55			AW769893	AW407608 AW075982 AJ248207 AJ762509 AJ812	070 AJ249937 AW083561 AW080697 BF663046 BG745612 BG979546 AW793245
				ALS19126 BE675314 AW806520 BIB70778 BF8795 R09703 BI013066	49 BE714919 BF847786 BG684161 AV695278 BG491029 BE793244 BE830893
	400264	1145_1	X58141 N	M_001119 AI246786 BE645243 AI685698 AI20859	8E222576 AI191715 AI423108 BF064068 BG057819 AI208589 AI880535 AI262890
60	•		AI246261 AI871126	BF939926 AI282848 AI802409 BE301053 AI88482 AW080375 AI350160 AI300855 AI818598 AI08526:	A160385 A335983 BF440017 BG231884 A3343699 A1280745 A1871338 A1123739 AJ306653 AW571658 BF109839 AW273280 A1888380 A1571860 A1357126 AW194105
			AL131474	AW316548 AW128942 AW571682 AI583962 AW30	0674 BF509394 AI891077 BF221538 AI651874 F25731 AW881176 AI685962 D44938
					D1 AI908017 AI378261 AA975416 R16732 H47612 H45402 AA668719 AA722441 H40630 NM_014190 BM469282 AL524786 AL527067 BF313768 AL042441 AL037806
65			B1195013	BE219292 BF055534 T95785 BE833037 AV64805	AA382588 W67987 H46049 R92289 H47699 AA380016 AL532433 BG958742 Al292151
05			R92185 H	18680 R43192 AA401390 AA977941 Al091944 AA	19407 B1044500 H18771 H22071 R09985 R75803 H42172 BE770251 AL529310 F03180 193369 AA617840 H14351 A1866242 A1915028 AA780787 AA506995 AA827496 AA634305
			AA846358	AA470463 AA618163 AA601963 W74212 AA0215	20 AA421274 AA903521 AA411402 AA044448 AA983449 AA076114 AA633470 AA581793
-					342340 AA976636 AA360268 AA976223 T95786 AA527774 A1620298 AA180888 2994 AA299572 A1092819 A1291438 AA459586 AA136373 R50213 BE622752 AA401414
70	400720		AA180973	AA766800 W96432 BI550308 H52236 AA491029	
	406729 407347	0_0 810943_	AA069711 1 T23514 A		
				•	•
75	TABLE 3 Pkey:	<b>7</b> 4:	Unique number e	orresponding to an Eos probeset	
	Ref:		Sequence source	. The 7 digit numbers in this column are Genbank	dentifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
	Strand:			an chromosome 22" Dunham, et al. (1999) <u>Nature</u> « rand from which exons were predicted.	UZ:48 <del>3-4</del> 50.
80	Nt_positi	on:		de positions of predicted exons.	
30	Pkey	Ref	Strand	Nt position	
	404240	5002624	Minus	116132-116407,116653-116922	
	404277	1834456	Minus	91665-91946	

	401179	9438647	Plus	113477-113893
	405102	8076881	Minus	120922-121296
	402575	9884830	Minus	109742-109883
_	402901	8894222	Minus	175428-175667
>	405204	7230116	Plus	126569-126754
	403857	7708910	Minus	2524-3408
	400847	9188605	Plus	44643-44835
	404030	7671252	Plus	149362-151749
	405517	9454624	Plus	114757-114877
10	402559	9864273	Plus	33539-33715
	403966	8568881	Plus	158193-158277,160116-160290
	402424	9796344	Minus	64925-65073

15

TABLE 40A: ABOUT 977 GENES UP-REGULATED IN STOMACH CANCER
Table 40A 6sts about 977 genes up-regulated in stomach cancer compared to normal adult fissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03
GeneChip array such that the ratio of "average" stomach cancer to "average" normal adult fissues was greater than or equal to 2.0. The "average" stomach cancer level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Picey:

Unique Eos probeset identifier number
Exacm:
Unique Eos probeset identifier number
Unique Fitac:
Unique Fitac:
Unique Fitac:
R1: 20

25

	Pkey	ExAcon	UnigenelD	Unigene Title	R1
	411243	AB039886	Hs.69319	CA11	30.66
30	418007	M13509	Hs.83169	matrix metalloproteinase 1 (Interstitial	16.94
50	444325	AW152618	Hs.16757	ESTs	13.51
	445891	AW391342	Hs.199460	ESTs	11.92
	448811	AI590371	Hs.174759	EST ₅	11.08
	431723	AW058350	Hs.16762	Homo saplens mRNA; cDNA DKFZp564B2062 (f	10.84
35	409757	NM_001898	Hs.123114	cystatin SN	10.38
33	421110	AJ250717	Hs.1355	cathepsin E	9.11
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	8.66
	446998	N99013	Hs.16762	Homo sepiens mRNA; cONA DKFZp564B2062 (f	8.50
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	7,11
40	428651	AF198478	Hs.188401	annexin A10	6.86
40	425211	M18667	Hs.1887	progastricsin (pepsinogen C)	6.51
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	6.49
	409683	U33317	Hs.711	defensin, alpha 6, Paneth cell-specific	8.39
	422260	AA315993	Hs.105484	ESTs, Wealty similar to LITB_HUMAN LITHO	6.31
45	428554	AK001666	Hs.189095	similar to SALL1 (sat (Orosophila)-like	6.25
45	409041	AB033025	Hs.50081	KIAA1199 protein	5.72
	408380	AF123050	Hs.44532	diabiquitin	5.72
	428953	AA306610	Hs.194676	DKFZP434C013 protein	5.46
	450685	L15533	Hs.423	pancreatitis-associated protein	5.40
50	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	5.34
50	434206	AW136973	Hs.288516	ESTs, Weakly similar to \$69890 mitogen i	5.16
	421346	Z34277	Hs.103707	apomucin	5.14
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	5.06
	425679	X05997	Hs.159177	lipase, gastric	4.94
	421582	Al910275	Hs.1406	trefoil factor 1 (breast cancer, estroge	4.93
55	434414	AJ798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	4.92
	422956	BE545072	Hs.122579	hypothetical protein FLJ 10461	4.89
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN TRANS	4.84
	423575	C18863	Hs.153443	Homo sapiens cDNA FLJ11576 fis, clone HE	4.72
<i></i>	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	4.72
60	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	4.68
	448693	AW004854	Hs.228320	Homo sapiens cDNA: FLJ23537 ffs, clone L	4.53
	441377	BE218239	Hs.202656	ESTs	4.51
	419278	AU076799	Hs.1247	apolipoprotein A-IV	4.48
	407811	AW190902	Hs.40098	cysteine knot superlamily 1, BMP antagon	4.47
65	403422				4.38
	403776				4.32
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	4.32
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	4.30
70	421341	AJ243212	Hs.279611	deleted in malignant brain tumors 1	4.30
70	451181	AI796330	Hs.207461	ESTs .	4.26
	432168	AK000563	Hs.272805	hypothetical protein FLJ20556	4.23
	454464	AW811606	Hs.271819	Homo sapiens cDNA: FLJ22751 fis, clone K	4.20
	448844	AI581519	Hs.177164	ESTs	4.14
	428434	AW383590	Hs.65551	ESTs, Wealty similar to AF172993 1 PLUNC	4.13
75	452461	N78223	Hs.108106	transcription factor	4.08
	409420	Z15008	Hs.54451	taminin, gamma 2 (nicein (100kD), kelini	4.04
	431611	U58766	Hs.264428	tissue specific transplantation antigen	4.04
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	4.03
	430044	AA484510	Hs.152812	ESTs	4.02
80	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	4.01
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superlami	4.00
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis. clone C	3.98
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	3.91
				· · · · · · · · · · · · · · · · · · ·	J. 5 I

	422168	AA586894	Hs.112408	\$100 calcium-binding protein A7 (psorias	3.87
	452304	AA025386	Hs.61311	ESTs. Weakly similar to S10590 cysteine	3.84
	412140	AA219691	Hs.73625	RAB6 Interacting, kinesin-like (retkines	3.82
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.81
5	419833	AA251131	Hs.220697	ESTs	
•	446232	AJ281848	Hs.165547	ESTs	3.81
	432398	AA307808	Hs.2979		3.74
	451105		113.23/3	trefoil factor 2 (spasmolytic protein 1)	3.70
	413281	AI761324	11- 04000	gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens	3.67
10		AA861271	Hs.34396	ESTs	3.66
10	432867	AW016936	Hs.233364	ESTs	3.66
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	3.65
	457465	AW301344	Hs.195969	ESTs	3.65
	414918	AI219207	Hs.72222	Homo sapiens cDNA FLJ13459 fts, clone PL	3.61
1.5	418738	AW388633	Hs.6682	ESTs .	3.60
15	427778	AA412323	Hs. 105323	ESTs	3.60
	454293	H49739	Hs.134013	ESTs, Moderately similar to NK homeobox	3.59
	452194	AI694413	Hs.298262	ESTs. Wealtly similar to dJ88J8.1 [H.sapi	3.57
	442577	AA292998	Hs. 163900	ESTs	3.57
	426174	AA547959	Hs.115838	ESTs	3.53
20	452862	AW378065	Hs.8687	ESTs	3.51
	418869	AW516565	Hs.258279	ESTs	3.48
	430178	AW449612	Hs.152475	ESTs	3.48
	430397	AI924533	Hs.105607	ESTs	
	418054	NM_002318	Hs.83354		3.46
25	442295	AJ827248		lysyl oxidase-like 2	3.45
	425921	NM_007231	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	3.44
			Hs.162211	solute carrier family 6 (neurotransmitte	3.44
	431764	AA515212	Hs.271819	Homo sepiens cDNA: FLJ22751 fis, clone K	3.43
	421948	L42583	Hs.111758	keratin 6A	3.43
30	444381	BE387335	Hs.283713	ESTs, Wealthy similar to CA54_HUMAN COLLA	3.41
50	442896	R37725	Hs.261108	ESTs	3.41
	452281	T93500	Hs.28792	Homo seplens cDNA FLJ11041 fis, clone Pt.	3.39
	444783	AK001458	Hs.62180	anillin (Drosophila Scraps homolog), act	3.39
	408832	AW085690	Hs.63428	ESTs .	3.39
26	406685	M18728		gb:Human nonspecific crossreacting antig	3.37
35	437527	AJ241019	Hs. 145644	ESTs	3.37
	433084	M18079	Hs. 282265	fatty acid binding protein 2, intestinal	3.37
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.36
	441318	AI078234	Hs.176130	ESTs	3.35
	458897	U85642	Hs.138506	ESTs	3.33
40	413808	J00287	Hs.182183	caldesmon 1	3.33
	411274	NM_002776	Hs.69423	kallikrein 10	3.32
	418406	X73501	Hs.84905	cytokeratin 20	3.32
	419559	Y07828	Hs.91096	ring finger protein	3.32
	423217	NM_000094	Hs. 1640	collagen, type VII, alpha 1 (epidermolys	
45	423271	W47225	Hs.126256	interteukin 1, beta	3.31
	411558	AA102670	Hs.70725		3.31
	427722	AK000123	Hs.180479	gamma-aminobutyric acid (GABA) A recepto	3.30
	422310	AA316622	Hs.98370	hypothetical protein FLJ20116	3.30
	430704	AW813091	115.36370	cytochrome P540 family member predicted	3.30
50	411263	BE297802	Lin COOCO	gb:RC3-ST0186-240400-111-d07 ST0186 Homo	3.29
50	443211		Hs.69360	kinesin-like 6 (mitotic centromere-assoc	3.29
	443426	AJ128388	Hs.143655	ESTS	3.29
	441085	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.28
		AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.28
55	452121	NM_004081	Hs.70936	deleted in azoospermia	3.27
55	408633	AW963372	Hs.46677	PRO2000 protein	3.27
	447342	Al199268	Hs.19322	ESTs	3.25
	419229	AI827237	Hs.282884	ESTE	3.24
	443957	AA521049	Hs.34487	hypothetical protein FLJ23412	3.23
60	452699	AW295390	Hs.213062	ESTs	3.23
UU	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	3.23
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.21
	408524	D87942	Hs.46328	fucosyltransferase 2 (secretor status in	3.20
	437897	AA770561	Hs.146170	hypothetical protein FLJ22969	3.20
45	453922	AF053306	Hs.38708	budding uninhibited by benzimidazotes 1	3.19
65	453160	AI263307	Hs.146228	ESTs	3.19
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	3.19
	430187	A1799909	Hs.158989	ESTs	118
	416209	AA235776	Hs.79078	MAD2 (mitolic arrest deficient, yeast, h	3.16
	447048	AW393080	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone L	3.14
70	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fls, clone A	3.14
	425465	L18964	Hs.1904	protein kinase C, iota	3.13
	425826	U97698	Hs.159593	mucin 6, gastric	3.13
	431662	AA513406	Hs.152307	ESTs	
	419216	AU076718	Hs.164021	small inducible cytokine sublamily B (Cy	3.13
75	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.13
. •	417315	AI080042	Hs.180450	ribosomal protein S24	3.12
	433001	AF217513	Hs.279905		3.11
	459587	AA031956	113.41 7303	clone HQ0310 PRO0310p1	3.11
	450159	AI702416	Ma 200774	gb:zk15e04.s1 Soares_pregnant_uterus_NbH	3.11
80	434370		Hs.200771	ESTs. Weakly similar to CAN2_HUMAN CALPA	3.11
		AF130988	Hs.58346	downless (mouse) homolog	3.10
	421190	U95031	Hs.102482	mucin 5, subtype 8, tracheobronchial	3.10
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	3.10
	420380	AA640891	Hs.102406	ESTs	3.10

	41474	V00410	LI. 9303 ·	about the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and	
	414774 415989	X02419 AJ267700	Hs.77274 Hs.111128	plasminogen activator, uroldnase ESTs	3.10 3.09
	407137	T97307	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	3.09
_	407289	AA135159	Hs.203349	Homo sepiens cDNA FLJ12149 fis, clone MA	3.09
5	420297	AI628272	Hs.88323	ESTs	3.08
	447519	U46258	Hs.23448	ESTs	3.08
	448045 431956	AJ297436	Hs.20165	prostate stem cell antigen	3.07
	431936	AK002032 AJ739159	Hs.272245 Hs.61898	Homo sapiens cDNA FLJ11170 fis, clone PL DKFZP586N2124 protein	3.06 3.05
10	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	3.05
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3	3.05
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.05
	430573	AA744550	Hs.136345	ESTs	3.05
15	428987	NM_004751	Hs.194710	glucosaminyl (N-acetyl) transferase 3, m	3.04
13	424252 436291	AK000520 BE568452	Hs.143811 Hs.5101	hypothetical protein FLJ20513	3.04
	415992	C05837	Hs.145807	protein regulator of cytokinesis 1 Homo saciens cDNA FLJ13593 fis, clone PL	3.03 3.03
	411789	AF245505	Hs.72157	Homo sapiens adican mRNA, complete cds	3.02
20	417956	AA210704	Hs.190465	ESTs .	3.02
20	408908	8E296227	Hs.48915	serine/threonine kinase 15	3.01
	422330	030783	Hs.115263	epiregulin	3.01
	425071 425761	NM_013989 AW664214	Hs.154424 Hs.196729	deiodinase, iodothyronine, type II	3.00
	432978	AF126743	Hs.279884	ESTs DNAJ domain-containing	2.99 2.99
25	418546	AA224827	10.275004	gb:nc32g04.s1 NCI_CGAP_Pr2 Homo sapiens	2.99
	425371	D49441	Hs.155981	mesothelin	2.99
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B11	2.98
	439453	BE264974	Hs.6566	thyroid hormone receptor Interactor 13	2.98
30	413278 428450	BE563085 NM_014791	Hs.833	interferon-stimulated protein, 15 kDa	2.97
50	424345	AK001380	Hs.184339 Hs.145479	KIAA0175 gene product Homo sapiens cDNA FLJ10518 fis, clone NT	2.96 2.95
	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	294
	432269	NM_002447	Hs.2942	macrophage stimulating 1 receptor (c-met	2.94
25	432917	NM_014125	Hs.279812	PRO0327 protein	2.94
35	433384 432731	AI021992	Hs.124244	ESTS	2.93
	420552	R31178 AK000492	Hs.287820 Hs.98806	fibronectin 1 ,	2.93
	428303	AW974476	Hs.183601	hypothetical protein regulator of G-protein signalling 16	2.92 2.92
	409687	T51125	Hs.8493	ESTs	2.91
40	434377	AW137148	Hs.136348	osteoblast specific factor 2 (fasciclin	2.89
	417791	AW965339	Hs.111471	ESTs	2.89
	457288	AA521458	Hs.192738	ESTs	2.89
	456181 450190	L36463 T51387	Hs.1030	ras inhibitor	2.89
45	411573	AB029000	Hs.70823	gb:yb20e08.r1 Stratagene fetal spieen (9 KIAA1077 protein	2.88 2.88
	430204	AA618335	Hs.146137	ESTs, Wealthy similar to putative [C.eleg	2.88
	434808	AF155108	Hs.256150	ESTs, Highly similar to NY-REN-41 entige	2.87
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.87
50	418670	AA601036	Hs.285083	ESTs	2.87
50	416661 409723	AA634543 AW885757	Hs.79440 Hs.257862	IGF-II mRNA-binding protein 3	2.87
	435099	AC004770	Hs.4756	ESTs flap structure-specific endonuclease 1	2.87 2.86
	408660	AA525775	Hs.292523	ESTs	2.86
	434032	AW009951	Hs.206892	ESTs	2.85
55	418216	AA66Z240	Hs.283099	AF15q14 protein	2.85
	453331	AJ240665	Hs.8895	ESTs	2.85
	450221 402075	AA328102	Hs.24641	cytosketeton associated protein 2	2.84
	410145	AW886300		gb:RCS-OT0078-100400-023-C11 OT0078 Homo	2.84 2.83
60	410681	AW246890	Hs.65425	calbindin 1, (28kD)	2.83
	439867	AA847510	Hs.161292		2.83
	443715	AI583187	Hs.9700	cyclin E1	2.83
	420005	AW271106	Hs.133294	ESTs	2.83
65	417366 422283	BE185289 AW411307	Hs.1076 Hs.114311	small profine-rich protein 18 (comifin)	2.83
05	404567	A11411307	NS.114311	CDC45 (cell division cycle 45, S.cerevis	2.82
	422158	L10343	Hs.112341	protesse inhibitor 3, skin-derived (SKAL	2.82 2.82
	449224	AW995911	Hs.299883		2.81
70	407584	W25945	Hs.18745	ESTs	2.81
70	453884	AA355925	Hs.36232	KIAA0186 gene product	2.81
	449032 422809	AA045573 AK001370	Hs.22900	nuclear factor (erythroid-derived 2)-lik	2.80
	449722	AK001379 BE280074	Hs.121028 Hs.23960	hypothetical protein FLJ10549 cyclin B1	2.79
	445676	Al247763	Hs.16928	ESTs	2.79 2.79
75	424308	AW975531	Hs.154443		2.78
	453028	AB006532	Hs.31442	RecQ protein-like 4	2.78
	421777	BE562088	Hs.108196	HSPC037 protein	2.78
	452571	W31518	Hs.34665	ESTs	2.77
80	420759 422675	T11832 BE018517	Hs.127797 Hs.119140		2.77
- •	412723	AA548459	Hs.179912		2.77 2.76
	439670	AF088076	Hs.59507	ESTs, Wealthy similar to AC004858 3 U1 sm	2.76
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	2.76

	414569	AF109298	Hs.118258	prostate cancer associated protein 1	2.76
	449378	AW664026	Hs.59892	ESTS	2.75
	423903 412059	M57765	Hs.1721	Interleukin 11	2.75
5	431104	AA317962 AW970859	Hs.249721	ESTS	2.75
_	439759	AL359055	Hs.269109 Hs.67709	ESTs Home seniors month full beauth insent after	2.75
	450701	H39960	Hs.288467	Homo sepiens mRNA full length insert cDN Homo sepiens cDNA FLJ12280 fis, clone MA	2.75 2.75
	452940	AA029722	Hs.20279	ESTs	274
	408690	AW864542	. 10.202.0	gb:PM4-SN0016-120500-003-h02 SN0016 Homo	2.74
10	407777	AA161071	Hs.71465	squalene epoxidase	2.73
	432201	AI538613	Hs.135557	ESTs	2.73
	414416	AW409985	Hs.76084	tamin 82	2.73
	414617	Al339520	Hs.20524	ESTs, Moderately similar to hexokinase I	273
1.5	432407	AA221036	Hs.285026	HERV-H LTR-associating 1	273
15	444301	AK000136	Hs.10760	hypothetical protein FLJ20129	2.72
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	2.72
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	2.72
	408298 426711	AI745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	2.72
20	429432	AA383471 Al678059	Hs.180669 Hs.202676	conserved gene amplified in osteosarcoma	271
20	450506	NM_004460	Hs.418	synaptonemal complex protein 2	2.71
	427528	AU077143	Hs.179565	fibroblast activation protein, alpha minichromosome maintenance deficient (S.	2.71 2.71
	418801	AA228366	Hs.115122	ESTs	271
	440283	AJ732892	Hs.190489	ESTs	271
25	429486	AF155827	Hs.203963	hypothetical protein FLJ 10339	271
	408366	AW511255	Hs.258082	ESTs	270
	406399				2.69
	434217	AW014795	Hs.23349	ESTs	2.68
20	449785	AJ225235	Hs.288300	Homo sapiens cDNA: FLJ23231 fis, clone C	2.68
30	446269	AW263155	Hs.14559	hypothetical protein FLJ 10540	2.68
	443349	Al052572	Hs.269864	ESTs	2.68
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic	2.67
	417079 444754	U65590	Hs.81134	Interleukin 1 receptor antagonist	2.67
35	424687	T83911 J05070	Hs.11881 Hs.151738	transmembrane 4 superfamily member 4	2.67
	439979	AW600291	Hs.6823	matrix metalloproteinase 9 (gelatinase 8 hypothetical protein FLJ10430	2.66
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	2.65 2.65
	430832	AJ073913	Hs.100686	ESTs. Weakly similar to secreted cement	2.65
	427217	AA399272	Hs.144341	ESTs	2.65
40	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	2.64
	450400	A1694722	Hs.279744	ESTs	2.64
	435380	AA679001	Hs.192221	ESTs	2.64
	432375	8E536069	Hs.2962	S100 calcium-binding protein P	2.63
15	453700	AB009426	Hs.560	apolipoprotein B mRNA editing enzyme, ca	2.63
45	422938	NM_001809	Hs.1594	centromere protein A (17kD)	2.63
	453134	AA032211	Hs.118493	ESTs	2.63
	420727	H75701	Hs.99886	complement component 4-binding protein,	2.62
	408868 414972	AW292286 BE263782	Hs.255058	ESTS	2.62
50	440255	A1932285	Hs.77695 Hs.160569	KIAA0008 gene product	2.62
-	403055	74352203	ns.100003	ESTs	2.62 2.62
	443247	BE614387	Hs.47378	ESTs, Moderately similar to hypothetical	2.62
	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	2.61
	413753	U17760	Hs.301103	Human DNA sequence from clone 272L16 on	2.61
55	445114	AW991959	Hs.254664	ESTs	2.61
	422397	AJ223366	Hs.116051	myeloma overexpressed gene(in a subset o	2.60
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequ	2.60
	432009	AL137424		gb:Homo sapiens mRNA; cDNA DKFZp761G2123	2.60
60	440249	A1246590	Hs.125325	ESTs	2.60
OU	433220	AJ076192	Hs.131933	EST:	2.60
	438533 436251	AI440266	Hs.170673	ESTs, Wealdy similar to AF126780 1 retin	2.60
	424717	BE515065 H03754	Hs.5092	nucleolar protein (KKE/D repeat)	2.60
	448988	Y09763	Hs.152213 Hs.22785	wingless-type MMTV integration site fami	2.60
65	425463	AK000740	Hs.157986	gamma-aminobutyric acid (GABA) A recepto hypothetical protein FLJ20733	2.60
	435370	AI964074	Hs.225838	ESTs	2.60 2.59
	432215	AU076609	Hs.2934	ribonucleotide reductase M1 polypeptide	2.59
	409142	AL136877	Hs.50758	chromosome-associated polypeptide C	2.59
	443919	AI091284	Hs.135224	ESTs	2.58
70	413268	AL039079	Hs.75256	regulator of G-protein signatting 1	2.58
	404519				2.58
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	2.57
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	2.57
75	426841	AI052358	Hs.193726	ESTs .	2.57
75	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	2.57
	417933	X02308	Hs.82962	thymidylate synthetase	2.56
	433675	AW977653	Hs.110771	Homo sapiens cDNA: FLJ21904 fis, clone H	2.58
	441384	AA447849	Hs.288660		2.56
80	451939 418867	U80456 D31771	Hs.27311	single-minded (Drosophila) homolog 2	2.56
~	449042	AW294985	Hs.89404 Hs.301148	msh (Drosophila) homeo box homolog 2	2.55
	416065	BE267931	Hs.78996	potassium voltage-gated channel, isk-rel proliferating cell nuclear antigen	2.55
	414132	AI801235	Hs.48480	ESTs	2.55
				20.0	2.55



	431890	X17033	Hs.271986	integrin, alpha 2 (CO498, alpha 2 subuni	2.55
	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	2.55
	434815 415250	AF155582 F02614	Hs.46744 Hs.27319	core1 UDP-galactose:N-acetytgalactosamin ESTs	2.54
5	435647	AI653240	Hs.49823	ESTs	2.54 2.54
	459306	AW578452	Hs.232988	ESTs, Wealthy similar to mucin (H.sapiens	2.54
	414381	A1088138	Hs.204044	ESTs	2.54
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	2.53
10	416984 431183	H38765 NM_006855	Hs.80706	diaphorase (NADH/NADPH) (cytochrome b-5	2.53
10	436043	AW963838	Hs.250696 Hs.168830	KDEL (Lys-Asp-Gh-Leu) endoplasmic retic Homo sapiens cDNA FLJ12136 fis, clone MA	2.53 2.53
	456743	AI630124	Hs.7434	ESTs	253
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	2.52
15	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	2.52
13	411734 432657	AW374954 AA831815	Hs.71779	Homo sapiens DNA from chromosome 19, cos	2.52
	434080	AI820719	Hs.270940 Hs.154662	ESTs hypothetical protein PRO1472	251 251
	438190	AA780020	Hs.136798	ESTs	2.51
20	418969	W33191	Hs.28907	hypothetical protein FLJ20258	2.51
20	446405	AW451259	Hs.57851	ESTs	2.51
	450002 431808	A1879524 M30703	Hs.201629	ESTs, Moderately similar to ALU8_HUMAN A	2.51
	429093	NM_000253	Hs.270833 Hs.195799	amphiregulin (schwannoma-derived growth microsomal triglyceride transfer protein	2.51 2.50
~ -	447634	AW967902	Hs.5152	Homo sapiens cDNA: FLJ22518 fis, clone H	2.50
25	436393	AW022213	Hs.143617	ESTs	2.50
	453751	R36762	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434B102 (fr	249
	445669 445865	A1570830 A1262584	Hs.174870 Hs.145575	ESTS	2.49
	448437	AW470125	ris. 143373	ESTs gb:xw60c04.x1 NCI_CGAP_Pan1 Homo sapiens	2.49 2.49
30	414883	AA926960	Hs.77550	CDC28 protein kinase 1	2.49
	406747	Al925153	Hs.217493	annexin A2	2.49
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	2.49
	426322 412903	J05068 BE007967	Hs.2012 Hs.155795	transcobalamin I (vitamin B12 binding pr ESTs	2.48
35	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	2.48 2.48
	447030	AW444659	Hs.232184	ESTs	2.48
	448454	NM_005879	Hs.21254	TRAF interacting protein	2.48
	419092	J05581	Hs.89603	mucin 1, transmembrane	2.48
40	406671 409640	AA129547 U78722	Hs.285754 Hs.55481	met proto-oncogene (hepatocyte growth fa	2.48
	424639	Al917494	Hs.131329	zinc finger protein 165 ESTs	2.48 2.48
	404171			30.0	2.47
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin	2.47
45	407839	AA045144	Hs. 161566	ESTs	2.47
73	410406 452220	AI969703 BE158006	Hs.301842 Hs.212296	ESTs ESTs	2.47
	427691	AW194426	Hs.20726	ESTs	2.46 2.45
	421493	BE300341	Hs.104925	ectodermal-neural cortex (with BTB-like	2.46
50	444838	AV651680	Hs.208558	ESTs	2.46
JU	413816 408296	AW958181	Hs.189998	ESTs	2.46
	436513	AL117452 AA972691	Hs.44155 Hs.192974	DKFZP586G1517 protein Homo sepiens cDNA FLJ12735 fis, clone NT	2.46 2.45
	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	2.45
<i></i>	432874	W94322	Hs.279651	melanoma inhibitory activity	2.45
55	425268	AI807883	Hs.156932	ESTs	2.45
	425397 408308	J04088 AL033377	Hs.156346 Hs.44197	topolsomerase (ONA) II alpha (170kD)	2.45
	427961	AW293165	Hs.143134	hypothetical protein DKFZp564D0462 ESTs	2.45 2.45
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	2.45
60	433083	AL042759	Hs.191762	ESTs	2.45
	439848 431924	AW979249	11. 070000	gb:EST391359 MAGE resequences, MAGP Homo	2.44
	431457	AK000850 NM_012211	Hs.272203 Hs.256297	Homo sapiens cDNA FLJ20843 fis, clone AD integrin, alpha 11	2.44
	443949	AW827419	Hs.235070	ESTs	2.44
65	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	2.44
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	243
	431958 413833	X63629	Hs.2877	caonenn 3, lype 1, P-cadherin (placenta	2.43
	407243	Z15005 AA058357	Hs.75573 Hs.74466	centromere protein E (312tD) carcinoembryonic antigen-related cell ad	2.43
70	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	243 243
	424273	W40450	Hs.144442	phospholipase A2, group X	2.42
	409533	AW969543	Hs.21291	mitogen-activated protein kinase kinase	2.42
	453966	BE148734 AA397679	Hs.252833	ESTS	2.42
75	427043 419741	NM_007019	Hs.298460 Hs.93002	ESTs ubiquitin carrier protein E2-C	2.42
	449987	AW079749	Hs.184719	ESTs, Weakly similar to AF116721 112 PRO	2.42 2.42
	433159	AB035898	Hs. 150587	kinesin-like protein 2	2.42
	439396	BE562958	Hs.74346	ESTs. Weakly similar to /prediction	2.42
80	426427	M86599 AK000796	Hs. 169840	TTK protein kinase	2.41
-55	434725 427719	AK000796 AJ393122	Hs.4104 Hs.134726	hypothetical protein ESTs	2.41 2.41
	433312	AJ241331	Hs. 131765	ESTs	241
	432615	AA557191	Hs.55028	ESTS	2.41

	407047	X65965		abilit engines SOD 2 com for more sure ou	2.41
	419220	AA811938	Hs.291759	gb:H.sapiens SOD-2 gene for manganese su ESTs	2.40
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	2.40
_	435219	AA676349	Hs.190331	ESTs	2.40
5	447164	AF026941	Hs.17518	Homo sepiens cig5 mRNA, partial sequence	2.40
	416713 418322	T70174 AA284166	Hs.84113	gb:yc18b03.s1 Stratagene lung (937210) H cyclin-dependent kinase inhibitor 3 (CDK	2.40 2.40
	409902	A1337658	Hs.156351	ESTs	2.40
10	443597	AI078418		gb:oz05e03.x1 Soares_fetzi_liver_spleen_	2.40
10	404253	0500000			2.40
	428970 443462	BE276891 AJ064690	Hs.194691 Hs.171176	retinoic acid induced 3 ESTs	2.40 2.39
	418693	AJ750878	Hs.87409	firambospondin 1	2.39
	451237	AW500293		gb:EST00049 pGEM-T fibrary Homo sapiens	2.39
15	407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.39
	437935 445625	AW939591 8E246743	Hs.5940 Hs.288529	hypothetical protein FLJ20063 Homo sapiens cDNA: FLJ22635 fis, clone H	2.39
	435937	AA830893	Hs.119769	ESTs	2.39 2.39
20	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	2.38
20	422082	AA016188	Hs.111244	hypothetical protein	2.38
	435849 407242	BE305242 M18728	Hs.112442	ESTs, Wealdy similar to CLDE_HUMAN CLAUD gb:Human nonspecific crossreacting antig	2.38 2.38
	450396	AU077002	Hs.24950	regulator of G-protein signatting 5	2.38
25	430354	AA954810	Hs.239784	human homolog of Drosophila Scribble	2.38
25	422578 446342	AF239666 8E298655	Hs.1545	caudal type homeo box transcription fact	2.38
	450737	AWD07152	Hs.14846 Hs.203330	Homo sapiens mRNA; cDNA DKFZp564D016 (fr ESTs	2.38 2.38
	428070	T63918	Hs.182313	retinal-binding protein 2, cellular	2.38
30	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	2.37
30	433345 427557	AI681545 NM_002659	Hs.152982 Hs.179657	Homo sepiens cDNA FLJ13117 fis, clone NT	2.37
	423554	M90516	Hs.1674	plasminogen activator, urokinase recepto glutarnine-fructose-6-phosphate transamin	2.37 2.37
	453204	R10799	Hs.191990	ESTs	2.37
35	453876	AW021748	Hs.110406	ESTs	2.36
23	425081 434682	X74794 AA827165	Hs.154443 Hs.191958	minichromosome maintenance deficient (S. ESTs	2.36 2.38
	439737	AJ751438	Hs.41271	Homo sepiens mRNA full length insert cDN	2.36
	414108	AJ267592	Hs.75761	SFRS protein kinase 1	2.36
40	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	2.36
40	428046 . 448826	AW812795 AI580252	Hs.155381 Hs.293245	ESTs, Moderately similar to 138022 hypot ESTs, Wealdy similar to putative p150 [H	2.36 2.36
	441020	W79283	Hs.35962	ESTs	2.36
	448019	AW947164	Hs.195641	ESTs	2.36
45	431753	X76029 AW390054	Hs.2841	neuromedin U	2.36
73	441703 410361	8E391804	Hs.192843 Hs.62661	ESTs guanylate binding protein 1, interferon-	2.36 2.36
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	2.36
	444478	W07318	Hs.240	M-phase phosphoprotein 1	2.36
50	421878 428388	AA299652 AA729827	Hs.111496 Hs.101265	Homo sapiens cDNA FLJ11643 fis, clone HE Homo sapiens cDNA: FLJ22593 fis, clone H	2.35
	436961	AW375974	Hs.156704	ESTs	2.35 2.35
	408194	AA601038	Hs.191797	ESTs	2.35
	438578 429183	AA811244 AB014604	Hs.164168	ESTs	2.35
55	435663	AI023707	Hs.197955 Hs.134273	KIAA0704 protein ESTs	2.35 2.35
	430290	AI734110	Hs.136355	ESTs	2.34
	423441	R68649	Hs.278359	absent in melanoma 1 like	2.34
	453900 450378	AW003582 AW249181	Hs.226414 Hs.19954	ESTs, Wealdy similar to ALUS_HUMAN ALU S ESTs, Wealdy similar to cONA EST yk386e1	2.33 2.33
60	432877	AW974111	Hs.292477	ESTS	2.33
	451928	AI823801	Hs.30315	ESTs	2.33
	426227 418245	U67058	Hs.168102		2.33
	415083	AA088767 AI632683	Hs.83883 Hs.27179	transmembrane, prostate androgen induced Homo sapiens cDNA FLJ12933 fis, clone NT	2.33 2.33
65	435106	AA100847	Hs.193380		2.33
	432193	AA372264	Hs.273193		2.33
	458531 449532	AA367718 W74653	Hs.159083 Hs.271593		2.33
	446354	AW449650	Hs.202249		2.33 2.33
70	409703	NM_006187	Hs.56009	2-5 oligoadenylate synthetase 3	2.33
	419373	NM_003244		TG-interacting factor (TALE family homeo	2.32
	435607 405818	W73428	Hs.8750	uncharacterized bone marrow protein BM04	2.32 2.32
7.5	423132	AF070647	Hs.124126	Homo sapiens clone 24438 mRNA sequence	2.32
75	444371	BE540274	Hs.239	forkhead box M1	2.32
	432675	AI791855 NM_006799	Hs.105884		2.32
	411773 448569	BE382657	Hs.72026 Hs.21486	protease, serine, 21 (testisin) signal transducer and activator of trans	2.31 2.31
00	434775	AA648983	Hs.212911	ESTs	2.31
80	407378	AA299264		gb:EST11752 Uterus Homo sepiens cONA 5	2.31
	442353 422611	BE379594 AA158177	Hs.49138 Hs.118722	ESTs burneytranstarasa A (alaba (1.6) 6 mass	2.31
	409965	AA079229	14,110/22	tucosyltransterase 8 (alpha (1,6) fucosy gb:zm95f04,r1 Stratagene colon HT29 (937	2.31 2.31
				4 4 4 4 land	2.01

	421677	H64092	Hs.38282	ESTs	2.31
	419493 424435	AF001212 AB011167	Hs.90744	proteasome (prosome, macropain) 26S subu	2.31
	446880	AI811807	Hs.146957 Hs.108646	KIAA0595 protein Homo saplens cONA FLJ12534 fis, clone NT	2.30 2.30
5	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	2.30
_	452834	AI638627	Hs.105685	ESTs	2.30
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	2.30
	428125	AA393071	Hs.182579	leucine aminopeptidase	2.30
10	417655	AA760791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	2.29
10	407287	AI678812	Hs.201658	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.29
	428923 452203	BE047698 X57522	Hs.188785 Hs.158164	ESTs	2.29
	409402	AF208234	Hs.695	ATP-binding cassette, sub-family 8 (MDR/ cystatin 8 (stefin 8)	2.29 2.29
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.29
15	451999	AW176401	Hs.27424	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.29
	400811	AF219139	Hs.87726	KIAA0154 protein; ADP-ribosylation facto	2.29
	436396	Al583487	Hs.299112	Homo sapiens cDNA FLI11441 fis, clone HE	2.28
	442152	R39246	Hs.239666	Homo sapiens cDNA FLJ13495 ffs, clone PL	2.28
20	420931 410174	AF044197 AA306007	Hs.100431	smail inducible cytokine B subfamily (Cy	2.28
20	425247	NM_005940	Hs.59461 Hs.155324	DKFZP434C245 protein matrix metalloproteinase 11 (stromelysin	2.28 2.28
	438170	AI916685	Hs.194601	ESTs	2.28
	445378	AV653564	Hs.226948	ESTs	2.28
0.0	428048	AA705745	Hs.185070	ESTs	2.28
25	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	2.27
	444665	BE613126	Hs.47783	ESTs, Wealdy similar to T12540 hypotheti	2.27
	427660 422128	AI741320 AW881145	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	2.27
	433535	AF111106	Hs.3382	gb:QV0-OT0033-010400-182-a07 OT0033 Homo protein phosphatase 4, regulatory subuni	2.27 2.27
30	415857	AA866115	Hs.301646	Homo sapiens cDNA FLJ11381 fis, done HE	2.27
	421155	H87879	Hs.102267	lysyl oxidase	2.27
	405545				2.27
	449467	AW205006	Hs.197042	ESTs	2.27
35	445537	AJ245671 AF131784	Hs.12844	EGF-like-domain, multiple 6	2.27
33	450680 423634	AP131784 AW959908	Hs.25318 Hs.1690	Homo sapiens clone 25194 mRNA sequence	2.26 2.26
	443868	W88483	Hs.293650	heparin-binding growth factor binding pr ESTs	2.26
	407742	AF186252	Hs.38084	sulfotransferase family, cytosolic, 1C,	2.26
40	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	2.26
40	432655	AA832195	Hs.292266	ESTs	2.26
	429731 400514	AK001592	Hs.212172	beta,beta-carotene 15,15-dioxygenase ho	2.26
	431846	BE019924	Hs.271580	uroplakin 1B	2.26 2.26
	439521	AI808955	Hs.58248	ESTs	2.26
45	426010	AA136563	Hs.1975	Homo sapiens cDNA: FLJ21007 fis, clone C	2.26
	437641	AA811452	Hs.291911	ESTs	2.26
	418982	AJ348838	Hs.13073	ESTs	2.26
	411393	AW797437	Hs.69771	B-factor, properdin	2.26
50	414809 419488	AI434699 AA316241	Hs.77356 Hs.90691	transferrin receptor (p90, CO71)	2.25
70	434540	NM_016045	Hs.5184	nucleophosmin/nucleoplasmin 3 TH1 drosophila homolog	2.25 2.25
	449962	AA004879	Hs.187820	ESTS	2.25
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	2.25
E E	456844	AI264155	Hs.152981	COP-diacylglycerol synthase (phosphatida	2.25
55	414368	W70171	Hs.75939	uridine monophosphate kinase	2.25
	408353 439223	BE439838	Hs.44298 Hs.23945	hypothetical protein	2.25
	448753	AW238299 AL048858	Hs.224355	ESTs ESTs, Weakly similar to A39650 protein k	2.25 2.25
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	2.24
60	432403	AA550815	Hs.124840	ESTs	2.24
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	2.24
	432673	AB028859	Hs.278605	ER-associated DNAJ; ER-associated Hsp40	2.24
	446887	AI346656	Hs.156652	Homo sapiens cDNA: FLJ22800 fis, clone K	2.24
65	452833 409432	BE559681 D49372	Hs.30736 Hs.54460	KIAA0124 protein small inducible cytokine subfamily A (Cy	2.24
0.5	422039	BE567832	Hs.82148	hypothetical protein	2.24 2.24
	429925	NM_000786			2.24
	445413	AA151342	Hs.12677	CGI-147 protein	2.23
70	423645	AI215632	Hs.147487	EST\$	2.23
70	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	2.23
	423515	AA327017	Hs.162204		2.23
	444743 434518	AA045648 H56995	Hs.11817 Hs.37372	nudix (nucleoside diphosphate linked moi Homo sapiens DNA binding peptide mRNA, p	2.23 2.23
	435602	AF217515	Hs.283532		2.23
75	449974	AW970948	Hs.269403		2.23
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	2.23
	457982	AW856093	Hs.183617	' ESTs	2.23
	414420	AA043424	Hs.76095	immediate early response 3	2.23
80	449019 431840	AI949095 AA534908	Hs.67776 Hs.2860	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.23
	452930	AW195285	Hs.194097	POU domain, class 5, transcription facto ESTs	2.23 2.23
	436391	AJ227892	Hs.146274		2.23
	439186	A1697274	Hs.6487	Xq28, 2000bp sequence contg. ORF	2.23

	427254	AL121523	Hs.97774	ESTs .	2.22
	424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	2.22
	414732 411835	AW410976 U29343	Hs.77152 Hs.72550	minichromosome maintenance deficient (S.	222
5	427647	W19744	Hs. 180059	hyaluronan-mediated motility receptor (R	222
_	438223	AA781171	rs. 160039	Homo sapiens cDNA FLJ20653 fis, clone KA gb:aj24d05.s1 Soares_testis_NHT Homo sap	2.22 2.22
	434504	AI887341	Hs.121590	Homo sepiens cDNA FLJ12827 fls, clone NT	2.22
	450149	AW969781	Hs.293440	ESTs, Moderately similar to ZIC2 protein	2.22
	439211	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	2.22
10	401519				2.22
	441794	AW197794	Hs.253338	ESTs	2.22
	412108	AA100293	Hs.185043	ESTs	222
	431849	A1670823	Hs.85573	Homo saplens mRNA; cDNA DKFZp566N034 (fr	2.22
15	444969	AJ203334	Hs.160628	ESTs	2.21
13	408901	AK001330	Hs.48855	hypothetical protein FLJ10458	221
	434423 439328	NM_006769	Hs.3844 Hs.118212	LIM domain only 4	2.21
	400021	W07411	ns.110212	ESTs, Moderately similar to ALU3_HUMAN A AFFX control; STAT1	2.21 2.21
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	221
20	434170	AA626509	Hs.122329	ESTs	2.21
	423453	AW450737	Hs.128791	CGI-09 protein	2.21
	428438	NM_001955	Hs.2271	endothelin 1	2.21
	433102	AI343966	Hs.158528	ESTs	2.21
~ ~	421470	R27496	Hs.1378	annexin A3	2.21
25	425499	T62489		gb:yc03f09.r1 Stratagene lung (937210) H	2.21
	438280	AW015534	Hs.217493	ennexin A2	2.21
	440381	AA917608	Hs.190495	ESTs	2.20
	453779	N35187	Hs.43388	ESTs	2.20
30	433627 417944	AF078866	Hs.284296	Homo sapiens cDNA: FLJ22993 fis, clone K	2.20
50	452299	AU077196 AW206330	Hs.82985	collagen, type V, alpha 2	2.20
	422689	AW856665	Hs.73239	hypothetical protein FLJ10901	2.20
	448457	H65629	Hs.245997	gb:RC3-CT0297-290100-013-d03 CT0297 Homo ESTs	2.20 2.20
	416221	BE513171	Hs.79088	mitochondrial ribosomal protein L3	2.20
35	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	2.20
	430603	AA148164	Hs.247280	HBV associated factor	2.20
	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mi	2.20
	452679	242387	Hs.4299	Homo sapiens cDNA: FLJ20965 fis, clone A	2.20
40	410619	BE512730	Hs.65114	keratin 18	2.20
40	424332	AA338919	Hs.101615	ESTs	2.20
	442490	AW965078	Hs.30212	thyroid receptor interacting protein 15	2.20
	418661	NM_001949	Hs.1189	Human mRNA for KIAA0075 gene, partial cd	2.20
	419341	N71463	Hs.118888	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.20
45	427920 413879	Z11502 AA132961	Hs.181107 Hs.212533	annexin A13	2.19
7.2	419752	AA249573	Hs.152618	Homo sapiens cDNA: FLJ22572 fts, clone H ESTs	2.19
	441438	AW137772	Hs.185980	ESTS	2.19 2.19
	413095	AA494359	Hs.30715	ESTa	2.19
	403208			2013	2.19
50	422596	AF063611	Hs.118633	2-5 oligoadenylate synthetase-like	2.19
	444261	AA298958	Hs.10724	MDS023 protein	2.19
	419474	AW968519	Hs.155849		2.19
	453883	AI638516	Hs.77448	aldehyde dehydrogenase 4 (glutamate gamm	2.18
55	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	2.18
33	453450	AW797627	Hs.89474	ADP-ribosylation factor 6	2.18
	440250 444334	AA876179	Hs.134650		2.18
	437616	BE296785 AJ797163	Hs.10848 Hs.207954	KIAA0187 gene product	2.18
	451807	W52854	Hs.27099	ESTs OKFZP564J0863 protein	2.18 2.18
60	430441	8E398091	Hs.6880	DKFZP434D156 protein	2.18
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (I	2.18
	411678	AI907114	Hs.71465	squalene epoxidase	2.18
	453735	AI066629	Hs.125073		2.18
65	450499	AA235207	Hs.250456		2.18
65	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	2.18
	421532	AW138207	Hs.146170		2.18
	444342	NM_014398	Hs.10887	similar to lysosome-essociated membrane	218
	451099 444207	R52795 Al565004	Hs.25954	interteukin 13 receptor, alpha 2	218
70	425873	NM_013390	Hs.79572 Hs.160417	cathepsin D (lysosomal aspartyl protease	218
. •	417404	NM_007350			217
	449437	AI702038	Hs.100057	pleckstrin homology-lika domain, family Homo sapiens cDNA: FLJ22902 fis, clone K	2.17 2.17
	446995	AI355012		gb:qu16d10.x1 NCI_CGAP_Ov23 Homo sapiens	2.17
	431548	AJ834273	Hs.9711	Homo sapiens cDNA FLJ13018 fis, clone NT	2.17
75	411127	AA668995	Hs.218329		2.17
	439961	AA857451	Hs.269696		217
	429125	AA446854	Hs.271004		2.17
	407103	AA424881	Hs.256301	ESTs	217
20	435990	AJ015852	Hs.131793		2.17
80	415116	AA160363	Hs.269956		2.17
	440052	AI633744	Hs.195648		2.17
	423961	D13666	Hs.136348		217
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	2.16

	443599	AI079559	Hs.134125	ESTs	216
	423623 427258	AB011117 AA400091	Hs.129943 Hs.39421	KIAA0545 protein ESTs	2.16
	418113	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	2.16 2.16
5	450835	BE262773	Hs.25584	hypothetical protein FLJ 10767	216
	428698	AA852773	Hs.297939	ESTs, Wealdy similar to T17344 hypotheti	2.16
	421408	AI688223	Hs.104114	H.sapiens HCG I mRNA	2.16
	449057 408947	AB037784 AL080093	Hs.22941 Hs.49117	KIAA1363 protein	2.16
10	443552	N65982	Hs.109434	Homo sopiens mRNA; cONA DKFZp564N1662 (I ESTs	2.16 2.16
••	448153	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	2.16
	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	2.16
	431341	AA307211	Hs.251531	proteasome (prosome, macropain) subunit.	2.16
15	452865 432789	AF924046 D26361	Hs.119567	ESTS	2.16
1.0	438580	AA811262	Hs.3104 Hs.299202	KIAA0042 gene product ESTs	2.16 2.16
	422192	AA305159	Hs.113019	fis485	215
	425607	U09860	Hs.158333	protease, serine, 7 (enterokinase)	2.15
20	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	2.15
20	447674 441021	BE270640 AW578716	Hs.19192	cyclin-dependent kinase 2	2.15
	442432	BE093589	Hs.7644 Hs.38178	H1 histone family, member 2 Homo sepiens cDNA: FLJ23468 fis, clone H	2.15 2.15
	426471	M22440	Hs.170009	transforming growth factor, alpha	2.15
26	431941	AK000106	Hs.272227	Homo sepiens cDNA FLJ20099 fis, clone CO	2.15
25	414761	AU077228	Hs.77256	enhancer of zesta (Orosophila) homolog 2	2.15
	447033 410407	Al357412 X66839	Hs.157601 Hs.63287	ESTs carbonic anhydrase IX	2.15
	446077	BE251048	Hs.22579	Homo sapiens clone CDABP0036 mRNA sequen	2.15 2.15
••	420900	AL045633	Hs.44269	ESTs	2.15
30	411975	AJ916058	Hs.144583	ESTs, Weakly similar to gag [H.sapiens]	215
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	2.15
	449571 452721	AW016812 AJ269529	Hs.200266 Hs.30377	ESTs Homo sapiens EST from clone 470080, full	2.15
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.15 2.14
35	410664	NM_006033	Hs.65370	lipase, endothelial	2.14
	435730	AB020635	Hs.4984	KIAA0828 protein	2.14
	452835 452092	AK001269	Hs.30738	hypothetical protein FLJ10407	2.14
	401708	BE245374	Hs.27842	hypothetical protein FLJ11210	2.14 2.14
40	411400	AA311919	Hs.69851	GAR1 protein	2.14
	448526	AB028948	Hs.21361	KIAA1023 protein	2.14
	421175	AJ879099	Hs. 102397	GIOT-3 for gonadotropin inducible transc	2.14
	412338	AA151527	Hs.69485	Homo sapiens cDNA FLJ12436 fis, clone NT	2.14
45	420894 409235	AA744597 AA188827	Hs.88854 Hs.7988	ESTs ESTs, Weakly similar to endo-alpha-D-man	2.14 2.14
	412870	N22788	Hs.82407	Horio sepiens HSPC296 mRNA, partial cds	214
	447760	AJ431328	Hs.291179	ESTs, Weally similar to topoisomerase !	2.14
	413511	AJ627178	Hs.75412	Arginine-rich protein	2.13
50	432945 418592	AL043683 X99226	Hs.271357 Hs.284153	ESTs, Wealdy similar to unnamed protein	213
	441790	AW294909	Hs.132208	Fanconi anemia, complementation group A ESTs	2.13 2.13
	425298	AK000209	Hs.155556	hypothetical protein FLJ20202	2.13
	450956	AW193531	Hs.205647	ESTs. Moderately similar to ALU1_HUMAN A	2.13
55	419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	2.13
55	421508 453975	NM_004833 AW009808	Hs.105115 Hs.270829	absent in melanoma 2 ESTs	2.13
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	2.13 2.13
	422783	AA598956	Hs.120439	ethanotamine kinase	2.13
60	444542	Al161293	Hs.146862	ESTs, Weakly similar to KIAA0525 protein	2.13
UU	410418 4197 <del>9</del> 1	031382 A1579909	Hs.63325 Hs.105104	transmembrane protease, serine 4 ESTs	2.13
	414860	BE255593	Hs.77502	methionine adenosytransferase II, alpha	2.13 2.13
	425860	L29339	Hs.1964	solute carrier farminy 5 (sodium/glucose	2.13
65	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyttransferase 1	2.13
05	437050 430217	AA766420 N47863	Hs.291606	ESTs	2.13
	420923	AF097021	Hs.180450 Hs.273321	ribosomal protein S24	2.13
	409012	AL117435	Hs.49725	differentiafly expressed in hematopoieti OKFZP434I216 protein	2.12 2.12
70	450645	AL117441	Hs.25264	DKFZP434N126 protein	212
70	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	2.12
	451356 429534	AA748418 AW976987	Hs.164577	ESTs	2.12
	428365	AA295331	Hs.163327 Hs.183861	ESTs Homo sapiens cDNA FLJ20042 fis, clone CO	2.12 2.12
~-	441495	AW294603	Hs.127039	ESTs	2.12
75	443564	AI921685	Hs.199713		2.12
	410839	NM_006849	Hs.66581	protein disuffide isomerase	2.12
	433640 442947	AW390125 R40800	Hs.240443		2.12
	414987	AA524394	Hs.21303 Hs.165544	ESTs ESTs	2.12 2.12
80	450510	AA010056	Hs.242998		2.12
	427475	AA403151	Hs.191605	ESTs	2.12
	444670	H58373	Hs.37494	ESTs	2.12
	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	2.12

415138		433748	R12244		gb:yl33c12.r1 Soares fetal liver spleen	2.12
141768					tissue factor pathway inhibitor 2	2.11
154 141949 AN(0.01452) Ha. 196457 shut carrier family 25 (millichondrid) 2.11 (1294) AN(0.0156) Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha. 198050 Ha.						
A16972	5					
10		416472				
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15   433849   84645884   hs.19416   ESTs   Weatly similar to TAZR HUMAN, BETA   211						
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450747   A0664821   Hs. 48306   SSTs, Highly similar to EWS_HUMAN RNA-BI   2.10						
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75 429504 X99133 Hs. 204238 Fipocalin 2 (oncogene 2493) 2.08 Hs. 58879 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 27693 Hs. 2				Hs.51233		
80 438394 BE379623 Hs.27693 CGI-124 protein 2.08 413092 AA126856 Hs.118665 ESTs 2.08 413715 AW851121 Hs.75497 Homo sapiens cDNA: FLJ22139 fis, clone H 2.08 423020 AA383092 Hs.1608 replication protein A3 (14kD) 2.07 433379 AW970529 Hs.88434 Homo sapiens cDNA: FLJ21816 fis, clone H 2.07 432125 AW972667 Hs.287510 Homo sapiens cDNA FLJ12300 fis, clone MA 2.07	75		X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	2.08
80 43379 AW95121 Hs.75497 AM95267 Hs. 18665 ESTs 2.08 43377 AW851121 Hs.75497 Hs. 1608 replication protein A3 (14kD) 2.07 433378 AW970529 Hs. 88434 Homo sepiens cDNA: FLJ2139 fis, clone H 2.07 433125 AW972667 Hs. 81753 ESTs 2.07 432125 AW972667 Hs. 287510 Homo sepiens cDNA FLJ12300 fis, clone MA 2.07	13					
80 43715 AW851121 Hs.75497 Homo sapiens cDNA: FLJ22139 fis, clone H 2.08 replication protein A3 (14kD) 2.07 AA38378 AW970529 Hs.86434 Hs.861743 AA35261 Hs.61743 ESTS CONA: FLJ21816 fis, clone H 2.07 432125 AW972667 Hs.287510 Homo sapiens cDNA: FLJ21816 fis, clone H 2.07 2.07 A03125 AW972667 Hs.287510 Homo sapiens cDNA: FLJ21800 fis, clone MA 2.07						
80 423020 AA383092 Hs.1608 replication protein A3 (14kD) 2.07 438378 AW970529 Hs.86434 Horno sepiens cDNA: FLJ21816 fis, clone H 2.07 433179 AA035/261 Hs.81753 EST8 EST8 LOTNA: FLJ21816 fis, clone H 2.07 432125 AW972667 Hs.287510 Horno sepiens cDNA FLJ12300 fis, clone MA 2.07		413715	AW851121			
453379 AA035261 Hs.61753 ESTs 2.07 432125 AW972667 Hs.287510 Homo septens cDNA FLJ12300 fis, clone MA 2.07	ጸብ					
432125 AW972667 Hs.287510 Homo sapiens cDNA FLJ12300 fis, clone MA 2.07	50					
		449370	AK002114		hypothetical protein FLJ11252	

	449318	AW236021	Hs.108788	ESTs, Wealthy similar to zeste [D.metanog	2.07
	450096 454011	A1682088 M31008	Hs.223368	ESTs	2.07
	427876	Al494291	Hs.37009 Hs.111977	alkatine phosphatase, intestinal ESTs	2.07
5	422901	R81936	Hs.121576	aspartate beta-hydroxytase	2.07 2.07
-	419235	AW470411	Hs.288433	neurotrimin	207
	449207	AL044222	Hs.23255	nucleoporin 15SkD	2.07
	408243	Y00787	Hs.624	interleukin 8	2.07
10	415652	T79213	Hs.272073	ESTs	2.07
10	446546 411765	BE167687	Hs.156628	ESTs	2.07
	423472	H43346 AFQ41260	Hs.129057	gb:yp09a04.r1 Soares breast 3NbHBst Homo	2.07
	436211	AK001581	Hs.80961	breast carcinoma amplified sequence 1 polymerase (DNA directed), gamma	2.07 2.07
	456157	AW979153		gb:EST391263 MAGE resequences, MAGP Homo	2.06
15	407143	C14076	Hs.248968	EST	2.06
	454269	AI961060	Hs.296411	ESTs, Moderately similar to KF1A_HUMAN K	2.06
	432440	X63597	Hs.2996	sucrase-isomaltase	2.06
	410668 422765	BE379794 AW409701	Hs.65403 Hs.1578	hypothetical protein	2.06
20	450434	AA166950	Hs.18645	baculoviral IAP repeat-containing 5 (sur ESTs, Weakly similar to partial CDS [C.e	2.06 2.06
	439832	T81829	Hs.14870	ESTs	206
	456264	AW974175	Hs.105251	ESTs	2.06
	431201	AA678405	Hs.8854	Human transcription unit PVT gene, exons	2.06
25	445021 438714	AK002025 AA814859	Hs.12251	Homo sapiens cDNA FLJ11163 fis, clone PL	2.06
	445318	AW500652	Hs.294112 Hs.200885	ESTs ESTs	2.06 2.06
	439951	AI347067	Hs.124636	ESTs	2.06
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	2.06
20	428307	W27393	Hs.183648	protein tyrosine phosphalase, receptor t	2.06
30	426874 451295	N67325	Hs.247132	ESTs	2.06
	432584	AIS57212 AA928829	Hs.17132 Hs.47099	ESTs	2.06
	433027	AF191018	Hs.279923	Horno sapiens cDNA: FLJ21212 fs, clone C putative nucleotide binding protein, est	2.06 2.06
	433716	AA608808	Hs.225118	ESTs	2.06
35	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	2.06
•	426235 449026	AJ531964	Hs.34447	ESTs	2.06
	437016	BE500946 AU076916	Hs.209105 Hs.5398	ESTs	2.06
	400019	A0070310	rus.3330	guanine monphosphate synthetase AFFX control: STAT1	2.06
40	408873	AL045017	Hs.23247	ESTs	2.06 2.06
	442547	AA306997	Hs. 268362	ESTs, Weakly similar to hypothetical pro	2.06
	455778	BE068746		gb:CM2-BT0693-210300-123-d09 BT0693 Homo	2.06
	439975	AW328081	Hs.6817	Homo saplens putative oncogene protein m	2.06
45	433037 440086	NM_014158 NM_005402	Hs.279938 Hs.288757	HSPC067 protein v-ral simian leukernia viral oncogene hom	2.06
	436414	BE264633	Hs.143638	WD repeat domain 4	2.06 2.05
	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	2.05
	407293	AA602234	Hs.270551	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.05
50	409459 436238	D86407	Hs.54481	low density lipoprotein receptor-related	2.05
50	400517	AK002163 AF242388	Hs.301724 Hs.149585	ESTs, Highly similar to unnamed protein	2.05
	439943	AW083789	Hs.124620	lengsin ESTs	2.05 2.05
	421904	BE143533	Hs.109309	hypothetical protein FLJ20035	2.05
55	417850	AA215724	Hs.82741	primase, polypeptide 1 (49kO)	2.05
55	417491	AW376842	Hs.1085	guanylate cyclase 2C (heat stable entero	2.05
	453775 435525	NM_002916 AJ831297	Hs.35120 Hs.123310	replication factor C (activator 1) 4 (37	2.05
	412627	BE391959	Hs.74276	ESTs chloride intracellular channel 1	2.05
	439702	AW085525	Hs.134182	ESTs	2.05 2.05
60	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	2.05
	432979	AA573263	Hs.120860	ESTs	2.05
	417308 432925	H60720 AA878324	Hs.81892	KIAA0101 gene product	2.05
	446311	AW007294	Hs.192734 Hs.149795	ESTs ESTs, Wealdy similar to ALU1_HUMAN ALU S	2.05 2.05
65	427871	AW992405	Hs.59622	ESTs, Wealdy similar to unknown [H.sapie	2.05
	453804	AA300204	Hs.35276	KIAA0852 protein	2.05
	449939	T86420	Hs.272139	ESTs	2.05
	455666 417819	BE065813	4- 122540	gb:RC2-BT0318-110100-012-a08 BT0318 Homo	2.05
70	427747	AJ253112 AW411425	Hs.133540 Hs.180655	ESTs serine/threonine kinase 12	2.04
-	415009	C75253	Hs.220950	ESTs	2.04 2.04
	437829	AI358522	Hs.270188	ESTs	2.04
	435381	AW136397	Hs.247572	ESTs	2.04
75	439778 428753	AL109729 AM030363	Hs.18948	ESTs, Highly similar to HPS1_HUMAN PROTE	2.04
, ,	426753 446475	AW939252 AI908188	Hs.192927 Hs.209245	hypothetical protein FLJ20251 ESTs	2.04
	431394	AK000692	Hs.252351	HERV-H LTR-associating 2	2.04 2.04
	423701	AA329856	Hs.143022	ESTs	2.04
QΛ	430680	AW138724	Hs.168974	ESTs. Highly similar to ALU7 HUMAN ALU S	2.04
80	422369	AF005216	Hs.115541	Janus kinase 2 (a protein tyrosine kinas	2.04
	432481 443746	AW451645 AW861379	Hs.151504 Hs.160602	Homo sapiens cDNA FLJ11973 fis, clone HE ESTs	2.04
	400792	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp43400515 (f	2.04
					201

	432393	AW205863	Hs.133988	ESTs, Wealdy similar to 152825 gene MAC2	2.04
	430785	Z30201	14. 40704	gb:HHEA22G Atrium cDNA library Human hea	2.04
	428343 419329	AL043021 AY007220	Hs.12705	ESTs, Weakly similar to plakophilin 26	2.04
5	452488	N74921	Hs.288998 Hs.184389	S100-type calcium binding protein A14 ESTs	2.04
•	403485	1114321	113.104309	2018	2.04
	413313	NM_002047	Hs.75280	glycyl-IRNA synthetase	2.04 2.04
	407634	AW016569	Hs.301280	ESTs, Highly similar to AF241B31 1 intra	2.04
• •	433326	A1379486	Hs.159430	ESTs	2.03
10	451129	BE072881		gb:RC2-8T0548-200300-012-e09 BT0548 Homo	2.03
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	2.03
	422963	M79141	Hs.13234	ESTs	2.03
	418684	U82987	Hs.87246	Bcl-2 binding component 3	2.03
15	407824 434551	AA147884 BE387162	Hs.9812	ESTs	2.03
15	440246	W52010	Hs.280858 Hs.191379	ESTs, Highly similar to XPB_HUMAN ONA-RE ESTs	203
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	2.03 2.03
	431301	AA502384	Hs.151529	ESTs	2.03
	452705	H49805	Hs.246005	ESTs	203
20	421724	AB037832	Hs.107287	KIAA1411 protein	203
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo	2.03
	450200	AW975625	Hs.173088	ESTs	2.03
	447474 418852	AW614220	Hs.189402	ESTs .	2.03
25	445019	BE537037 Al205540	Hs.273294	hypothetical protein FLJ20069	2.03
2.7	435202	AI971313	Hs.281295 Hs.170204	ESTs KIAA0551 protein	2.03 2.03
	431842	NM_005764	Hs.271473	epithelial protein up-regulated in card	2.03
	436198	AK001125	Hs.300922	Homo sapiens cDNA FLJ10263 fis, clone HE	2.03
~~	440773	AA352702	Hs.37747	hypothetical protein FLJ12484	2.03
30	443425	AI056776	Hs.133397	ESTs	2.03
	454166	AW993356	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	2.03
	407975	X89426	Hs.41716	endothelial cell-specific molecule 1 (NO	2.03
	428299 418735	AL038004	Hs.29419	ESTs	2.03
35	442053	N48769 R35343	Hs.44609 Hs.24968	ESTs	2.03
-	415757	AA830854	Hs.187810	Human DNA sequence from clone RP1-233G16 ESTs .	2.03 2.03
	432559	AW452948	Hs.257631	ESTa	2.03
	425912	AL137629	Hs.162189	serine/threonine kinase with Dbl- and pl	2.02
40	419395	BE268326	Hs.90280	5-aminolmidazote-4-carboxamide ribonucte	2.02
40	417576	AA339449	Hs.82285	phosphoribosylgtycinamide formyltransfer	2.02
	418559	AA225048	Hs.104207	ESTs	2.02
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	2.02
	433906 422072	AI167816 AB018255	Hs.43355	ESTs	2.02
45	419546	AA244199	Hs.111138	KIAA0712 gene product	2.02
	446229	A1744964	Hs.14449	gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sapiens KIAA1609 protein	2.02 2.02
	450516	AA902656	Hs.21943	NIF3 (Ngg1 interacting factor 3, S.pombe	2.02
	431721	AB032996	Hs.268044	KIAA1170 protein	2.02
50	419807	R77402		gb:yi75f11.s1 Soares placenta Nb2HP Homo	2.02
50	438192	AI859065	Hs.16808	ESTs, Wealtly similar to paraplegin-like	2.02
	401866	0.0075			2.02
	443129 426991	R16075	Hs.21668	ESTs	2.02
	414731	AK001536 AI890434	Hs.285803 Hs.77135	Homo sapiens cDNA FLJ12852 fis, clone NT	2.01
55	424783	AA913909	Hs.153088	Homo sapiens mRNA; cDNA DKFZp586A191 (tr TATA box binding protein (T8P)-essociate	201
	413293	AL047483	Hs.75270	GTP-binding protein homologous to Saccha	2.01 2.01
	435787	AW162767	Hs.100914	hypothetical protein FLJ10352	2.01
	422599	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	2.01
60	442660	AW138174	Hs.130651	ESTs	2.01
UU	456553	AA721325	Hs.189058	ESTs, Weakly similar to cAMP-regulated g	2.01
	431530 431300	NM_002204 AA502348	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	2.01
	443180	R15875	Hs.70945	gb:ne26b03.s1 NCI_CGAP_Co3 Homo sapiens ESTs	2.01
	450914	AJ743761	Hs.142528	ESTS	2.01 2.01
65	448275	BE514434	Hs.20830	synaptic Ras GTPase activating protein 1	201
	405484			The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	2.01
	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	2.01
	451273	NM_014811	Hs.26163	KIAA0649 gene product	201
70	439696	W95298	Hs.171882	ESTs	201
70	432378	AI493046	Hs.146133	ESTs	201
	417975 453665	AA641836 AA626250	Hs.30085	Homo sapiens cDNA: FLJ23186 fis, clone L	2.01
	419981	AA897581	Hs.181165 Hs.128773	eukaryotic translation elongation factor ESTs	2.01
	445808	AV655234	Hs.298083	ESTS	2.01 2.01
75	435767	H73505	Hs.117874	ESTs	2.01
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.01
	452747	BE153855	Hs.61460	ESTs	2.01
	422790	AA809875	Hs.25933	ESTs	2.01
80	443303 433929	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	2.01
~~	410008	A1375499 AA079552	Hs.27379	ESTs	2.01
	448954	AB014564	Hs.22616	gb:zm20h12.s1 Stratagène pancreas (93720 KIAA0664 protein	2.01
	440774	AJ420611	Hs.127832	ESTs	2.00 2.00
					2.00

	451351	AW058261	H- 400313	EST- West	• • •
			Hs. 168213	ESTs. Weatly similar to ALU1_HUMAN ALU S	2.00
	442961	BE614474	Hs.289074	Homo sapiens cDNA FLI 13985 fis, clone Y7	2.00
	424420	BE614743	Hs.146688	prostaglandin E synthase	2.00
	407154	H79677		gb:yu76g10.s1 Soares fetal tiver spleen	2.00
5	410240	AL157424	Hs.61289	Synaptojanin 2	
•	426830	AA385751			2.00
			Hs.160392	ESTs	2.00
	435014	BE560898	Hs.10026	ribosomal protein L17 isotog	2.00
	408520	Ai918693	Hs.81848	RAD21 (S. pombe) homolog	2.00
	432829	W60377	Hs.57772	ESTs	2.00
10	406752	AI285598	Hs.217493	annexin A2	2.00
				GHICAITAL	200
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1.5	TABLE 404	Ŀ			
15	Pkey:	Uniqu	ue Eas probes	et identifier number	
	CAT number	er. Gene	cluster numbe	er ·	
	Accession:		ank accession		
				, manage	
	Pkey	CAT number	Accession		
20					
20	408690	107490_1		NA056567 AW882724	
	409955	116301_1	AA079229 A	A079201 AA078874	
	410008	116812_1	AA079552 E	E142525 BE142527	
	410145	1178960_1	AW886300	AW887902 AW887893 AW886291 AW592641	
	411765	125700_1	H43346 AA2	248302 AA095182	
25	416713	1610889_1		244 T69850 H79151	
	418546	176677_1			
	419546			59708 T59843 BE156903	
		185766_1		A244272 H57440	
	419807	188252_1		262462 AA250988 R06794	
20	420637	195241_1	AW976153	AA278945 AA747691	
30	422058	210815_1	AA862231 A	VA659033 AA302799 AA302798	
	422128	211994_1	AWB81145	AA490718 M85637 AA304575 T06067 AA331991	
	422689	219896_1		AA315006 AW954733	
	425499	252539_1		634 AA828581 AA358569	
	430704	322217_1		AW206655 AA484440	
35	430785	323486_1			
23				86132 T72025	
	431120	328264_1	AA492588 /	M492498 AA492571	
	431300	331217_1	AA502346 (	BE159863	
	431322	331543_1	AW970622	AA503009 AA502998 AA502989 AA502805 T9218	8
40	432009	34025_1	AL137424 E	E007148 T52277	
40	432093	341283_1		/972670 H28359 AA525808	
	433748	37385_1		1290 AJ110858 AF090916 AF075357 AA011531	
	434414	38585_1			ALMOSTO ALMOST ALMOSTO ALMOSTO ALMOST ALGADO ALMOST ALGADO ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST ALMOST
	40 14 14	20202_1	AMBETEAA	10000 ATTO 1017 ATTO 1010 WUUDD/ BE14224D	AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231
			AW85/541	AWB14172 H56214 AWB14398 AF134164 AA243	93 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139
45			AA149//6/	AA699829 AW879188 AW813567 AW813538 AI26	7168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730
43			AA157715	4A053524 AW849581 AW854566 C05254 AW882	336 T92637 AWB12621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957
			N66951 AA	527374 H66215 AA045564 AI694265 H60808 AA1	49726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659
			BE081531 I	H59570	
	437549	438403_1		AW751068 AW844938	
	438223	452646_1		AI202139 AI202098	
50	438993	467651_1		AA834879 AI926361	
	439848	477806_1			
	443597			D63277 AAB46968	
		574739_1		V80626 AW387769	
	446995	702707_1	AI355012 A		
55	447197	711623_1		866546 R36167	
33	448437	763310_1	AW470125	A1734872 A1749559 AW856504 A1583942 AW779	336 AW843429 AW844876 AI520713 AW847236
	450190	827655_1	T51387 AV	/191595 T51271 AI686285	
	451105	859083_1	AJ761324 A	W880941 AW880937	
	451129	859870_1		BE072946 AI762181	
	451237	883269_1	AW600293		
60	455666	1349545_1		8E065788 BE065889 BE065832	
•	455778		00000013	DECOURAGE DECOURSES DECOURSES DECOURSES DE COURSES DE C	
		1364506_1	DEU00/40	BE088802 BE088755 BE088876 BE088947 BE08	881 BE088952
	456157	158261_1	AW9/9153	AA176967 AA826015	
		_			
15	TABLE 40	IC:			
65	Pkey:	Uni	que number co	rresponding to an Eos probeset	
	Ref:	Sec	uence source.	The 7 digit numbers in this column are Genhank t	dentifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
		880	uence of huma	n chromosome 22" Dunham, et al. (1999) Nature 4	107.480.40C
	Strand:	Indi	cates DNA str	and from which exons were predicted.	AC-401-17
	Nt_positio				
70	прози	41. (1941)	Cales nucleous	le positions of predicted exons.	
. 0	Otari	0-4		A4- 14	
	Pkey	Ref	Strand	Nt_position	
	400514	9796594	Minus	78844-79025,80850-80991,89754-89941,93750	<b>-93891</b>
	401519	6649315	Plus	157315-157950	
	401708	2951946	Plus	154511-155298	
75	401856	8018106	Plus	73126-73623	
_	402075	8117407	Plus		1 124455 124610 125522 125025
	403055	8748904		121907-122035,122804-122921,124019-12416	1,124433-144010,123012-120010
			Minus	109532-110225	
	403208	7630829	Minus	147706-147903,148667-148804	
90	403422	9665041	Minus	151169-151561	
80	403485	9966528	Plus	2888-3001,3198-3532,3655-4117	
	403776	7770611	Minus	1414-1513,1624-1756	
	404171	9930793	Plus	173667-173783,176876-177055	
	404253	9367202	Minus	55675-56055	
		646	ramină	and Publish	

	404519	8152000	Plus	12817-13000
	404567	7249169	Minus	101320-101501
	405484	5922025	Ptus	199214-199579,199672-199920,200262-200495
_	405545	1054740	Plus	118677-118807.119091-119296.121625-121823
5	405818	4071056	Plus	29055-29196
	406399	9256288	Minus	63448-63554

TABLE 41A: ABOUT 634 SEQUENCES UP-REGULATED IN STOMACH CANCER
Table 41A lists about 634 genes up-regulated in stomach cancer compared to normal adult fissues that are likely to be extracellular or cell-surface proteins. These were selected as for Table 40A and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig. th3, egf, 7tm domains). Predicted protein domains are 10

15

tor Table 40A a noted. Pikey: ExAcon: UnigenetD: Unigene Tide: PSDomain: R1:

Unique Eos probeset identifier number Exemptar Accession number, Genbank accession number Unigene number Unigene gene title Protein Structural Domain Ratio of turnor to normal adult tissues

	141.	14000	01 (W10) W10	IIII GOOM 029083		
20	Pikey	ExAcon	UnigenetD	Unigene Title	PS0omain .	RI
	411243	AB039886	Hs.69319	CA11	SS	30.66
	418007	M13509	Hs.83169	matrix metallop	hemopexin,Peptidase_M10,SS	16.94
	448811	A1590371	Hs.174759	ESTs	TM	11.08
26	409757	NM_001898	Hs.123114	cystatin SN	cystatin,SS	10.38
25	421110	AJ250717	Hs.1355	cathepsin E	asp.SS	9.11
	428368	BE440042	Hs.83326	matrix metallop	hemopexin,Peptidase_M10,SS	8.66
	406687	M31126	Hs.272620	pregnancy speci	hemopexin,TM,	7.11
	428651	AF196478	Hs.188401	annexin A10	annexin,TM,	6.86
30	425211	M18667	Hs. 1867	progastricsin (	asp,TM,SS	6.51
30	423673	BE003054	Hs.1695	matrix metallop	hemopexin,Peptidase_M10,SS	6.49
	409683 428664	U33317 AK001666	Hs.711	defensin, alpha	defensins,Defensin_propep,SS	6.39
	408380	AF 123050	Hs.189095 Hs.44532	similar to SALL diubiquitin	zf-C2H2,TM,SS	6.25
	428953	AA306610	Hs.194676	OKFZP434C013 pr	ubiquitin,7tm_3,ANF_receptor,sushi,7tm_1,TM, arf,TNFR_c6,DEAD,Stathmin,TM,SS	5.72
35	450685	L15533	Hs.423	pancreatitis-as	lectin_c,TM,SS	5.46 5.40
~~	409187	AF154830	Hs.50966	carbamoyl-phosp	GATase,CPSase_L_chain,CPSase_sm_chain,MGS,TM,	5.34
	434206	AW136973	Hs.288516	ESTs, Weakly si	PH,TM,	5.16
	421346	Z34277	Hs.103707	apomucin	Cys_knot.vwd.	5.14
	427585	D31152	Hs.179729	collagen, type	C1q,Collagen,TM,SS	5.06
40	425679	X05997	Hs.159177	lipase, gastric	abhydrolase, SS	4.94
	421582	AI910275	Hs.1406	trefoil factor	trefoil,trypsin,TM,SS	4.93
	422956	BE545072	Hs.122579	hypothetical pr	TM	4.89
	448105	AW591433	Hs.170675	ESTs, Wealdy si	trypsin,TM,	4.84
45	413385	M34455	Hs.840	Indoleamine-pyr	IDO,TM,	4.72
45	417866	AW067903	Hs.82772	collagen, type	TSPN,Collagen,COLFI,SS	4.68
	419278	AU076799	Hs.1247	apolipoprotein	Apolipoprotein, SS	4.48
	407811	AW190902	Hs.40098	cysteine knot s	SS	4.47
	403422				SS	4.38
50	403776 418478	1120046			IL8,TM,SS	4.32
50	428242	U38945 H55709	Hs.1174	cyclin-dependen	ank, TM, SS	4.32
	421341	AJ243212	Hs.2250 Hs.279611	leukemia inhibi	UF_OSM.SS	4.30
	428434	AW363590	Hs.65551	deleted in mail	SS	4.30
	409420	215008	Hs.54451	ESTs, Weakly si taminin, gamma	SS laminin_EGF.laminin_B.SS	4.13 4.04
55	431611	U58766	Hs.264428	tissue specific	Epimerase, TM, SS	4.04
	413719	BE439580	Hs.75498	small inducible	ILB.SS	4.03
	409956	AW103364	Hs.727	inhibin, beta A	TGF-beta,TGFb_propeptide,SS	4.01
	422420	U03398	Hs.1524	turnor necrosis	TNF,TM,	4.00
	428227	AA321649	Hs.2248	small inducible	ILB,TM,SS	3.91
60	422168	AA586894	Hs.112408	S100 catcium-bi	efhand,TM,	3.87
	412140	AA219691	Hs.73625	RAB6 interaction	kinesin,TM,SS	3.82
	414812	X72755	Hs.77367	monokine induce	ILB,SS	3.81
	419833	AA251131	Hs.220697	ESTs	WHEP-TRS,TM,	3.81
65	445232	AJ281848	Hs.165547	ESTs	7tm_3,TM,	3.74
UJ	432398	AA307808	Hs.2979	trefoil factor	trefoil,TM,SS	3.70
	432867 424046	AW016936 AF027856	Hs.233364	ESTs	GSHPx,TM,SS	3.66
	414918	AI219207	Hs.138202 Hs.72222	serine (or cyst	serpin,TM,	3.65
	454293	H49739	Hs.134013	Homo sapiens cD	TM	3.61
70	442577	AA292998	Hs.163900	ESTs, Moderatel ESTs	TM TM	3.59
	426174	AA547959	Hs.115838	ESTs	SS	3.57
	418869	AW516565	Hs.258279	ESTs	Sema,TM,	3.53 3.48
	418054	NM_002318	Hs.83354	lysyl oxidase-l	Lysyl_oxidase.SRCR.SS	3.45
	442295	AJ827248	Hs.224398		Collagen, COLFI, vwc, TM, SS	3.44
75	425921	NM_007231	Hs.162211	solute carrier	SNF,TM,	3.44
	421948	L42583	Hs.111758		filament, TM,	3.43
	444783	AK001468	Hs.62180	anillin (Drosop	PH,TML	3.39
	437527	AJ241019	Hs.145644	ESTs	PIPSKTM,SS	3.37
0.0	433084	M18079	Hs.282265		fipocalin,SS	3.37
80	452401	NM_007115	Hs.29352	turnor necrosis	Xlink, CUB, TM, SS	3.36
	458897	U85642	Hs.138506		TM	3.33
	413808	J00287	Hs.182183		esp,TM,SS	3.33
	411274	NM_002776	Hs.69423	kalikrein 10	trypsin,TM,	3.32

	418406	X73501	Hs.84905	cytokeratin 20	filament,TM,	3.32
	419559	Y07828	Hs.91096	ring finger pro	zf-C3HC4,zf-B_box,TM,	3.32
	423217	NM_000094	Hs.1640	collagen, type	fn3,Collagen,Kunitz_BPTL,vwa,SS	3.31
5	411558	AA102670	Hs.70725	gamma-aminobuty	neur_chan,TM,SS	3.30
,	427722 422310	AK000123 AA316622	Hs.180479 Hs.98370	hypothetical pr	PHSS	3.30
	411263	BE297802	Hs.69380	cytochrome P\$40 kinesin-like 6	p450,SS	3.30
	443426	AF098158	Hs.9329	chromosome 20 o	kinesin,TM, TM	3.29 3.28
	452121	NM_004081	Hs.70936	deleted in azoo	TM	3.27
10	447342	Al199268	Hs.19322	ESTs	TM,SS	3.25
	452699	AW295390	Hs.213062	ESTs	TM	3.23
	425188	AK002052	Hs.155071	hypothetical pr	TM	3.23
	400289	X07820	Hs.2258	matrix metallop	hemopexin, SS	3.21
1.5	408524	D87942	Hs.46328	fucosyltransfer	Glyco_transf_11,TM,SS	3.20
15	437897	AA770561	Hs.145170	hypothetical pr	TM	3.20
	453922	AF053306	Hs.36708	budding uninhib	TM	3.19
	406690	M29540	Hs.220529	carcinoembryoni	ig.TM,SS	3.19
	416209 408113	AA236776	Hs.79078	MAD2 (mitotic a	HORMA,SS	3.16
20	425465	T82427 L18964	Hs.194101 Hs.1904	Homo sapiens cD	7tm_3,TM.	3.14
20	419216	AU076718	Hs.164021	protein kinase small inducible	Ski_Sno,DAG_PE-bind,OPR.pkise,phise_C,TM,SS	3.13
	418203	X54942	Hs.83758	CDC28 protein k	ILB,TM,SS CKS,TM,	3.13 3.12
	417315	AI080042	Hs.180450	ribosomal prote	TMSS	3.12
	433001	AF217513	Hs.279905	clone HQ0310 PR	TMSS	3.11
25	459587	AA031956		gb:zk15e04.s1 S	UNETM	3.11
	421379	Y15221	Hs.103982	small inducible	ILB,TM,SS	3.10
	414774	X02419	Hs.77274	plasminogen act	kringte, trypsin, SS	3.10
	407289	AA135159	Hs.203349	Homo saplens cD	TM	3.09
20	447519	U46258	Hs.23448	ESTs	histone,Ribosomal_L22e,TM,	3.08
30	448045	AJ297438	Hs.20166	prostate stem c	TM,SS	3.07
	431956	AK002032	Hs.272245	Homo sapiens cD	RASS	3.06
	409632 454034	W74001 NM_000691	Hs.55279 Hs.575	serine (or cyst	serpin,TM,	3.05
	436481	AA379597	Hs.5199	aldehyde dehydr HSPC150 protein	aldedh,TM,	3.05
35	428987	NM_004751	Hs.194710	glucosaminyl (N	UQ_con,TM, Branch,TM,SS	3.05 3.04
	424252	AK000520	Hs.143811	hypothetical pr	casein_kappa,SS	3.04
	436291	BE568452	Hs.5101	protein regulat	TM	3.03
	411789	AF245505	Hs.72157	Homo sapiens ad	ig,LRRCT,SS	3.02
40	417956	AA210704	Hs.190465	ESTs	sushi,SS	3.02
40	408908	BE296227	Hs.48915	serine/threonin	pkise,TM,SS	3.01
	422330	D30783	Hs.115263	epiregulin	EGF,TM,SS	3.01
	425071	NM_013989	Hs.154424	deiodinase, iod	T4_deiodise,TM,SS	3.00
	425761	AW664214	Hs. 196729	ESTs	SH3,TM,	2.99
45	432978	AF126743	Hs.279884	DNAJ domain-con	DJ,TM,	2.99
70	418546 425371	AA224827 D49441	Un 155001	gb:nc32g04.s1 N	vwa.integrin_A.FG-GAP,TM,SS	2.99
	422440	NM_004812	Hs.155981 Hs.116724	mesothelin aldo-keto reduc	TM,SS	299
	439453	BE264974	Hs.6566	thyroid hormone	aldo_ket_red,TM, AAA_TM,	2.98 2.98
	413278	BE563085	Hs.833	interferon-stim	ubiquitin,TM,	2.90
50	428450	NM_014791	Hs.184339	KIAA0175 gene p	pkise,KA1,TM,	2.95
	424345	AK001380	Hs.145479	Homo sapiens cD	TM,SS	2.95
	433133	AB027249	Hs.104741	PD2-binding kin	pkise,TM,	294
	432269	NM_002447	Hs.2942	macrophage stim	pkise,Sema,Plexin_repeat,TIG,TM,SS	294
55	432917	NM_014125		PRO0327 protein	TM	2.94
55	432731	R31178	Hs.287820	fibronectin 1	SS	2.93
	420552	AK000492	Hs.98806	hypothetical pr	SS	2.92
	428303	AW974476	Hs.183601	regulator of G-	RGS,TM,	2.92
	409687	T51125	Hs.8493	ESTs	ELS, SAM_PNT, TM,	291
60	457288 456181	AA521458 L36463	Hs.192738 Hs.1030	ESTs ras inhibitor	TM PA VBCD TM CC	2.89
00	450190	T51387	H3. 1030	gb:yb20e08.r1 S	ra.vps9.tm.ss sh3.tm.	2.89
	430204	AA618335	Hs.146137	ESTs, Weakly si	TM	2.68 2.68
	434808	AF155108	Hs.256150	ESTs, Highly si	TM	2.87
	450983	AA305384	Hs.25740	ERO1 (S. cerevi	SS	2.87
65	418670	AA601036	Hs.285083	ESTs	TM	2.87
	416661	AA634543	Hs.79440	IGF-II mRNA-bin	KH-domain,TM,	2.87
	435099	AC004770	Hs.4756	flap structure-	XPG_I,XPG_N,TM,	2.86
	402075				serpin,TM,	2.84
70	410681	AW246890	Hs.65425	calbindin 1, (2	efhand,FHA,BRCT,adh_short,adh_short_C2,TM,	2.83
70	439867	AA847510	Hs.161292		TM	2.83
	443715	AI583187	Hs.9700	cyclin E1	cyclin,TM,SS	2.83
	417366 422283	BE185289	Hs.1076	small proline-r	Cornifin,TM,	2.83
		AW411307	Hs.114311	CDC45 (cell div	CDC45,TM,SS	2.82
75	404567 422158	L10343	He 117741	aminaca inhihi	HECT,zf-UBR1,TM,	2.82
. 5	449224	AW995911	Hs.112341 Hs.299883	protease inhibi	wap,SS	2.82
	407584	W25945	Hs.18745	hypothetical pr ESTs	fn3,TM,	2.81
	453884	AA355925	Hs.36232	KIAA0186 gene p	PKSS TM	281
	449032	AA045573	Hs.22900	nuclear factor	bZIP,Chromo_shadow,TM,SS	2.81 2.80
80	422809	AK001379	Hs.121028		IQ,TM,	2.79
	449722	BE280074	Hs.23960	cyclin B1	cyclin,TM,	2.79
	453028	AB006532	Hs.31442	RecQ protein-ti	DEAD,helicase_C,TM,	2.78
	421777	BE562088	Hs.108196		TM	2.78



	452571	W31518	No 24555	CCT		
	422875	BE018517	Hs.34665 Hs.119140	ESTs eukaryotic tran	TM elf-5a.TM.	277
	400298	AA032279	Hs.61635	six transmembra	TM	2.77 2.76
_	414569	AF109298	Hs.118258	prostate cancer	TM	2.76
5	449378	AW664026	Hs.59892	ESTs	TM	2.75
	423903	M57765	Hs.1721	interleukin 11	TM,SS	2.75
	431104	AW970859	Hs.269109	ESTs .	Sema,TM,SS	2.75
	452940	AA029722	Hs.20279	ESTs	7tm_1,TM,SS	2.74
10	432201 414617	AI538613	Hs.135657 Hs.20524	ESTs	trypsin,TM,	2.73
10	444301	AI339520 AK000136	Hs.10760	ESTs, Moderatel	hexokise,TM,	2.73
	426711	AA383471	Hs.180669	hypothetical pr conserved gene	LRR, TM, TM	2.72
	429432	AI678059	Hs.202676	synaptonemal co	TM	2.71 2.71
	450506	NM_004450	Hs.418	fibroblast acti	Peplidase_S9,DPPIV_N_term,SS	2.71
15	427528	AU077143	Hs.179565	minichromosoma	MCMTMSS	2.71
	418801	AA228366	Hs.115122	ESTs	integrin_A,FG-GAP,TM,SS	2.71
	429486	AF155827	Hs.203963	hypothetical pr	SNF2_N,helicase_C,TM,	2.71
	408366	AW511255	Hs.258082	ESTs	SS	2.70
20	406399 446269	AW263155	Hs.14559	hunathariani an	kazal,TM,SS	2.69
20	426514	BE616633	Hs.301122	hypothetical pr bone morphogene	TM	2.68
	417079	U65590	Hs.81134	interleukin 1 r	TGF-beta,TGFb_propeptide,TM,SS IL1.SS	2.67 2.67
	444754	T83911	Hs.11881	transmembrane 4	TM,SS	2.67
25	424687	J05070	Hs.151738	matrix metallop	fn2,hemopexin,Pep5dase_M10,SS	2.66
25	439979	AW600291	Hs.6823	hypothetical pr	TM	2.65
	430832	AI073913	Hs.100686	ESTs, Weakly si	TM,SS	2.65
	429170	NM_001394	Hs.2359	dual specificit	DSPc,Rhodanese,TM,	2.64
	450400 435380	AI694722 AA679001	Hs.279744	ESTs	TM	2.64
30	432375	BE536069	Hs.192221 Hs.2962	ESTs S100 catclum-bi	Occludin, TM, SS	2.64
	453700	AB009426	Hs.560	apolipoprotein	S_100,efhand,TM,SS dCMP_cyt_deam,sugar_tr,TM,SS	263 263
	422938	NM_001809	Hs.1594	centromere prot	histone, TM,	263
	453134	AA032211	Hs.118493	ESTs	adh_short,TM,SS	2.63
25	420727	H75701	Hs.99886	complement comp	şushi,	2.62
35	408868	AW292286	Hs.255058	ESTs	TM	2.62
	414972	BE263782	Hs.77695	KIAA0008 gene p	TM	2.62
	403055 447400	AK000322	Hs.18457	August and and	filament, TM, SS	2.62
	413753	U17760	Hs.301103	hypothetical pr Human DNA seque	zf-C3HC4,TM, laminin_EGF,laminin_Nterm,SS	2.61
40	433220	AI076192	Hs.131933	ESTs	TM	2.61 2.60
	436251	BE515065	Hs.5092	nucleolar prote	Nop,TM,SS	2.60
	448988	Y09763	Hs.22785	gamma-aminobuty	neur_chan,TM,SS	2.60
	425463	AK000740	Hs.157986	hypothetical pr	TM	2.60
45	435370	A1964074	Hs.225838	ESTs	EGF,fn3,fibrinogen_C,TM,SS	2.59
45	432215	AU076609	Hs.2934	ribonucleatide	ribonucleo_red,ribonuc_red_lg,TM,	2.59
	409142 443919	AL136877 AI091284	Hs.50758	chromosome-asso	SMC_N,TM,SS	2.59
	413268	AL039079	Hs.135224 · Hs.75256		adh_short,TM,SS	2.58
	404519	11000010	115.7 3230	regulator of G-	RGS,TM, defensins,SS	2.58
50	414998	NM_002543	Hs.77729	oxidised low de	TM	2.58 2.57
	429597	NM_003816	Hs.2442	a disintegrin a	TM,SS	2.57
	426841	AI052358	Hs.193726	ESTs	asp,TM,SS	2.57
	416768	AA363733	Hs.1032	regenerating is	lectin_c,SS	2.57
55	417933	X02308	Hs.82962	thymidylate syn	thymidylat_synt.SS	2.56
"	441384 451939	AA447849 U80456	Hs.288660	protease, serin	TM	2.56
	418867	D31771	Hs.27311 Hs.89404	single-minded (	PAC,PAS,BPL,BPL_C,TM,	2.56
	416065	BE267931	Hs.78996	msh (Drosophila proliferating c	homeobox,TM, TM	2.55 2.55
	431890	X17033	Hs.271986	integrin, alpha	wa,integrin_A.F.G.GAP,TM,SS	2.55 2.55
60	407830	NM_001086	Hs.587	arytacetamide d	COesterase,7tm_1,TM,SS	2.55
	434815	AF155582	Hs.46744	core1 UDP-galac	SS	2.54
	435647	AI653240	Hs.49823	ESTs	TM	2.54
	459306	AW578452	Hs.232988	ESTs, Weakly si	TM,SS	2.54
65	414361 425782	AI086138 U66468	Hs.204044	ESTs	TM	2.54
05	416984	H38765	Hs.159525 Hs.80706	cell growth reg	SS TM	2.53
	431183	NM_006855	Hs.250696	diaphorase (NAD KDEL (Lys-Asp-G		2.53
	456743	AI630124	Hs.7434	ESTs	ER_turnen_recept, iRK, DEAD, helicase_C, TM, SS TM	2.53 2.53
70	410268	AA316181	Hs.61635	six transmembra	TM	2.52
70	424905	NM_002497	Hs.153704	NIMA (never in	pkise,TM,	2.52
	432657	AA831815	Hs.270940	ESTs	TM	2.51
	434080	AJ820719	Hs. 154662	hypothetical pr	DU_CXXCXGXG,TM,SS	2.51
	418969 431808	W33191 M30703	Hs.28907	hypothetical pr	SH3.TM,	251
75	429093	NM_000253	Hs.270833 Hs.195799	amphiregulin (s microsomal trig	EGF,TM,SS	2.51
-	447634	AW967902	Hs.5152	Homo sapiens cD	Vitellogenin_N,TM,SS TM	2.50
	436393	AW022213	Hs.143617	ESTs	Galactosyl_T_2,TM,SS	2.50 2.50
	453751	R36762	Hs.101282	Homo sapiens mR	TM	2.49
00	445865	AI262584	Hs.145575	ESTs	SS	2.49
80	414883	AA926960	Hs.77550	CDC28 protein k	CKS,TM,	2.49
	406747 446921	AI925153	Hs.217493		TM	2.49
	426322	AB012113 J05068	Hs.16530	small inducible	ILB,SS Condomin No.4 TA SS	2.49
	720022	***************************************	Hs.2012	transcobalamin	Cobalamin_bind,TM,SS	2.48

	422515	AW500470	Hs.117950	multifunctional	AIRC.SAICAR_SYNLTM.	2.48
	447030 448454	AW444559 NM_005879	Hs.232184	ESTs	TM	2.48
	419092	J05581	Hs.21254 Hs.89603	TRAF Interactin	zi-c3HCA,TM,	2.48
5	409640	U78722	Hs.55481	mucin 1, transm zinc finger pro	SEA,TM,SS	2.48
-	404171	O. O. E.	113.30-101	zac mya po	zi-C2H2,SCAN,TM, sodie,TM,	2.48
	414747	U30872	Hs.77204	centromere prot	SS S	2.47 2.47
	410406	AI969703	Hs.301842	EST8	FGGY.TM.	247
• •	452220	BE158006	Hs.212296	ESTs	FG-GAP,TM,SS	246
10	421493	BE300341	Hs.104925	ectodermal-neur	BTB,Kelch,TM,	2.46
	444838	AV651680	Hs.208558	ESTs	integrin_A.FG-GAP,TM,SS	2.46
	413816	AW958181	Hs.189998	ESTa	AMP-binding,G_glu_transpept,TM,	2.46
	436613 432874	AA972691	Hs. 192974	Homo sapiens cD	TM,SS	2.45
15	425397	W94322 J04088	Hs.279651 Hs.156346	metanoma inhibi	SHO,SS	2.45
1.5	422353	T55979	Hs.115474	topoisomerase ( replication fac	HATPæe_c,SS	2.45
	431924	AK000850	Hs.272203	Homo sapiens cD	TM SH3.TML	2.45 2.44
	431457	NM_012211	Hs.256297	integrin, atpha	FG-GAP,vwa,TM,SS	244
	416498	U33632	Hs.79351	potassium chann	TM	244
20	428484	AF104032	Hs.184601	solute carrier	aa_permeases,TM,	243
	431958	X63629	Hs.2877	cadherin 3, typ	cadherin,Cadherin_C_term,TM.SS	2.43
	413833	Z15005	Hs.75573	centromere prot	kinesin, TM,	2.43
	407243 410044	AA058357	Hs.74466	carcinoembryoni	TMSS	2.43
25	424273	BE566742 W40460	Hs.58169	highly expresse	TMSS	243
	409533	AW969543	Hs.144442 Hs.21291	phospholipase A	phostip,TM,SS	2.42
	419741	NM_007019	Hs.93002	mitogen-activat ubiquitin carri	TM,SS UQ_con,efhand,TM,SS	2.42
	449987	AW079749	Hs. 184719	ESTs, Weakly si	ABC_tran_ABC_membrane,TM,	2.42 2.42
	433159	AB035898	Hs.150587	kinesin-like pr	kinesin, Myosin_tail, TM, SS	2.42
30	439396	8E562958	Hs.74346	ESTs, Weakly si	SS	2.42
	426427	M86699	Hs.169840	TTK protein kin	pkise,TM,	2.41
	434725	AK000796	Hs.4104	hypothetical pr	TM	2.41
	433312	AI241331	Hs.131765	ESTS	zi-CZH2,SS	2.41
35	407047 419220	X65965	N- 201750	gb:H.sapiens SO	sodfe,TM,	2.41
33	416530	AA811938 U62801	Hs.291759 Hs.79361	ESTs	TM,SS	2.40
	435219	AA676349	Hs.190331	kallikrein 6 (n ESTs	trypsin,pro_isomerase,TM,SS	2.40
	418322	AA284166	Hs.84113	cyclin-dependen	TM SS	2.40 2.40
	404253			ojust ocpanion.	histone,TM,SS	2.40
40	428970	BE276891	Hs.194691	retinoic acid i	7m_3,TM,	2.40
	418693	AI750878	Hs.87409	thrombospondin	EGF.TSPN,tsp_1,tsp_3,vwc,SS	2.39
	451237	AW600293		gb:EST00049 pGE	TM	2.39
	407756	AA115021	Hs.38260	ubiquitin speci	UCH-1,UCH-2,SS	2.39
45	437935	AW939591	Hs.5940 .	hypothetical pr	TM,SS	2.39
7,7	445625 435937	BE246743 AA830893	Hs.288529	Homo sapiens cD	TM	2.39
	438993	AA828995	Hs.119769	ESTs	TM	2.39
	422082	AA016188	Hs.111244	gb:od77b08.s1 N hypothetical pr	integrin_B,TM,SS TM	2.38
	450396	AU077002	Hs.24950	regulator of G-	RGS,TM,	2.38 2.38
50	422578	AF239666	Hs.1545	caudal type hom	homeobox_SS	2.38
	428070	T63918	Hs.182313	retinal-binding	lipocalin,TM,	2.38
	416111	AA033813	Hs.79018	chromatin assem	TM,SS	2.37
	433345	AJ681545	Hs.152982	Homo sapiens cD	TM	2.37
55	427557 423554	NM_002659	Hs.179657	plasminogen act	UPAR_LY6,SS	2.37
55	453204	M90516 R10799	Hs.1674 Hs.191990	glutamine-fruct	GATase_2,SIS,TM,SS	2.37
	425081	X74794	Hs.154443	ESTs minichromosome	TM	2.37
	434682	AA827165	Hs.191958	ESTs	MCM,TM, TM	2.36
	414108	AJ267592	Hs.75761	SFRS protein ki	pkise,TM,	2.36 2.36
60	417900	BE250127	Hs.82906	CDC20 (cell div	WD40.TM.	2.36
	428046	AW812795	Hs.155381	ESTs, Moderatel	ank,SS	2.36
	448019	AW947164	Hs.195641	ESTs	TM	2.36
	431753	X76029	Hs.2841	neuromedin U	NMU,TM,SS	2.36
65	410361 418526	BE391804	Hs.62661	guanylate bindi	GBP,TM,SS	2.36
03	444478	BE019020 W07318	Hs.85838 Hs.240	solute carrier	MCT,TM,SS	2.36
	436961	AW375974	Hs.156704	M-phase phospho ESTs	kinesin,SS	2.36
	408194	AA601038	Hs.191797	ESTs	TM TM	2.35
	438578	AA811244	Hs.164168	ESTs	formyl_transf,AIRS,GARS,TM,	2.35 2.35
70	429183	AB014604	Hs.197955	KIAA0704 protei	TM	2.35
	453900	AW003582	Hs.226414		TM	2.33
	432877	AW974111	Hs.292477	ESTs	EIS,SAM_PNT,TM,	2.33
	451928	AJ823801	Hs.30315	ESTs	TM	2.33
75	418245	AA088767	Hs.83883	transmembrane,	Id]_recept_e,TM,SS	2.33
, ,	435106 432193	AA100847 AA372264	Hs. 193380		TM	2.33
	449532	W74653	Hs.273193 Hs.271593		TM,SS	2.33
	409703	NM_006187	Hs.56009	ESTs 2-5oligoadeny	TM NTD brood 2 TM CC	2.33
	419373	NM_003244		TG-interacting	NTP_transf_2,TM,SS harneobox,SS	233
80	435607	W73428	Hs.8750	uncharacterized	SS SS	2.32 2.32
	405818				TM,SS	2.32
	444371	BE540274	Hs.239	forkhead box M1	Fork_head,SS	2.32
	432675	A1791855	Hs.105884	ESTs	PDEase,TM,	2.32

	411773	NM_006799	Hs.72026	protease, serin	trypsin,SS	2.31
	434775	AA648983	Hs.212911	ESTs	TM,SS	2.31
	422611 419493	AA158177 AF001212	Hs.118722 Hs.90744	tucosyltransfer	SS	231
5	424435	AB011167	Hs.146957	proteasome (pro KIAA0595 protei	SS .	2.31
•	409262	AK000631	Hs.52256	hypothetical pr	TM WD40.TM.SS	2.30 2.30
	428125	AA393071	Hs.182579	leucine aminope	Peptidase_M17,TM,SS	2.30
	417655	AA780791	Hs.14014	ESTs, Wealty si	TM	2.29
	407287	AI678812	Hs.201658	ESTs, Wealdy si	ras,TM,SS	2.29
10	428923	BE047698	Hs.188785	ESTS	TMLSS	2.29
	452203	X57522	Hs.158164	ATP-binding cas	ABC_tran,ABC_membrane,TM,	2.29
	409402		Hs.695	cystatin B (sta	cystatin,SS	2.29
	419359	AL043202	Hs.90073	chromosome segr	TMSS	2.29
15	451999 400811	AW176401	Hs.27424	DEAD/H (Asp-Glu	TMSS	2.29
13	420931	AF219139 AF044197	Hs.87726 Hs.100431	KIAA0154 protei	Cobalamin_bind,SS	2.29
	425247	NM_005940	Hs.155324	smali inducible matrix metallop	ILB,TM,SS hemopexin,Peptidase_M10,TM,SS	2.28
	438170	AI916685	Hs.194601	ESTs	2-Hacid OH.TM.	2.28 2.28
	445378	AV653564	Hs.226946	ESTs	TM	2.28
20	428048	AA705745	Hs.185070	ESTs .	AMP-binding, TM,	2.28
	414696	AF002020	Hs.76918	Niemann-Pick di	Patched,TM,SS	2.27
	433535	AF111106	Hs.3382	protein phospha	TM	2.27
	421155	H87879	Hs.102267	lysyl oxidase	Lysyl_oxidase,SS	2.27
25	405545	A 1015674			ABC_tran,ABC_membrane,TM,SS	2.27
23	445537 423634	AJ245671	Hs.12844	EGF-like-domain	EGF,SS	2.27
	407742	AW959908 AF186252	Hs.1690 Hs.38084	heparin-binding sulfotransferas	TMSS	2.26
	428330	L22524	Hs.2256	matrix metallop	Sulfatransfer, SS	2.26
	429731	AK001592	Hs.212172	beta,beta-carot	Paptidase_M10,SS TM	2.26 2.26
30	400514			ocationa on o	p450,TM,SS	2.26
	431846	BE019924	Hs.271580	uroplatin 18	transmembrane4,TM,SS	2.26
	425010	AA136563	Hs.1975	Homo sapiens cD	TM	2.26
	437641	AA811452	Hs.291911	ESTs	TM	2.26
35	411393	AW797437	Hs.69771	B-factor, prope	sushi,trypsin,vwa,DEAD,rm,EGF,fn3,fibrinogen_C,SS	2.26
22	414809	A1434599	Hs.77356	transferrin rec	PA,Ribosomat_S2,TM,	2.25
	419488 434540	AA316241	Hs.90691 Hs.5184	nucleophosmin/n	SS	2.25
	410196	NM_016045 AI936442	Hs.59838	TH1 drosophila	TM UBACT_repeat.TM.	2.25
	456844	AI264155	Hs.152981	hypothetical pr CDP-diacytgtyce	Cytidylytrans.TM.	2.25 2.25
40	408353	BE439838	Hs.44298	hypothetical pr	Ribosomal_S17,TM,	2.25
	448753	AL048858	Hs.224355	ESTs, Weakly si	TM	2.25
	428479	Y00272	Hs. 184572	cell division c	pkise,TM,SS	2.24
	424971	AA479005	Hs.154036	tumor suppressi	ion_trans,PH,TM,	2.24
45	432673	AB028859	Hs.278605	ER-associated D	DJ,DJ_C,TM,SS	2.24
45	409432	D49372	Hs.54460	small inducible	il8,TM,SS	2.24
	429925	NM_000786	Hs.226213	cytochrome P450	p450,TM,SS	2.24
	445413 447532	AA151342 AK000614	Hs.12677	CGI-147 protein	UPF0099,TM,SS	2.23
	423515	AA327017	Hs.18791 Hs.162204	hypothetical pr ESTs	TM SS	2.23 2.23
50	444743	AA045648	Hs.11817	nudix (nucleosi	mutī,TM,	2.23
	434518	H56995	Hs.37372	Homo sapiens DN	TM	2.23
	435602	AF217515	Hs.283532	uncharacterized	TM.SS	2.23
	449974	AW970948	Hs.269403	ESTs	TM,SS	2.23
55	424927	AW973668	Hs.153850	hypothetical pr	TM	2.23
23	414420	AA043424	Hs.76095	immediate early	TM	2.23
	431840 452930	AA534908	Hs.2860	POU domain, cla	homeobox,pou,TM,SS	2.23
	436391	AW195285 AJ227892	Hs.194097 Hs.146274	ESTs ESTs	SS SS	2.23
	439186	AI697274	Hs.6487	Xq28, 2000bp se	Epimerese,SS	2.23 2.23
60	414732	AW410976	Hs.77152	minichromosome	MCM,TM,	2.23
	411835	U29343	Hs.72550	hyaturonan-medi	TM	2.22
	438223	AA781171		gb:aj24d05.s1 S	myosin_head,TM,	2.22
	450149	AW969781	Hs.293440	ESTs, Moderatel	TM	2.22
65	401519				filament, TM,	2.22
0.5	441794	AW197794	Hs.253338	ESTs	ank,TM,	2.22
	408901	AK001330	Hs.48855	hypothetical pr	TM	2.21
	434423 432140	NM_006769 AK000404	Hs.3844	LIM domain only	LIM,TM,	2.21
	423453	AW450737	Hs.272688 Hs.128791	hypothetical pr CGI-09 protein	SS Carrie COR OM B. target TM	2.21
70	428438	NM_001955		endothelin 1	Granin,CDP-OH_P_transf,TM, endothelin,TM,SS	2.21 2.21
	421470	R27496	Hs.1378	annexin A3	annexin.TM.SS	2.21
	440381	AA917808	Hs.190495		TMSS	2.20
	453779	N35187	Hs.43388	ESTs	TM,SS	2.20
75	433627	AF078866	Hs.284296		SURF4,TM,	2.20
75	417944	AU077196	Hs.82985	collagen, type	COLFI, Collagen, vwc, TM, SS	2.20
	422689	AW856665		gb:RC3-CT0297-2	SNF2_N,TM.	2.20
	448457 426125	H65629 X87241	Hs.245997		TM,SS	2.20
	430603	AA148164	Hs.166994 Hs.247280		EGF,cadherin,taminin_G,TM,SS	2.20
80	425274	8E281191	Hs.155462		z-C3HC4,TM, MCM,TM,	2.20
	452679	Z42387	Hs.4299	Homo sapiens cD	TM	2.20 2.20
	410619	BE512730	Hs.65114	keratin 18	filament, TM,	2.20
	424332	AA338919	Hs.101615		SS	2.20

	418661	NM_001949	Hs.1189	Human mRNA for	E2F_TDP.TM.SS	2.20
	419341	N71463	Hs.118888	ESTs. Weakly si	UPF0016,TM,SS	2.20
	427920	Z11502	Hs.181107	annexin A13	annexin, TM,	2.19
5	403208 422596	AF063611	Hs.118633	2 Callanda	lectin_c,TM,SS	2.19
•	444261	AA298958	Hs.10724	2-5 otigoadeny MDS023 protein	ubiquitin,SS	2.19
	423401	NM_001992	Hs.128087	coagulation (ac	TM	2.19 2.18
	453450	AW797627	Hs.89474	ADP-ribosytatio	7tm_1,TM,SS SS	2.18
	444334	BE296785	Hs.10848	KIAA0187 gene p	SS	218
10	437616	AI797163	Hs.207954	ESTs	SMC_N,TM,SS	2.18
	451807	W52854	Hs.27099	DKFZP564J0863 p	TM	2.18
	430441	BE398091	Hs.6880	DKFZP434D156 pr	TM	2.18
	411678	AI907114	Hs.71465	squalene epoxid	Monoaxygese,TM,	2.18
1.6	452291	AF015592	Hs.28853	CDC7 (cell divi	pkise,TM,	2.18
15	444342	NM_014398	Hs.10887	similar to tyso	Lamp, TM, SS	2.18
	451099	R52795	Hs.25954	Interleukin 13	fn3,TM,SS	2.18
	425873	NM_013390	Hs.160417	transmembrane p	TM	2.17
	417404	NM_007350	Hs.82101	pleckstrin homo	TM	2.17
20	446995	AI355012		gb:qu16d10.x1 N	TM	217
20	439961 429125	AA857451 AA446854	Hs.269696 Hs.271004	ESTs	TM	217
	407103	AA424881	Hs.256301	ESTs ESTs	TM TM	217
	415116	AA160363	Hs.269956	ESTs	ER_lumen_recept,TM,SS	217
	440052	AI633744	Hs.195648	ESTs	PAC,TM,SS	2.17 2.17
25	423961	D13666	Hs.136348	osteoblast spec	Fascidin, TM, SS	2.17
	431070	AW408164	Hs.249184	transcription f	FHA.SS	2.16
	443599	AI079559	Hs.134125	ESTs	TM	2.16
	427258	AA400091	Hs.39421	ESTs	TM	216
20	418113	AJ272141	Hs.83484	SRY (sex determ	HMG_bax,TM,	2.16
30	450835	BE262773	Hs.25584	hypothetical pr	ArfGap,SS	2.18
	449057	AB037784	Hs.22941	KIAA 1363 protei	TM	2.16
	448153	Y10805	Hs.20521	HMT1 (hnRNP met	TM,SS	2.16
	424653	AW977534	Hs.151469	calcium/calmodu	Guanylate_kin,PDZ.pkise,SH3.TM,	2.16
35	431341	AA307211	Hs.251531	proteasome (pro	proteasome,TM,	216
55	452865 432789	A1924046 D26361	Hs.119567	ESTS	PMP22_Claudin,TM,SS	2.16
	438580	AA811262	Hs.3104 Hs.299202	KIAA0042 gene p ESTs	TM	2.16
	422192	AA305159	Hs.113019	fis485	pkise,TM, SS	216
	425607	U09860	Hs.158333	protease, serin	kil_recept_a,trypsin,CUB,SRCR,MAM,SEA,TM,SS	2.15 2.15
40	447289	AW247017	Hs.36978	melanoma antige	3Beta_HSD,Epimerase,MAGE,TM,	2.15
	447674	BE270640	Hs.19192	cyclin-dependen	pkise,TM,	2.15
	441021	AW578716	Hs.7644	H1 histone fami	linker_histone, TM,	2.15
	426471	M22440	Hs.170009	transforming gr	EGF.TM,SS	2.15
45	431941	AK000106	Hs.272227	Homo sapiens cD	pkise, Furin-like, TM, SS	2.15
45	414761	AU077228	Hs.77256	enhancer of zes	SET,TM,	2.15
	410407	X66839	Hs.63287	carbonic anhydr	carb_anhydrase,TM,SS	2.15
	420900	AL045633	Hs.44269	ESTs	Ald_Xan_dh_C,FAD_binding_5,TM,	2.15
	419239	AA468183	Hs.184598	Homo sapiens cD	TM	215
50	452721 410664	AJ269529	Hs.30377	Horno sapiens ES	TM	2.15
50	452835	NM_006033 AK001269	Hs.65370	fipase, endothe	Ribosomal_L22,fipase,PLAT,TM,SS	2.14
	452092	BE245374	Hs.30738 Hs.27842	hypothetical pr	TM	2.14
	401708	044444	FIS.27042	hypothetical pr	Acyltransferase, TM, SS SS	2.14
	411400	AA311919	Hs.69851	GAR1 protein	TM	2.14 2.14
55	448526	AB028946	Hs.21361	KIAA 1023 protei	TM	2.14
	421175	AI879099	Hs.102397	GIOT-3 for gona	zi-C2H2,KRAB,TM,SS	214
	413511	AI627178	Hs.75412	Arginine-rich p	TM	2.13
	432945	AL043683	Hs.271357	ESTs, Wealdy si	PK,SS	2.13
40	418592	X99226	Hs.284153	Fanconi anemia,	TM	2.13
60	425298	AK000209	Hs.155556	hypothetical pr	TM	2.13
	450956	AW193531	Hs.205647	ESTs, Moderatel	pkise,TM,SS	2.13
	419569	AI971651	Hs.91143	jagged 1 (Alagi	EGF,DSL,TM,SS	2.13
	421508	NM_004833	Hs.105115	absent in melan	TM	2.13
65	413670 422783	AB000115 AA598956	Hs.75470	hypothetical pr	TM	213
05	410418	D31382	Hs.120439 Hs.63325	ethanolamine ki	Choline_kise,TM,	2.13
	414860	BE255593	Hs.77502	transmembrane p methionine aden	trypsin,ld1_recept_a,TM,SS	2.13
	425860	L29339	Hs.1964	solute carrier	S-AdoMet_synt,SS SSF,Ribosomal_S17e,TM,	213 213
	414839	X63692	Hs.77462	DNA (cytosine-5	zi-CXXC.BAH,TM,SS	2.13
70	437050	AA766420	Hs.291606	ESTs	TM	2.13
	430217	N47863	Hs.180450	ribosomal prote	TM,SS	2.13
	409012	AL117435	Hs.49725	DKFZP4341216 pr	RhoGEF.TM,	2.12
	428365	AA295331	Hs.183861	Homo sapiens cD	TM	2.12
75	410839	NM_006849	Hs.66581	protein disulfi	thiored,TM,	2.12
75	450510	AA010056	Hs.242998	EST ₅	TM,SS	2.12
	427475	AA403151	Hs.191605		\$S	2.12
	433748	R12244		gb:yf33c12.r1 S	AMP-binding,TM,	2.12
	415138	C18356	Hs.78045	tissue factor p -	Kunitz_BPTI.G-gamma,TM,SS	2.11
80	414788 415474	X78342 NM 014353	Hs.77313	cyclin-dependen	pkise,TM,SS	2.11
-	416472	NM_014252 AA180756		Solute carrier	mito_carr,TM,	2.11
	410718	AI920783	Hs.193094 Hs.191435		TM SOC BEY THEE	211
	425811	AL039104	Hs.159557		SOS_PSY,TM,SS	2.11 2.11
				Industrial dela	Armadiilo_seg,iBB,TM,SS	4.11

	447197	R36075		gb:yh88b01.s1 S	SDF.TM.	2.11
	431621	AW292329	Hs.163481	ESTs	PH,Band_41,TM,SS	211
	433849	BE465884	Hs.280728	ESTs	SS	2.11
5	438038 422032	A1732629	Hs.194161	ESTs, Weakly si	Cytidylyltrans,TM,	2.11
_	409717	AA476966 AW452871	Hs.110857 Hs.56043	polymerase (RNA CGI-115 protein	TFIIS,TM,SS TM	211 211
	445837	AI261700	Hs.145544	ESTS	TM	2.11
	423880	BE278111	Hs.134200	DXFZP564C186 pr	TM	2.10
10	421574 437103	AJ000152	Hs.105924	defensin, beta	Defensin_beta,TM,SS	2.10
10	450747	AW139408 Al064821	Hs.152940 Hs.48306	ESTs ESTs, Highly si	Chaline_kise,TM, rrm,TM,	2.10 2.10
	437033	AW248364	Hs.5409	RNA polymerase	TM	2.10
	417640	D30857	Hs.82353	protein C recep	TM,SS	2.10
15	431120	AA492588	11-044530	gb:ng99c08.s1 N	TM,SS	2.10
13	430510 429669	AW162916 BE185499	Hs.241576 Hs.2471	hypothetical pr KIAA0020 gene p	TM TM	2.10 2.10
	407881	AW072003	Hs.40968	heparan sulfate	SS	2.10
	436415	BE265254	Hs.5181	proliferation-a	Peptidase_M24,TM,SS	2.10
20	407887	AA579668	Hs.41072	serine (or cyst	serpin,TM,	2.10
20	447815 434274	AM32199 AA628539	Hs.247084 Hs.116252	ESTs ESTs, Moderatel	LIM,TM, rm,TM,SS	2.09
	411571	AA122393	Hs.70811	hypothetical pr	SS	2.0 <del>9</del> 2.09
	442525	AF150282	Hs.145945	EST\$	pkise,TM,	2.09
25	423750	AF165883	Hs.132415	prefoldin 2	TM	2.09
23	449199 415363	AI990122 AI670947	Hs.196988 Hs.78406	ESTs	ras,TM,	2.09
	418462	8E001596	Hs.85266	phosphatidylino integrin, beta	PIP5K,pkise,TM,SS integrin_B,fn3,TM,SS	2.09 2.09
	430335	D80007	Hs.239499	KIAA0185 protei	S1.TM.	2.08
30	443450	N66045	Hs.133529	ESTs	TM	2.08
30	418753 439018	BE217818 AW300887	Hs.87016 Hs.26638	Homo sapiens cD	TM	2.08
	431628	AF146277	Hs.255561	ESTs, Weakly si CD2-associated	TM,\$\$ \$H3,\$\$	2.08 2.08
	446528	AU076640	Hs.15243	nucleolar prote	Nol1_Nop2_Sun,TM,	2.08
25	411372	A1147861	Hs.213289	low density lip	EGF,id1_recept_a,id1_recept_b,TM,SS	. 2.08
35	459319 408730	NM_000059	Hs.47144	gb:Homo saplens	BRCA2_repeat,TM,	2.08
	409220	AV660717 BE243323	Hs.51233	DKFZP586N0819 p tumor necrosis	TM,SS TNFR_c6,death,TM,	2.08 2.08
	429504	X99133	Hs.204238	fipocalin 2 (on	Spocalin, SS	2.08
40	409686	AK000002	Hs.55879	Homo sapiens mR	ABC_tran,ABC_membrane,TM,	2.08
40	413092 413715	AA126856	Hs.118665	ESTS	EGF,TM,SS	2.08
	423020	AW851121 AA383092	Hs.75497 Hs.1608	Homo sapiens cD replication pro	cyclin,TM, TM	2.08 2.07
	438378	AW970529	Hs.86434	Homo sapiens cD	TM,SS	2.07
45	432125	AW972667	Hs.287510	Homo sapiens cO	Band_41,TM,SS	2.07
45	449370	AK002114	Hs.23495	hypothetical pr	TM.SS	2.07
	454011 427876	M31008 AI494291	Hs.37009 Hs.111977	alkaline phosph ESTs	alk_phosphatase,TM,SS TM	2.07 2.07
	422901	R81936	Hs.121576	aspartate beta-	SS	207
60	449207	AL044222	Hs.23255	nucleoporin 155	TM,SS	2.07
50	408243	Y00787	Hs.624	interleukin 8	IL8,TM,SS	2.07
	446548 423472	BE 167687 AF041260	Hs.156628 Hs.129057	ESTs breast carcinom	Sulfotransfer,TM,SS TM	2.07
	436211	AK001581	Hs.80961	polymerase (DNA	TM	2.07 2.07
	456157	AW979153		gb:EST391263 MA	transmembrane4,TM,	2.06
55	407143	C14078	Hs.248968	EST	TM	2.06
	432440 410668	X63597 BE379794	Hs.2996 Hs.65403	sucrase-isomati hypothetical pr	Glyco_hydro_31,trefoil,TM,SS	2.06
	422765	AW409701	Hs.1578	bacutoviral IAP	TM BIR,TM,	2.06 2.06
<b>.</b>	439832	T81829	Hs.14870	ESTs	SS	2.06
60	445318	AW500652	Hs.200885		TM	2.06
	439951 428307	AI347067 W27393	Hs.124636 Hs.183648	ESTs	TM,SS TM	2.06
	432584	AA928829	Hs.47099	protein tyrosin Homo sapiens cD	SS	2.06 2.06
	433027	AF191018	Hs.279923	putative nucleo	MMR_HSR1,TM,	2.06
65	433716	AA608808	Hs.225118	ESTs	TM	2.06
	429412	NM_006235		POU domain, da	IM	2.06
	449026 437016	BE500948 AU076916	Hs.209105 Hs.5398	ESTs guanine monphos	TM GATase,GMP_synt_C,TM,	2.06 2.06
	442547	AA306997	Hs.268362		SS	2.06
70	455778	BE088746		gb:CM2-BT0693-2	TM	2.06
	439975	AW328081	Hs.6817	Homo sapiens pu	TM,SS	2.06
	433037 440086	NM_014158 NM_005402			TM ras,TM,	2.06
-	436414	BE264633	Hs.143838		WD40,TM,	2.06 2.05
75	411770	NM_014278	Hs.71992	heat shock prot	HSP70,TM,	2.05
	409459	D86407	Hs.54481	low density lip	EGF,kdl_recept_a,kdl_recept_b,TM,SS	2.05
	436238 400517	AK002163 AF242388	H\$.301724		MMR_HSR1,TM.	2.05
	421904	BE143533	Hs.149585 Hs.109309		TM SS	2.05 2.05
80	417850	AA215724	Hs.82741	primase, polype	SS	2.05
	417491	AW376842	Hs.1085	guanylate cycla	pkise.guanylate_cyc,ANF_receptor,TM,SS	2.05
	453775 435525	NM_002916 AI831297		replication fac	AAATMSS	2.05
	*33363	~~~1231	Hs.123310	ESTs	TM	2.05

	412627	BE391959	Hs.74276	chloride Intrac	G-patch.ig.MutS_C,TM,	2.05
	439702	AW085525	Hs.134182	ESTs	A2M,SS	2.05
	440006	AK000517	Hs.6844	hypothetical pr	TM	2.05
5	417308 446311	H60720	Hs.81892	KIAA0101 gene p	TM	2.05
	427871	AW997294 AW992405	Hs.149795	ESTs, Wealty si	pkise,TM,	2.05
	453804	AA300204	Hs.59622 Hs.35276	ESTs, Weakly si KIAA0852 protei	SS	2.05
	449939	T86420	Hs.272139	ESTs	TM,SS	2.05
	417819	AI253112	Hs.133540	ESTs	OIL,myosin_head,TM,SS TM	2.05 2.04
10	427747	AW411425	Hs.180655	serine/threonin	pkise,TM,	2.04
	415009	C75253	Hs.220950	ESTs	TM	204
	437829	AI358522	Hs.270188	ESTs	TM	2.04
	428753	AW939252	Hs. 192927	hypothetical pr	TM	2.04
1.5	445475	AI908188	Hs.209245	ESTs	OPR,TM,	2.04
15	431394	AK000692	Hs.252351	HERV-H LTR-asso	ig.TM,SS	2.04
	423701	AA329856	Hs.143022	ESTs	TM	2.04
	422369	AF005216	Hs.115541	Janus kinase 2	SH2.pkise,TM,	204
	432481	AW451645	Hs.151504	Homo sapiens cD	TSPN,Collagen,TM,SS	2.04
20	443746	AW861379	Hs.160602	ESTs	TM	2.04
20	400792	AA635062	Hs.50094	Homo seplens mR	z-C3HC4,CARD,BIR,TM	2.04
	428343 419329	AL043021 AY007220	Hs.12705	ESTs, Wealty si	TM	2.04
	403485	A100/220	Hs.288998	S100-type calci	TM	2.04
	413313	NM_002047	Hs.75280	obered sONA man	filament,TM,	2.04
25	433326	AJ379485	Hs.159430	glycyl-tRNA syn ESTs	WHEP-TRS,7tm_2,TM,SS TM	2.04
	440246	W52010	Hs.191379	ESTs	serpin,TM,	2.03
	444005	BE395085	Hs.10086	type I transmem	TM,SS	2.03 2.03
	452705	H49805	Hs.246005	ESTs	TM	203
••	421724	AB037832	Hs.107287	KIAA1411 protei	TM	2.03
30	447474	AW614220	Hs.189402	ESTs	SS	2.03
	418852	BE537037	Hs.273294	hypothetical pr	TM	2.03
	431842	NM_005764	Hs.271473	epithelial prot	TM,SS	2.03
	440773	AA352702	Hs.37747	hypothetical pr	TM	2.03
35	443425	AI056776	Hs.133397	ESTs	TM,SS	2.03
33	407975	X89426	Hs.41716	endothelial cel	IGFBP.SS	2.03
	428299	AL038004	Hs.29419	ESTs	TMSS	2.03
	415757 432559	AA830854	Hs.187810	ESTs	TM	2.03
	425912	AW452948 AL137629	Hs.257631	ESTs	PAC,TM,SS	2.03
40	419395	BE268326	Hs.162189 Hs.90280	serine/threonin 5-aminoimidazol	h3.ig.PH,RhoGEF,TM,SS	2.02
	417576	AA339449	Hs.82285	phosphoribosytg	AICARFT_IMPCHas,MGS,TM,	2.02
	418559	AA225048	Hs.104207	ESTs	AIRS,formyl_transI,GARS,TM, TM	2.02
	410855	X97795	Hs.66718	RAD54 (S.cerevi	SNF2_N,helicase_C,TM,	2.02
	422072	AB018255	Hs.111138	KIAA0712 gene p	TM	2.02 2.02
45	419546	AA244199		gb:nc06c05.s1 N	Y_phosphatase,TM,	2.02
	450516	AA902656	Hs.21943	NIF3 (Ngg1 inte	DUF34,TM	2.02
	419807	R77402		gb:yi75/11.s1 S	TM	2.02
	438192	A1859065	Hs.16808	ESTs, Weakly si	TM,SS	2.02
50	401866			•	filament, TM, SS	2.02
50	443129	R16075	Hs.21668	ESTs	TM,SS	2.02
	424783	AA913909	Hs.153088	TATA box bindin	TM	2.01
	413293	AL047483	Hs.75270	GTP-binding pro	ras,TM,SS	2.01
	435787 422599	AW162767	Hs. 100914	hypothetical pr	SS	2.01
55	431630	BE387202 NM_002204	Hs.118638 Hs.265829	non-metastatic	NDK,SS	2.01
55	448275	BE514434	Hs. 20830	integrin, sipha	FG-GAP,integrin_A,TM,SS	2.01
	405484	54514151	115.20000	synaptic Ras GT	kinesin,PHD,abhydrolase_2,TM,SS filament,SS	201
	436469	AK001455	Hs.5198	Down syndrome c	TM	2.01 2.01
	451273	NM 014811	Hs.26163	KIAA0649 gene p	TM	2.01
60	432378	A1493046	Hs.146133	ESTs	TM	2.01
	419981	AA897581	Hs.128773	ESTs	Ski_Sno,SS	201
	445808	AV655234	Hs.298083	ESTs	sushi, TM, SS	2.01
	435767	H73505	Hs.117874	ESTs	Peptidase_S8,P,TM,	2.01
45	430468	AF052573	Hs.241517	polymerase (DNA	TM	2.01
65	422790	AA809875	Hs.25933	ESTs	TM	2.01
	443303	U67319	Hs.9216	caspase 7, apop	ICE_p10.ICE_p20,TM,	2.01
	410008	AA079552	14- 400000	gb:zm20h12.s1 \$	FG-GAP.TM,SS	2.01
	440774 442961	A1420611	Hs.127832	ESTs	zf-MYND,TM,SS	2.00
70	424420	BE614474 BE614743	Hs.289074	Homo sepiens cD	TM	2.00
. 5	410240	AL157424	Hs.146688 Hs.61289	prostaglandin E	MAPEG,TM,SS	2.00
	435014	BE560898	Hs.10026	synaptojanin 2 ribosomal prote	TM Photograph 1.17 The	2.00
	406752	AI285598	Hs.217493	annexin A2	Ribosomal_L17,TM, TM	2.00
				- III MAINT F III.	• •••	2.00
75	TABLE 4	18:				
	Pkey:	Unit	que Eos probes	set identifier number		
	CAT num	ber: Ger	e cluster numb	er		
	Accession	n: Ger	bank accessio	n numbers		
80	Observ	CAT				
90	Pkey 410008	CAT number 116812_1		DE440000 DE440000		
	418546	176677_1		BE142525 BE142527 T59708 T59843 BE156903		
	419546	185768_1		AA244272 H57440		•
			- V-244 133	TW. 77616 1141 990		
					ACA	

	419807	188252_1	R77402 AA26	2462 AA250988 R06794					
	422689	219896_1	AW856665 A	A315006 AW954733					
	431120	328264_1		A92498 AA492571					
5	433748 438223	37385_1 452646_1		90 Al110858 AF090916 AF075357 AA011531 202139 Al202098					
_	438993	467651_1		834879 Al926361					
	446995	702707_1	AI355012 AW	Al355012 AW812856					
	447197	711623_1	R36075 Al36						
10	450190 451237	827655_1 863269_1	AW600293 A	91595 T51271 AI686285					
	455778	1364506_1		5088802 BE088755 BE088876 BE088947 BE08888	RF088952				
	458157	158261_1		A176967 AA826015					
	TABLE 410								
15	Pkey:		e number com	sponding to an Eos probaset					
	Ref:	Şequ	ence source. 1	he 7 digit numbers in this column are Genbank iden	ifier (GI) numbers. "Dunham, et at." refers to the publication entitled "The DNA				
	Chand	seque	LEGITURE OF DUTTERS	chromosome 22° Dunham, et al. (1999) <u>Nature</u> 402:	189-495				
	Strand: Nt_position			from which exons were predicted. positions of predicted exons.					
20			ALLS TIBLECOOLS	positions of production districts.					
	Pkey	Ref	Strand	Nt_position					
	400514 401519	9796594 6649315	Minus Plus	78844-79025,80850-80991,89754-89941,93750-93	891				
	401708	2951946	Phus	157315-157950 154511-155298					
25	401866	8018106	Plus	73126-73623					
	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,12	4455-124610,125672-126076				
	403055 403208	8748904 7630829	Minus Minus	109532-110225					
	403422	9665041	Minus	147706-147903,148667-148804 151169-151561					
30	403485	9966528	Plus	2888-3001,3198-3532,3655-4117	·				
	403776 404171	7770611	Minus	1414-1513,1624-1756					
	404253	9930793 9367202	Plus Minus	173667-173783,176876-177055 55675-56055	•				
25	404519	8152000	Plus	12817-13000	•				
35	404567	7249169	Minus	101320-101501					
	405484 405545	5922025 1054740	Plus Plus	199214-199579,199672-199920,200262-200495					
	405818	4071056	Plus	118677-118807,119091-119296,121626-121823 29055-29196					
40	406399	9256288	Minus	63448-63554					
40									
	TABLE 42	A: ABOUT 561	GENES UP-RE	GULATED IN STOMACH CANCER					
	Table 42A	lists about 561	genes up-regul	ated in stomach cancer compared to normal stomaci	n. These were selected as for Table 40A except using various non-malignant atomach				
45	ahemiens	in determining	the denominati	Y value	· · · · · · · · · · · · · · · · · · ·				
	Pkey: ExAcon;	Uniq	ue Eos probese	et identifier number					
	ExAcon: Unigenel©	Uniq Exen Unig	ue Eos probeso optar Accession ene number						
	ExAcon: Unigenet© Unigene T	Uniq Exen t. Unig itle: Unig	ue Eos probeso aplar Accession and number and gene title	el identifier number n number, Genbank accession number					
50	ExAcon: Unigenel©	Uniq Exen t. Unig itle: Unig	ue Eos probeso optar Accession ene number	el identifier number n number, Genbank accession number					
50	ExAccn: UnigenelC Unigene T R1: Pkey	Uniq Exen t. Unig itle: Unig Ratio	ue Eos probeso aplar Accession and number and gene title	et identifier number i number, Genbank accession number irmal tissue Unigene Title	Ri				
50	ExAccn: UnigenelD Unigene T R1: Pkey 42836B	Uniq. Exen t. Unig. Ratio ExAccn BE440042	ue Eos probest optar Accession ene number ene gene title of turnor to no UnigeneID Hs.83326	et identifier number number, Genbank accession number rmal tissue Unigene Title matrix metalloproteinase 3 (stromelysin	60.4				
	ExAccn: Unigenel D Unigene T R1: Pkey 42836B 448693	Uniq Exen t: Unig itle: Unig Ratio ExAcon BE440042 AW004854	ue Eos probest nplar Accession ene number ene gene title of turnor to no UnigeneID Hs.83326 Hs.228320	el identifier number i number, Genbank accession number irmal tissue Unigene Title matrix metalloproteinase 3 (stromelysin Homo sapiens cDNA: FLJ23537 fis, clone L	60.4 28.6				
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<ul><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	ExAccn: Unigene I Unigene I Unigene I R1:  Pkey 428368 448694 422330 415989 403776 424905 414132 450372 45032 44598 416861 414972 44590 441377 419423 44503 415138 424539 4124758 418379 423020 419948 41177	Unique Executive Control of the Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of 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factor pathway inhibitor 2 ESTs Homo sapiens cDNA: FLJ/23537 fis, clone L fidgeth-like 1 replication protein A3 (14kD) sertnet/hrecoince kinase 15 NADPH oxidase 4 KIAA0112 protein; homolog of yeast ribos gbill3-C10214-291299-052-A12 C10214 Homo	50.4 28.6 26.8 22.0 21.2 19.0 17.1 14.9 14.8 14.2 14.0 13.8 13.1 12.5 12.2 10.6 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 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	409041	AB033025	Hs.50081	KIAA1199 protein	
	450480	X82125	Hs.25040	zinc linger protein 239	8.0 7.6
	417655	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	7.6
•	453878	AW964440	Hs, 19025	ESTs	7.6
5	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfami	7.5
	427961	AW293165	Hs.143134	ESTs	7.4
	428330 426235	L22524 A1631964	Hs.2256 Hs.34447	matrix metalloproteinase 7 (matritysin, ESTs	7.3
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	7.1 7.0
10	418205	L21715	Hs.83760	troponin I, skeletal, fast	7.0 7.0
	409757	NM_001898	Hs.123114	cystatin SN	6.9
	430044	AA464510	Hs.152812	ESTs	6.6
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	6.5
15	416209 449020	AA236776	Hs.79078 Hs.192699	MAD2 (mitotic arrest deficient, yeast, h	6.5
13	431958	AJ621170 X63629	Hs.2877	ESTs	6.3
	434699	AA643687	Hs.149425	cadherin 3, type 1, P-cadherin (placenta Homo sapiens cDNA FLJ11980 fs, clone HE	5.8 5.7
	424345	AK001380	Hs.145479	Homo sapiens cONA FLJ10518 fis, clone NT	5.6
20	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	5.4
20	434551	BE387162	Hs.280858	ESTs, Highly similar to XPB_HUMAN DNA-RE	5.3
	427660 424960	AJ741320 BE245380	Hs.114121	Homo sapiens cDNA: FLJ23228 fs, clone C	5.0
	400268	BE245300	Hs.153952	5 nucleofidase (CD73)	4.9
	408427	AW194270	Hs.177236	ESTs	4.B 4.7
25	453785	AJ368236	Hs.283732	ESTs	4.7
	411274	NM_002776	Hs.69423	katlikrein 10	4.7
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	4.7
	415752 434370	BE314524 AF130988	Hs.78776 Hs.58346	putative transmembrane protein	4.6
30	431806	AF186114	Hs.270737	downless (mouse) homolog tumor necrosis factor (ligand) superfami	4.6
	400205		113.2.107.07	union nociona ractor (againt) superiora	4.6 4.6
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	4.5
	406587	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	4.4
35	453160	AJ263307	Hs.146228	ESTs	4.4
33	423871 431211	AA331906 M86849	11- 5555	gb:EST35805 Embryo, 8 week I Homo sapien	4.4
	446638	AL133063	Hs.5566 Hs.15783	gap junction protein, beta 2, 26kD (conn Homo sapiens mRNA; cDNA DKFZp434P1115 (f	4.4
	406741	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	4.3 4.3
40	411560	AW85118B		gb:8L3-CT0220-150200-071-H05 CT0220 Homo	4.1
40	433159	AB035898	Hs.150587	kinesin-like protein 2	4.1
	445142	AI754693	Hs.145968	ESTs	4.1
	414727	8E456904		gb:hz28f03.x1 NCI_CGAP_GC6 Homo sepiens	4,1
	422285 451807	AI803103 W52854	Hs.27099	gb:tc14e06.x1 Soares_NhHMPu_S1 Homo sapi	4.1
45	411558	AA102670	Hs.70725	DKFZP564J0863 protein gamma-aminobutyric acid (GABA) A recepto	4.1 4.0
	415701	NM_003878	Hs.78619	gamma-glutarnyl hydrolase (conjugase, fol	4.0
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	3.9
	452909	NM_015368	Hs.30985	pannexin 1	3.9
50	443211	AI128388	Hs.143655	ESTs	3.9
50	442896 407788	R37725 8E514982	Hs.261108 Hs.38991	ESTs	3.8
	406671	AA129547	Hs.285754	S100 catclum-binding protein A2 met proto-oncogene (hepatocyte growth fa	3.8
	421155	H87879	Hs. 102267	lysyl oxidase	3.8 3.8
	420552	AK000492	Hs.98806	hypothetical protein	3.8
55	420727	H75701	Hs.99886	complement component 4-binding protein,	3.7
	422665	AJ011812	Hs.119018	transcription factor NRF	3.7
	447425 41 <i>7</i> 715	AI963747 AW969587	Hs.18573 Hs.86366	acylphosphatasa 1, erythrocyte (common)	3.7
	406076	AL390179	Hs.137011	ESTs Homo saplens mRNA; cDNA DKFZp547P134 (fr	3.7
60	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6 3.6
	412723	AA648459	Hs.179912	ESTs	3.6
	452461	N78223	Hs.108106	transcription factor	3.6
	453331	A1240665	Hs.8895	ESTs	3.6
65	406434 417956	AA210704	Hs.190465	COT.	3.6
00	410102	AW248508	Hs.279727	ESTS	3.6
	426471	M22440	Hs.170009	Homo sapiens cDNA FLJ14035 fts, clone HE transforming growth factor, alpha	3.6 3.5
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	3.5
70	442556	AL137761	Hs.8379	Homo sapiens mRNA; cDNA DKFZpS86L2424 (f	3.5
70	426957	AA393676	Hs.97459	ESTs, Weakly similar to KIAA0819 protein	3.5
	448105	AW591433	Hs.170675	ESTs. Weakly similar to TMS2_HUMAN TRANS	3.5
	414998 442942	NM_002543 AW167087	Hs.77729 Hs.131562	oxidised low density fipoprotein (lectin	3.5
	416391	A1878927	Hs.79284	mesoderm specific transcript (mouse) hom	3.4
75	420230	AL034344	Hs.298020	Homo sapiens cONA FLJ11796 fis, clone HE	3.4 3.4
	408243	Y00787	Hs.624	Interleukin 8	3.4
	412978	AI431708	Hs.820	homeo bax C6	34
	412851	AI826502	Hs.106149		3.4
80	417720 414812	AA205625 X72755	Hs.208067	ESTs	3.4
-0	453884	AA355925	Hs.77367 Hs.36232	monokine induced by gamma interferon	3.4
	436396	AI683487	Hs.299112	KIAA0186 gane product Homo sapiens cDNA FLJ11441 fis, clone HE	3.4
	425921	NM_007231	Hs.162211	solute certier family 6 (neurotransmitte	3.4 3.4
					4.7

	400000				
	420092 423441	AA814043 R68649	Hs.88045	ESTs	3.3
	421787	AA227068	Hs.278359 Hs.108301	absent in melanoma 1 like nuclear receptor subfamily 2, group C, m	3.3 3.3
	447342	Al199268	Hs.19322	ESTs	3.3
5	430178	AW449612	Hs.152475	ESTs	3.3
	452826	BE245286	Hs.301636	ESTs, Moderately similar to PEX6_HUMAN P	3.3
	414821	M53835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	3.3
	413339 448756	AI818080 AI739241	Hs.194290 Hs.171480	ESTs ESTs	3.3
10	421948	L42583	Hs.111758	keratin 6A	3.3 3.3
••	431453	AW753917		gb:RC0-CT0299-291199-031-F02 CT0299 Homo	3.3
	438538	AA832203	Hs.291955	ESTs	3.3
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	3.3
15	431721	A8032996	Hs.268044	KIAA1170 protein	3.3
13	436391 442025	AJ227892 AW887434	Hs.146274 Hs.11810	ESTS Wankly similar to CD4 2 IC sleaves	3.3
	418007	M13509	Hs.83169	ESTs, Weakly similar to CD4.2 [C.elegans matrix metafloproteinase 1 (interstital	3.3 3.2
	411678	AI907114	Hs.71465	squalene epoxidase	3.2
20	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	3.2
20	450400	A1694722	Hs.279744	ESTs	3.2
	453857 423528	AL080235 AB011137	Hs.35861 Hs.129740	DKFZP586E1621 protein	3.2
	440659	AF134160	Hs.7327	KIAA0565 gene product claudin 1	3.2 3.2
	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.2
25	412022	Al005043	Hs.24143	ESTs .	3.2
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.1
	416111 408633	AA033813 AW963372	Hs.79018	chromatin assembly factor 1, subunit A (	3.1
	445808	AV655234	Hs.46677 Hs.298083	PRO2000 protein ESTs	3.1 3.1
30	414618	AI204600	Hs.96978	ESTs	3.1
	421340	F07783	Hs.1369	decay accelerating factor for complement	3.1
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	3.1
	456508 420759	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 8M-01	3.1
35	452637	T11832 AW971231	Hs.127797 Hs.291020	ESTs ESTs	3.1 3.1
	415857	AA866115	Hs.301645	Homo sapiens cDNA FLJ11381 fis, clone HE	31
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	3.1
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.1
40	440138 454456	AB033023	Hs.6982	hypothetical protein FLJ10201	3.1
40	429125	AW850984 AA446854	Hs.271004	gb:IL3-CT0220-150200-068-H08 CT0220 Homo ESTs	3.0 3.0
	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fts, clone NT	3.0
	438394	BE379623	Hs.27693	OGI-124 protein	3.0
45	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	3.0
43	439453 414696	BE264974	Hs.6566	thyroid hormone receptor interactor 13	3.0
	422746	AF002020 NM_004484	Hs.76918 Hs.119651	Niemann-Pick disease, type C1 glypican 3	3.0
	424947	R77952	Hs.239625	integral membrane protein 2B	3.0 3.0
60	453775	NM_002918	Hs.35120	replication factor C (activator 1) 4 (37	3.0
50	449386	AA001308	Hs.193213	ESTs	3.0
	430687 428862	BE274217	Hs.249247	heterogeneous nuclear protein similar to	2.9
	401747	NM_000346	Hs.2316	SRY (sex-determining region Y)-box 9 (ca	2.9 2.9
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	2.9
55	444735	BE019923	Hs.243122	hypothetical protein FLJ13057 similar to	2.9
	413385	M34455	Hs.840	indolearnine-pyrrole 2,3 dioxygenase	2.9
	436222 442961	AI208737	Hs.122810	Home sapiens cDNA FLJ11489 fs, clone HE	2.9
	454798	BE614474 AW821295	Hs.289074	Homo sepiens cDNA FLJ13986 fis, clone Y7 gb:PM3-ST0307-241299-002-g03 ST0307 Homo	29 29
60	421550	AA781795	Hs.122587	EST8	29
	434398	AA121098	Hs.3838	serum-inducible kinase	29
	420153	N22120	Hs.75277	hypothetical protein FLJ13910	2.9
	435706 416065	W31254 BE267931	Hs.7045 Hs.78996	GL004 protein	2.9
65	423250	BE061916	Hs.125849	profiferating cell nuclear antigen chromosome 8 open reading frame 2	2.9 2.8
	423493	AI815965	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homo	2.8
	430242	U66669	Hs.236642		. 28
	436411	AW674352		gb:ba63c07.y1 NIH_MGC_12 Homo sapiens cD	2.8
70	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	2.8
. 0	437834 400440	AA769294 X83957	Hs.83870	gb:nz36g03.s1 NCI_CGAP_GCB1 Homo saplens nebulin	2.8 2.8
	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked moi	2.8
	428725	AI565937	Hs.98692	ESTs	2.8
75	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	2.8
75	449420 433929	AI854852	Hs.196562		2.8
	430287	Al375499 AW182459	Hs.27379 Hs.125759	ESTs ESTs, Wealdy similar to tumor suppressor	2.8 2.8
	423346	Al267677	Hs.127416		2.8 2.8
00	407824	AA147884	Hs.9812	ESTS	2.8
80	408482	NM_000676		adenosine A2b receptor	2.8
	425188 456999	AK002052 AA319798	Hs.155071		2.8
	408875	NM_015434	Hs.172247 Hs.48604	eukaryolic translation etongation factor DKFZP434B168 protein	2.8 2.8
				C protect	2.0

	407839	AA045144	Hs.161566	ESTs	2.7
	409012	AL117435	Hs.49725	DKFZP434I216 protein	2.7
	410762	AF226053	Hs.66170	HSKM-B protein	2.7
5	426925 410116	NM_001196	Hs.172894	BH3 interacting domain death agonist	2.7
,	428398	AW630671 AJ249368	Hs.58636 Hs.98558	squamous cell carcinoma antigen recogniz ESTs	2.7
	400048	74243000	115.50000	AFFX control: YEL002c/WBP1	2.7
	412140	AAZ19691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	2.7 2.7
	435664	AJ032087	Hs.269819	ESTs	2.7
10	405695			-4.0	2.7
	456655	AI376736	Hs.111779	secreted protein, acidic, cysteine-rich	27
	408670	AF160967	Hs.46784	potassium large conductance calcium-acti	2.7
	422576	BE54855S	Hs_118554	CGI-83 protein	2.7
15	431379	AA504264	Hs.182937	peptidylprotyl isomerase A (cyclophilin	2.7
13	429540	M85776		gb:EST02297 Fetal brain, Stratagene (cat	2.7
	426874	N67325	Hs.247132	ESTs	2.7
	433183 409902	AF231338 Al337658	Hs.222024 Hs.156351	transcription factor BMAL2	27
	422336	AI761322	Hs.115285	ESTs	2.7
20	408434	AW195317	Hs.107716	dihydrolipoamide S-acetyttransterese (E2 Horno sapiens cDNA: FLJ22344 fis, clone H	2.7 2.7
	432328	AI572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	2.7
	407633	NM_007069	Hs.37189	similar to rat HREV107	2.6
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	26
25	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	26
25	445564	AB028957	Hs.12896	KIAA1034 protein	2.5
	401644				2.6
	417479	AI057052	Hs.133554	ESTs	26
	434217 426514	AW014795	Hs.23349	ESTs	2.6
30	414800	BE616633 BE538690	Hs.301122	bone morphogenetic protein 7 (osteogenic	2.6
50	400289	X07820	Hs.2258	gb:601064676F1 NIH_MGC_10 Homo sapiens c matrix metalloproteinase 10 (strometysin	2.6
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	2.6 2.6
	421246	AW582962	Hs.300961	ESTs, Highly similar to AF151805 1 CGI-4	26
20	430397	AJ924533	Hs.105607	ESTs	2.6
35	428048	AA705745	Hs. 185070	ESTs	2.6
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	26
	440052	AI833744	Hs.195648	ESTs	2.6
	433077	AA314262	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	2.6
40	432407 452401	AA221036	Hs.285026	HERV-H LTR-associating 1	2.6
70	451813	NM_007115 NM_016117	Hs.29352 Hs.27182	turnor necrosis factor, alpha-induced pro	2.6
	410889	X91662	Hs.66744	phospholipase A2-activating protein twist (Drosophila) homotog (acrocephalos	26
	440100	BE382685	Hs. 158549	ESTs	2.6
	413746	AA133243	Hs.171553	ESTs	26 26
45	414737	AI160386	Hs.125087	ESTs	2.6
	422063	BE156476		gb:QV0-HT0368-040100-082-c05 HT0368 Homo	2.6
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	2.6
	437641	AA811452	Hs.291911	EST\$	2.6
50	436027	AI864053	Hs.39972	ESTs, Wealdy similar to 138588 reverse t	2.6
50	444381 452571	8E387335 W31518	Hs.283713	ESTs, Weakly similar to CA54_HUMAN COLLA	2.6
	452862	AW378065	Hs.34665 Hs.8687	ESTs ESTs	26
	411984	NM_005419	Hs.72988	signal transducer and activator of trans	2.6 2.6
	446440	AV658411	Hs.42656	Homo sapiens cDNA FLJ12667 fis, clone NT	2.6
55	448663	BE614599	Hs.106823	H.sapiens gene from PAC 42616, similar t	2.6
	426427	M86699	Hs.169840	TTK protein kinase	2.6
	445848	AA774824	Hs.13377	Homo sapiens clone 23649 and 23755 untino	2.6
	420022 451418	AA256253	Hs.120817	ESTs	2.6
60	428953	BE387790 AA306610	Hs.26369	hypothetical protein FLJ20287	26
	424008	R02740	Hs.194676 Hs.137555	DKFZP434C013 protein	2.6
	417863	AB000450	Hs.82771	putative chemokine receptor; GTP-binding vaccinia related kinase 2	2.6 2.6
	414987	AA524394	Hs.165544	ESTs	2.6
65	440249	AI246590	Hs.125325	ESTs	2.6
65	407966	AA295052	Hs.38515	ESTs	2.5
	406685	M18728		gb:Human nonspecific crossreacting antig	2.5
	403204			•	2.5
	436961	AW375974	Hs.156704	ESTs	2.5
70	422260 444471	AA315993 AB020684	Hs.105484	ESTs, Weakly similar to LITB_HUMAN LITHO	2.5
, 0	430290	AI734110	Hs.11217	KIAA0877 protein	25
	413670	AB000115	Hs.136355 Hs.75470	ESTs  hypothetical entire expressed in actor	2.5
	421928	AF013758	Hs.109643	hypothetical protein, expressed in osteo polyadenylate binding protein-interactin	25
	439580	AF086401	Hs.293847	ESTs	2.5 2.5
75	439963	AW247529	Hs.6793	platelet-activating factor acetythydrota	25
	457065	AJ476318	Hs.192480	ESTs	25
	439521	A1808955	Hs.58248	ESTs	2.5
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	2.5
80	422631	BE218919	Hs.118793	hypothetical protein FLJ 10688	2.5
55	417856	AW067903	Hs.82772	collagen, type XI, alpha 1	2.5
	416975 415947	NM_004131 U04045	Hs.1051	granzyme 8 (granzyme 2, cytotoxic T-lymp	2.5
	454678	AW813089	Hs.78934	mulS (E. coli) homolog 2 (colon cancer,	2.5
				gb:RC3-ST0186-240400-111-b05 ST0186 Homo	2.5

	424080	AW189983	Hs.139119	Homo sapiens cDNA FLJ 10967 fis, clone PL	2.5
	426572	AB037783	Hs.170623	hypothetical protein FLI11183	2.5
	440594 428264	AW445167 AA424839	Hs.126036 Hs.98484	ESTs, Wealdy similar to ALU1_HUMAN ALU S	2.5 2.5
5	408750	BE294069	Hs.93581	hypothetical protein FLJ 10512	2.5
	451177	AI969716	Hs.13034	ESTs .	2.5
	449318 434414	AW236021 AJ798376	Hs.108788	ESTs, Weakly similar to zeste [D.melanog	2.5
	400240	M120310		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	2.5 2.5
10	410519	AW612264	Hs.131705	ESTs	2.5
•	440953	AI683036	Hs.124135	KIAA1618 protein	2.5
	421190 444478	U95031 W07318	Hs.102482 Hs.240	mucin 5, subtype B, tracheobronchial M-phase phosphoprotein 1	2.5 2.5
	442295	AJ827248	Hs.224398	Home sepiens cDNA FLJ11469 fis, clone HE	25
15	420894	AA744597	Hs.88854	ESTs	2.5
	410094	8E147897	Hs.58593	general transcription factor IIF, polype	24
	413998 412281	AW103807 AI810054	Hs.243933 Hs.14119	ESTs ESTs	2.4 2.4
••	418105	AW937488	Hs.178000	ESTs	2.4
20	447335	8E617695	Hs.286192	protein phosphatase 1, regulatory (Inhib	24
	446852 408915	AW451643 NM_016651	Hs.257479 Hs.48950	ESTs, Wealdy similar to AF147747 1 BOG25	2.4 2.4
	442991	BE281238	H\$.8886	heptacellular carcinoma novel gene-3 pro hypothetical protein FLJ20424	2.4
0.5	410193	AJ132592	Hs.59757	zinc finger protein 281	24
25	410664 449264	NM_006033	Hs.65370	lipase, endothelial	24
	423453	A1637649 AW450737	Hs.196105 Hs.128791	ESTs CGI-09 protein	2.4 2.4
	433757	A1949974	Hs.152670	ESTs	2,4
30	411598	BE336654	Hs.70937	H3 histone family, member K	24
30	431657 429663	AJ345227 M68874	Hs.105448 Hs.211587	ESTs, Weakly similar to B34087 hypotheti phospholipase A2, group IVA (cytosolic,	24 24
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinemic	24
	419559	Y07828	Hs.91096	ring finger protein	2.4
35	419839 419713	U24577 AW968058	Hs.93304 Hs.92381	phospholipase A2, group VII (platelet-ac	2.4 2.4
33	413281	AA861271	Hs.34396	nudix (nucleoside diphosphate linked moi ESTs	24
	402819				2.4
	431457	NM_012211	Hs.256297	integrin, alpha 11	2.4
40	422564 443683	A1148006 BE241717	Hs.222120 Hs.9676	ESTs uncharacterized hypothalamus protein HT0	2.4 2.4
	407242	M18728	114.5070	gb:Human nonspecific crossreacting antig	2.4
	409235	AA188827	Hs.7988	ESTs, Wealtly similar to endo-alpha-D-man	2.4
	408938 422158	AA059013 L10343	Hs.22607 Hs.112341	ESTs protease inhibitor 3, skin-derived (SKAL	2.4 2.4
45	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermotys	24
	408321	AW405882	Hs.44205	cortistatin	24
	419086 452945	NM_000216 AW978187	Hs.89591 Hs.31086	Kalimann syndrome 1 sequence	24
	452234	AW084176	Hs.223296	Homo sapiens mRNA for cytochrome b5, par ESTs	24 24
50	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.4
	430399 450737	AI916284 AW007152	Hs.199671	ESTs	24
	428513	BE220806	Hs.203330 Hs.184697	ESTs Homo sapiens clone 23785 mRNA sequence	2.4 2.4
	405454				24
55	422168	AA586894	Hs.112408	S100 calclum-binding protein A7 (psorias	23
	421462 403416	AF016495 AI744626	Hs.104624 Hs.301506	aquaporin 9 ESTs, Highly similar to KIAA0564 protein	2.3 2.3
	422039	BE567B32	Hs.82148	hypothetical protein	2.3
60	448988 429145	Y09763 AI694923	Hs.22785 Hs.49031	gamma-aminobutyric acid (GABA) A recepto	2.3
00	423198	M81933	Hs.1634	ESTs cell division cycle 25A	23 23
	442914	AW188551	Hs.99519	Homo sapiens cDNA FLJ14007 fls, clone Y7	2.3
	449042 421308	AW294985	Hs.301148		2.3
65	419926	AA687322 AW900992	Hs.192843 Hs.93796	ESTs DKFZP586D2223 protein	2.3 2.3
	429992	AL050053	Hs.227397	Homo sapiens mRNA; cDNA DKF2p566E103 (fr	23
	440601	N62409	Hs.126688	ESTs	2.3
	445232 410174	A1281848 AA306007	Hs.165547 Hs.59461		2.3
70	452110	T47667	Hs.28005	DKFZP434C245 protein Homo seplens mRNA; cDNA DKFZp564G2463 (I	2.3 2.3
	422493	AW474183	Hs.233816	ESTs	23
	407047 411098	X65965 U80034	Hs.68583	gb:H.sapiens SOD-2 gene for manganese su	23
	411030	AW894667	Hs.169965	mitochondrial intermediate peptidase chimerin (chimaerin) 1	2.3 2.3
75	442029	AW956698	Hs.14456	neural precursor cell expressed, develop	2.3
	446545	AJ431798	Hs.164192		2.3
	422094 421933	AF129535 RS8881	Hs.272027 Hs.109655		2.3 2.3
00	430001	AI580056	Hs.98992	ESTs Control of Intellige (Crossophica) - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophical - Crossophi	23
80	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	2.3
	402053 415666	H72693		gb:yu03c11.r1 Soares fetal liver soleen	23 23
	432743	Al146966	Hs.101656		23

A03330		433409	A1278802	Hs.25661	ESTs	2.2
August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   August   A						2.3 2.3
Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Substitution   Subs			AL031427	Hs.40094		
433730 AK002135 Hs. 3342 hs. 3462 hs. 3462 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3463 hs. 3	5					
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415058 AW902848 Hs.273829 ESTs hypothetical protein FLI10120 2.2 436209 AW350417 Hs.254020 ESTs, Moderately similar to unnamed prot 4.22 425692 D90041 Hs.155959 Hs.155959 Home sapiens mRNA; cDNA DKFZo584A023 (fr 2.2 425657 NM_006731 Hs.55777 Fukuyama type congenital muscular dystro 2.2 428157 AJ738719 Hs.298668 ESTs 2.2 428157 AJ738719 Hs.298668 ESTs 2.2 42914747 U30872 Hs.298668 Hs.2488 hymphocyte cytosofic protein 2 (SH2 doma 2.2 425843 BE313280 Hs.159627 Home sapiens cDNA FLI13892 is, clone PL 2.1 436251 ESE515065 Hs.2092 Hs.1092 eath associated protein 3 2.2 42516 BE25862 Hs.117950 multifunctional polypeptide similar is 3 2.1 426787 AB032990 Hs.40719 hypothetical protein RIAA1164 2.1 427528 AU077143 Hs.179565 millichromosome maintenance deficient (S. 21 440092 AW294909 Hs.13208 ESTs 2.1 4400022 ESTs 12540020 Hs.19309 Hs.13208 ESTs 2.1	OU					
418049 A211467 Hs.190488 hypothetical protein FLJ10120 22 436209 AW850417 Hs.254020 ESTs, Moderately similar to unnamed prot 22 425692 D90041 Hs.155956 Hs.155956 NM_006731 Hs.55777 Fukuyama type congenital muscutar dystro 22 425693 NM_006731 Hs.55777 Fukuyama type congenital muscutar dystro 22 426157 AJ738719 Hs.298668 ESTs 22 427032 U20158 Hs.28880 tr.37204 Hs.77204 Hs.77204 Hs.77204 Hs.77204 Hs.77204 Hs.77204 Hs.155993 AJ910382 Hs.118727 Horn septems cOhn FLJ10120 22 425843 BES13280 Hs.195627 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.59867 Hs.5986						
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425692 D90041 Hs.155956 N-acetytiransferase 1 (arytamine N-acety 2.2 40965 NM,006731 Hs.55777 Fukuyama type congenital muscular dystro 2.2 428157 AJ738719 Hs.29868 ESTs 2.2 410480 F97457 Hs.69984 cadherin 13, H-cadherin (heart) 2.2 427932 U20158 Hs.2488 lymphocyte cytosofic protein 2 (St12 doma 2.2 425843 B62313280 Hs.159627 centromere protein F (350/400kD, mitosin 2.2 425843 B62313280 Hs.159627 death associated protein 3 426251 B6515065 Hs.50932 muscledar protein (NEXP to repeat) 2.1 nucleockar protein (FV to repeat) 2.1 nucleockar protein (FV to repeat) 2.1 430056 A99295659 Hs.207825 signal recognition particle 72kD 2.1 nucleockar protein (NEXP to repeat) 407870 AB032930 Hs.40719 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164 2.1 hypothetical protein KIAA1164	65				ESTs, Moderately similar to unnamed prot	
49865   NM_006731   Hs.55777   Fukuyama type congenital muscutar dystro   2.2	0.5					
A28157						
10480   R67457   Hs. 63984   cadherin 13, H-cadherin (heart)   2.2   429732   U20158   Hs. 2488   hs. 2488   hs. 2488   hs. 177204   425843   BE313280   Hs. 159627   death associated protein 3   2.2   445299   A910382   Hs. 159627   death associated protein 3   2.2   Horno sapiens cCNA FLJ13692 is, clone PL   2.1   430066   A929659   Hs. 237825   signal recognition particle 72xD   2.1   42516   BE258862   Hs. 17950   Hs. 40719   416109   A420311   Hs. 179565   Ms. 40787   A9032990   Hs. 40787   Hs. 179565   Hs. 173598   ESTs   2.1   4400022   A467945   Hs. 13208   ESTs   2.1   AFFX control: STAT1   2.1   AFFX control: STAT1   2.2   AFFX control: STAT1   2.2   AFFX control: STAT1   2.2   AFFX control: STAT1   2.2   AFFX control: STAT1   2.2   AFFX control: STAT1   A2208   A467945   AFFX control: STAT1   A2208   AFFX control: STAT1   A2208   AFFX control: STAT1   A2208   AFFX control: STAT1   A2208   A467945   AFFX control: STAT1   A2208   AFFX control: STAT1   A2208   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A467945   A4		428157	A1738719	Hs.298668		
414747 U30872	70					2.2
425843 BE313280 Hs.159627 death associated protein 3 22 436251 BE515065 Hs.5092 uncleotar protein (KKE/D repeat) 21 43065 A929659 Hs.237825 signal recognition particle 72x0 21 407870 AB032990 Hs.40719 hypothetical protein KIAA1164 2.1 416109 AI420311 Hs.179565 suppressor of K* transport defect 1 2.1 427528 AU077143 Hs.179565 minichromosome maintenance deficient (S. 2.1 440889 AI467945 Hs.173598 ESTs 2.1 4400022 ESTs 2.1 AFFX control: STAT1 2.1	70					
A45299						
15						
422516   BE258862   Hs.117950   multifunctional polypepiide similar to S   2.1	76	436251	BE515065	Hs.5092	nucleolar protein (KKE/D repeat)	21
80 407870 AB032990 Hs. 40719 hypothetical protein KIAA1164 2.1 427528 AU077143 Hs. 175550 suppressor of K * transport defect 1 2.1 427528 A46989 AI467945 Hs. 175596 ESTs 2.1 447790 AW294909 Hs. 132208 ESTs 2.1 400022 AFFX control: STAT1 2.1	13					
80 427528 AU077143 Hs.178565 suppressor of K+ transport defect 1 2.1 minichromosome maintenance deficient (S. 2.1 427528 AV294909 Hs.173566 ESTs 2.1 400022 AFFX control: \$TAT1 2.1						
80 427528 AU077143 Hs.179565 minichromosome maintenance deficient (S. 2.1 44089 AU47945 Hs.173596 ESTs 2.1 44092 AW294999 Hs.132208 ESTs 2.1 AFFX control: STAT1 2.1						
441790 AW294909 Ms.132208 ESTs 2.1 400022 AFFX control: STAT1 2.1	90			Hs.179565	minichromosome maintenance deficient (S.	2.1
400022 AFFX control: STAT1 2.1	٥٥					
			A114343U3	ns.132200		
			NM_016625	Hs.191381		

	44.4350	DEC. 404.40		-1.401074.464	
	414366 409929	BE549143 R38772	Hs.172619	gb:601076456F1 NIH_MGC_12 Homo sapiens c KIAA1106 protein	2.1 2.1
	405264				21
5	445625	BE246743	Hs.288529	Homo sapiens cDNA: FLJ 22635 fis, clone H	2.1
,	408949 424513	AF189011	Hs.49163	putative ribonuclease III	21
	433683	BE385864 At817723	Hs.149894 Hs.22678	mitochondrial translational initiation f hypothetical protein FLJ21832	2.1
	442952	AJ743261	Hs.131860	ESTs	2.1 2.1
••	441020	W79283	Hs.35962	ESTs	21
10	446770	AV660309	Hs.154986	ESTs, Wealdy similar to AF137386 1 plasm	21
	432378	AJ493046	Hs.146133	ESTs	2.1
	447769	AW873704	Hs.48764	ESTs	2.1
	412654 445669	AI093480 AI570830	Hs.29263 Hs.174870	Homo sapiens cDNA FLJ11896 fis, clone HE ESTs	21
15	417979	AU077284	Hs.83081	GTP cyclohydrolase I feedback regulatory	2.1 2.1
	433849	BE465884	Hs.280728	ESTs	2.1
	437928	NM_005476	Hs.5920	UOP-N-acetylglucosamine-2-epimerase/N-ac	21
	457341	BE181716		gb:QV1-HT0639-150500-198-e03 HT0639 Homo	2.1
20	452833 403055	BE559681	Hs.30738	KIAA0124 protein	2.1
20	414581	AA256213	Hs.72010	COT-	21
	432840	AK001403	Hs.279521	ESTs hypothetical protein FLJ20530	21 21
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecul	. 21
~~	440908	A1915225	Hs.126735	ESTs	2.1
25	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	21
	436895	AF037335	Hs.5338	carbonic anhydrase XII	21
	455716 408420	BE070263 NM_006915	U- 200484	gb:QV4-BT0407-280100-090-e07 BT0407 Homo	21
	435849	BE305242	Hs.299481 Hs.112442	Homo sapiens mRNA; cDNA DKFZpS8680118 (f ESTs, Weakly similar to CLDE_HUMAN CLAUD	2.1 2.1
30	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	21
	433644	AW342028	Hs.256112	ESTs	2.1
	400020			AFFX control: STAT1	2.1
	434064	AL049045	Hs.180758	hypothetical protein PRO0082	21
35	410660 404076	AI061118	Hs.65328	Fanconi anemia, complementation group F	2.1
55	44 1362	BE614410	Hs.23044	RAD51 (S. carevisiae) homolog (E coti Re	2.1
	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	2.1 2.1
	444863	AW384082	Hs.301323	ESTs	21
40	445867	AF272663	Hs.13405	gephyrin	2.1
40	441021	AW578716	Hs.7644	H1 histone family, member 2	2.1
	446595	T57448	Hs.15487	hypothetical protein FLJ20725	2.1
	417515 412429	L24203 AV650262	Hs.82237 Hs.75765	ataxia-telangiectasia group O-associated	21
	449207	AL044222	Hs.23255	GRO2 oncogene nucleoporin 155kD	21 21
45	412095	A1624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	21
	400861				2.1
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	2.1
	440591	AA431599	Hs.132799	Homo sapiens cDNA: FLJ23451 fis, clone H	2.1
50	426181 452880	AA371422 AA029332	Hs.69844	ESTs, Weakly similar to dJ191N21.1 (H.sa	21
50	421878	AA299652	Hs.87549 Hs.111496	ESTS	2.1 2.1
	442104	L20971	Hs.188	Homo sapiens cDNA FLJ11643 fis, clone HE phosphodiesterase 4B, cAMP-specific (dun	2.1
	427224	AL135554	Hs.101937	sine oculis homeobox (Drosophila) homolo	2.1
55	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	2.1
55	432487	AA550988	Hs.221472	ESTs	2.1
	429534	AW976987	Hs.163327	ESTs	2.1
	448051 447760	BE048061 AJ431328	Hs.153315 Hs.291179	ESTs Workly similar to toggic amounts a	2.1
	422675	BE018517	Hs.119140		21 21
60	415173	AW501735	Hs.253015	ESTs	2.1
	425170	AU077315	Hs.154970	transcription factor CP2	2.1
	453751	R38762	Hs.101282	Homo sepiens mRNA; cDNA DKFZp434B102 (fr	2.1
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	2.1
65	417874 449555	BE616160 AW450288	Hs.82829 Hs.195390	protein tyrosine phosphatase, non-recept	21
45	439699	AF086534	Hs. 187561	ESTs ESTs, Moderately similar to ALU1_HUMAN A	21 21
	427413	BE547647	Hs.177781	superoxide dismutase 2, mitochondrial	2.1
	424673	AA345051	Hs.294092	ESTs	21
70	407802	D84145	Hs.39913	novel RGD-containing protein	2.0
70	452834	A1638627	Hs.105685	ESTs	2.0
	438895 446035	AW007021	Hs.82894	ESTs .	2.0
	406981	NM_006558 S71129	Hs.13565 Hs.296844	Sam68-like phosphotyrosine protein, T-ST	20
	427001	NM_006482	Hs.173135		2.0 2.0
75	439223	AW238299	Hs.23945	ESTs	2.0
	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	2.0
	414890	BE281095	Hs.77573	uridine phosphorylase	2.0
	423019	AI640185	Hs.225816		2.0
80	435905 422278	AW997484 AF072873	Hs.5003 Hs.114218	KIAA0456 protein	2.0
	439608	AW864696	Hs.26198	frizzled (Orosophila) homolog 6 Homo saplens cDNA: FLJ23353 fis, clong H	2.0
	432114	AL036021	Hs.225597	ESTs	2.0 2.0
	405545				2.0

	418201	AA214345	Hs.98445	Homo sapiens cDNA: FLJ21652 fis, clone C	20
	442528	AF150317	Hs.134217	ESTS	2.0
	445237	AW270515	Hs.149596	ESTs	2.0
	428074	BE387770	Hs.182378	colony stimulating factor 2 receptor, al	2.0
5	423430	AF112481	Hs.128501	RAD54, S. cerevisiae, homolog of, B	20
-	435767	H73505	Hs.117874	ESTs	20
	432945		Hs.271357		
		AL043683		ESTs, Wealty similar to unnamed protein	20
	428792	BE535955	Hs.193602	chromosome condensation protein G	20
10	404170				20
ΙU	410286	AI739159	Hs.61898	OKFZP586N2124 protein	20
	434565	T52172		gb:yb22d01.s1 Stratagena fetal spleen (9	2.0
	422610	AF153820	Hs.1547	potassium inwardly-rectilying channel, s	2.0
	417933	X02308	Hs.82962	thymidylate synthetase	2.0
	441384	AA447849	Hs.288660	protease, serine, 23	2.0
15	437403	AI208149	Hs.121196	ESTs	2.0
	412673	AL042957	Hs.31845	ESTs	2.0
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	20
	438426	AA835936	Hs.269763	ESTs	2.0
	413943	AW294416	Hs.144687	ESTs	20
20	449001	AI619957	Hs.169854		20
	427674	NM_003528	Hs.2178	H2B histone family, member Q	20
	435425	H16263	Hs.31416	ESTs	20
	433364	AJ075407	Hs.296083	ESTs	
	429782				20
25		NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	20
23	417366	BE185289	Hs.1076	small proline-rich protein 1B (comilin)	2.0
	426746	J03626	Hs.2057	undine monophosphate synthetase (orotet	2.0
	411943	BE502436	Hs.7962	ESTs. Weakly similar to putative [C.eleg	2.0
	414266	BE267834		gb:601124428F1 NIH_MGC_8 Homo sapiens cD	2.0
20	432677	NM_004482		UDP-N-acetyl-alpha-O-galactosamine:polyp	2.0
30	450534	AI570189	Hs.25132	KIAA0470 gene product	2.0
	446715	A1337735	Hs.173919	ESTs	2.0
	TABLE 42	8:			
	Pkey:	Unia	ue Eos probes	et identifier number	
35	CAT numi		e cluster numb		
	Accession		bank accession		
				The field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the f	
	Pkey	CAT number	Accession		
	408432	1058667 1		R27868 AW811262	
40	411479	1247077_1			121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905
	411413	1241011_1	AW848214	ATTO-10202 ATTO-1003   ATTO-10142 ATTO-1010 ATTO-10	121 ATTO-10032 ATTO-10140 ATTO-1037 I ATTO-10003 ATTO-10007 ATTO-10003 ATTO-10303
	411560	10/0//2 1		411000007 0544045	
	414266	1249443_1		AW996967 BE143456	
		1430984_1		BE514180 BE514096	
45	414366	1438636_1		BE390613 BE277344	
47	414727	1481204_1	BE466904 \		•
	414800	1491863_1	BE538690		
	415666	1543492_1	H72693 R0	8673 H72694 F20990 R08580	
	422063	210852_1		BE156473 BE156474 BE156475 AA302839	
60	422285	214669_1	AI803103 A	J885143 AW470793 AW450703 AJ090784 AW271587	AW236950 AW242783
50	422689	219896_1	AW856665	AA315006 AW954733	
	423871	232749_1	AA331906	AA332484	
	429540	305828_1	M85776 AA	454535 AA456208 H90189	
	431453	333457_1		BE152926 AA505333 BE155673	
	434414	38585_1			858232 AW861851 AW858382 AA232351 AA218567 AA055556 AW858231
55					AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139
					8 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730
			AA157715	AADS357A AWRAGERI AWREASER COS2SA AWRE2936	T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957
			NECOET AA	.627974 WCC24E AAN4EEC4 MCN47CE WCN0NO AA44N	736 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659
			BE081531		20 AM 133050 BENB 1333 BEN13454 WAR 114065 WAR 111103 WAS 11103 AM 2111033
60	434565	200ng 4			
50	436411	38898_1		147324 T52248	
		419334_1		AA715374 Z25205	
	437834	443674_1			293 AW749298 AW749294 AW749288 AW749291 AW749297 AW749292 AW749295
				AW749287 BE535498	
65	438788	465159_1		AW978859 AA828841	
U)	454456	1207088_1		AW752835 M86124	
	454678	1228915_1	AW813089	W28102	
	454798	1235104_1	AW821295	AWB21272 AWB21282	
	454946	1245753_1	AW846376	i AW846375 AW846434 AW846287 AW846365 AW84	6554 AW846384 AW846290 AW846356 AW846474
~~	455716	1352695_1		BE070195 BE070265 BE070202 BE070233 BE07039	
70	457341	322221_1		AW948314 AW801848 AW948320 AW983981 AA484	
		_			
	TABLE 4	2C:			
	Pkey:		que number ca	prresponding to an Eos probeset	
	Ref:				ntifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
75		\$.Dr	wence of him	an chromosome 22" Dunham, et al. (1999) Nature 402	ARGLARS
	Strand:	ind	icates DNA ***	an Cultumpsome 22 Lounnam, et al. (1999) <u>Martila</u> 402 and from which exons were predicted.	70-7-04
	Nt_posit			de positions of predicted exons.	
			AARES HULIEOU	ne besieves or begoested ayou?	
	Pkey	Ref	Chand	M. maridan	
80	400861	9757506	Strand	Nt_position	
30			Plus	163855-164016	
	401644	8576138	Plus	82655-83959	AA (AA (AAAA) (BA(A) (BAAA) (BAAA) (BAAAA) (A) (AA (A) (A) (A) (A) (A) (A) (A
	401747	9789672	Minus		20422-120990,130161-130381,130468-130593,131097-131258,131866-31932,132451-
				132575,133580-134011	

	402053	8083229	Plus	62703-63179
	402819	6729581	Plus	29217-29422
	403055	8748904	Minus	109532-110225
_	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
5	403204	7622392	Plus	16214-16439
	403258	7770439	Minus	156251-156619
	403776	7770611	Minus	1414-1513.1624-1756
	404076	9931752	Minus	3848-3967
• •	404170	9930793	Plus	168836-169248
10	405264	7329374	Plus	28556-28684
	405454	7656675	Plus	133807-134053
	405545	1054740	Plus	118677-118807,119091-119296,121626-121823
	405695	4309958	Plus	51860-52162
	406434	9256651	Minus	17803-17931
15				

TABLE 43A: ABOUT 339 GENES UP-REGULATED IN STOMACH CANCER
Table 43A lists about 339 genes up-regulated in stomach cancer compared to normal stomach that are likely to be extracellular or cell-surface proteins. These were selected as for Table 42A and the predicted protein contained a structural domain that is indicative of surface or extracellular localization (e.g. ig. th3, egt. 7tm domains). Predicted protein domains

20

Table 42A and are noted. Picey: ExAccn: Unigene1D: Unigene Title: PSDomain: R1: Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Unigene number Unigene gene title Protein Structural Domain Ratio of turnor to normal tissue 25

	Pkey	ExAcon	UnigeneID	Unigene Title	PSDomain	R1
30	428368	BE440042	Hs.83326	matrix metallop	hemopexin,Peptidase_M10,,SS	60.4
30	428664	AK001666	Hs.189095	similar to SALL	zI-C2H2,TM,SS	26.8
	422330	D30783	Hs.115263	epiregulin	EGF,TM,SS	22.0
	439979	AW600291	Hs.6823	hypothetical pr	TM	19.0
	451099	R52795	Hs.25954	interleukin 13	tn3,TM,SS	17.1
25	403776				ILB,TM,SS	14.9
35	424905	NM_002497	Hs.153704	NIMA (never in	pkinase,TM,	14.8
	453922	AF053306	Hs.36708	budding uninhib	TM	13.6
	435032	AA150797	Hs.109276	latexin protein	TM	13.1
	427585	D31152	Hs.179729	collagen, type	C1q,Collagen,TM,SS	12.5
40	416661	AA634543	Hs.79440	IGF-II mRNA-bin	KH-domain, TM,	12.2
40	414972	BE2637B2	Hs.77695	KIAA0008 gene p	TM	10.6
	446619	AU076643	Hs.313	secreted phosph	Osteopontin, TM, SS	10.5
	415138	C18356	Hs.78045	tissue factor p	Kunitz_8PTI,G-gamma,TM,SS	9.6
	423020	AA383092	Hs.1608	replication pro	TM	8.6
	408908	BE296227	Hs.48915	serine/threonin	pkinase.TM.SS	8.5
45	419948	AB041035	Hs.93847	NADPH oxidase 4	Ferric_reduct,TM,SS	8.3
	411750	BE562298	Hs.71827	KIAA0112 protei	SS	8.3
	420900	AL045633	Hs.44269	ESTs	Ald_Xan_dh_C,FAD_binding_5,TM,	8.0
	450480	X82125	Hs.25040	zinc finger pro	zf-C2H2,TM,SS	7.6
	417655	AA780791	Hs.14014	ESTs, Westly si	TM	7.6
50	430403	AF039390	Hs.241382	tumor necrosis	TMSS	7.5
	428330	L22524	Hs.2256	matrix metallop	Peptidase_M10,,SS	7.3
	452291	AF015592	Hs.28853	CDC7 (cell divi	pkinase.TM.	7.0
	418205	L21715	Hs.83760	troponin I, ske	Troponin, SS	7.0
	409757	NM_001898	Hs.123114	cystatin SN	cystatin, SS	6.9
55	444783	AK001468	Hs.62180	anillin (Drosop	PH,TM,	6.5
	416209	AA236776	Hs.79078	MAD2 (mitotic a	HORMASS	6.5
	431958	X63629	Hs.2877	cadherin 3, typ	cadherin_C_term,TM,SS	5.8
	424345	AK001380	Hs.145479	Homo sapiens cD	TMSS	5.6
	428227	AA321549	Hs.2248	small inducible	ILB.TM.SS	5.4
60	424960	BE245380	Hs.153952	5' nucleotidase	5 nucleotidase.TM.SS	4.9
	400268	000.0000	14.150302	\$ 11420000130	Myosin_tail,,SS	4.8
	411274	NM_002776	Hs.69423	kaltikrein 10	typsin,TM,	4.7
	415752	BE314524	Hs.78776	putative transm	TM	4.6
	431806	AF186114	Hs.270737	tumor necrosis	TM.SS	4.6
65	400205		14.210/31	market recurses	SS	
••	422938	NM_001809	Hs.1594	centromere prot	histone,TM,	4.6
	406687	M31126	Hs.272620	pregnancy speci	hemopexin,TM,	4.5
	423871	AA331906	16.272020	gb:EST35805 Emb	тм	4.4
	431211	M86849	Hs.5566		connexin,TM.	4.4
70	446638	AL133063	Hs.15783	gap junction or		4.4
. •	406741	AA058357	Hs.74468	Homo sapiens mR	TM	4.3
	411560	AW851186	113.74400	carcinoembryoni	ig,TM,SS	4.3
	433159	AB035898	Hs.150587	gb:IL3-CT0220-1	TM	4.1
	422285	AI803103	UZ 100001	kinesin-like pr	kinasin,Myosin_tail,TM,SS	4.1
75	451807	W52854	Hs.27099	gb:tc14e06.x1 S	TM,SS	4.1
	411558	AA102670		DKFZP564J0863 p	TM	4.1
	415701		Hs.70725	gamma-aminobuty	neur_chan,TM,SS	4.0
	409420	NM_003878 215008	Hs.78619	gamma-glutamyl	TM,SS	4.0
	452909		Hs.54451	laminin, gamma	taminin_EGF,taminin_B,.SS	3.9
80	407788	NM_015368 BE514982	Hs.30985	pannexin 1	TM	3.9
00			Hs.38991	S100 calcium-bi	ethand,S_100,TM,SS	3.8
	421155 420552	H87879 AK000492	Hs.102267	lysyl oxidase	Lysyl_oxidæe,,SS	3.8.
	420727	H75701	Hs.98806	hypothetical pr	\$S	3.8
	420121	112101	Hs.99886	complement comp	sushi	3.7

	422665	AJ011812	Hs.119018	transcription f	R3H,G-patch,GTP_CDC,TM,SS	3.7
	447425	AJ963747	Hs.18573	acylphosphatase	Acytphosphatase,TM,	3.7
	406076	AL390179	Hs.137011	Homo sapiens mR	TM	3.6
•	406434				heme_1,TM,	3.6
5	417956	AA210704	Hs.190465	ESTs	sushi,,SS	3.6
	410102	AW248508	Hs.279727	Homo sapiens cD	TM,SS	3.6
	426471	M22440	Hs.170009	transforming gr	EGF,TM.SS	3.5
	425782	U66468	Hs.159525	cell growth reg	\$S	3.5
10	426957	AA393676	Hs.97459	ESTs, Wealdy si	SS	3.5
10	448105 414998	AW591433	Hs.170675	ESTs, Wealdy si	trypsin,TM,	3.5
	442942	NM_002543 AW167087	Hs.77729 Hs.131562	oxidised low de	TM	3.5
	416391	AI878927	Hs.79284	ESTs mesoderm specif	pkinase,TM,SS	3.4
	420230	AL034344	Hs.298020	Homo sapiens cD	abhydrolasa,TM,SS Fork_head,TM,	3.4 3.4
15	408243	Y00787	Hs.624	Interleukin 8	(LB,TM,SS	3.4
	412978	AH31708	Hs.820	homeo box C6	homeobox,TM,	3.4
	412851	AI826502	Hs.106149	ESTs	TM,SS	3.4
	414812	X72755	Hs.77367	monokina induce	IL8.,SS	3.4
20	453884	AA355925	Hs.36232	KIAA0186 gene p	TM	3.4
20	425921	NM_007231	Hs.162211	solute carrier	SNF,TM,	3.4
	421787	AA227068	Hs.108301	nuclear recepto	TM	3.3
	447342	A1199268	Hs.19322	ESTs .	TM,SS	3.3
	452826	BE245286	Hs.301636	ESTs, Moderatel	AAA,TM,	3.3
25	414821 448756	M63835 AJ739241	Hs.77424	Fc fragment of	ig,TM,SS	3.3
23	421948	L42583	Hs.171480 Hs.111758	ESTs keratin 6A	TM Sharet TM	3.3
	438538	AA832203	Hs.291955	ESTs	filament,TM, TM	3.3 3.3
	436391	AJ227892	Hs.146274	ESTs	SS	3.3 3.3
	418007	M13509	Hs.83169	matrix metallop	hemopexin,Peptidase_M10\$\$	3.2
30	411678	AJ907114	Hs.71465	squalene epoxid	Monooxygenase,TM,	3.2
	422956	BE545072	Hs.122579	hypothetical pr	TM	3.2
	450400	AI694722	Hs.279744	ESTs	ТМ	3.2
	440659	AF134150	Hs.7327	claudin 1	PMP22_Claudin,TM,SS	3.2
35	418203 416111	X54942 AA033813	Hs.83758	CDC28 protein k	CKS,TM,	3.1
55	445808	AV655234	Hs.79018 Hs.298083	chromatin assem ESTs	TM,SS	3.1
	421340	F07783	Hs.1369	decay accelerat	sushi,TM,SS sushi,,SS	3.1 3.1
	422689	AW856665		gb:RC3-CT0297-2	SNF2_N,TM,	3.1
40	439451	AF086270	Hs.278554	heterochromatin	chromo,Chromo_shadow,,SS	3.1
40	454456	AW850984		gb:IL3-CT0220-1	tn3,TM,SS	3.0
	429125	AA446854	Hs.271004	ESTs	TM	3.0
	409361	NM_005982	Hs.54416	sine oculis hom	homeobox,,SS	3.0
	439453 414696	BE264974	Hs.6566	thyroid hormone	AAA,TM,	3.0
45	422746	AF002020 NM_004484	Hs.76918 Hs.119651	Niemann-Pick di	Patched,TM,SS	3.0
	453775	NM_002916	Hs.35120	glypican 3 replication fac	Glypican,TM,SS AAA,TM,SS	3.0 3.0
	428852	NM_000346	Hs.2316	SRY (sex-determ	HMG_box,TM,	2.9
	401747	•••••			filament, TM,	2.9
	429682	NM_006306	Hs.211602	SMC1 (structura	SMC_C,SMC_N,TM,	2.9
50	413385	M34455	Hs.840	indoteamine-pyr	IDO,TM,	2.9
	442961	BE614474	Hs.289074	Homo sapiens cD	TM	2.9
	421650	AA781795	Hs.122587	ESTs	TM	2.9
	434398 435706	AA121098 W31254	Hs.3838	serum-inducible	pkinase,POLO_box,TM,	2.9
55	416065	BE267931	Hs.7045 Hs.78996	GL004 protein proliferating c	PDEase,TM, TM	2.9
-	423493	AI815965	Hs.129683	ubiquitin-conju	UQ_con,,SS	2.9 2.8
	430242	U66669	Hs.236642	3-hydroxylsobut	TM	2.8
	411770	NM_014278	Hs.71992	heat shock prot	HSP70,TM	28
<b>~</b>	400440	X83957	Hs.83870	nebulin	TM	2.8
60	444743	AA045648	Hs.11817	nudix (nucleosi	muT,TM,	2.8
	417771	AA804698	Hs.82547	retinoic acid r	TM	2.8
	430287	AW182459 NM_000676	Hs.125759	ESTs, Weakly si	TM,SS	2.8
	408482 425188	AK002052	Hs.45743 Hs.155071	adenosine A2b r	7tm_1,TM,SS	2.8
65	456999	AA319798	Hs.172247	hypothetical pr eukaryotic tran	TM SS	2.8 2.8
	408875	NM_015434	Hs.48604	DKFZP434B168 or	TM	2.8
	409012	AL117435	Hs.49725	DKFZP434I216 pr	RhoGEF,TM,	27
	410762	AF226053	Hs.66170	HSKM-8 protein	zi-MYND.,SS	27
70	426925	NM_001196	Hs.172894	BH3 interacting	TM	2.7
70	410116	AW630671	Hs.58636	squamous cell c	TM,SS	2.7
	428398	A1249368	Hs.98558	EST8	SS	2.7
	412140 456655	AA219691 AJ376736	Hs.73625 Hs.111779	RAB5 interaction	kinesin,TM,SS	2.7
	408670	AF160967	Hs.46784		kazalSS	2.7
75	422576	BE548555	Hs.118554	potassium farge CGi-83 protein	TM,SS lactamase_B,,SS	2.7 2.7
-	431379	AA504264	Hs.182937		TM	2.7
	433183	AF231338	Hs.222024		HLH,PAS,TM,SS	2.7
	432328	A1572739	Hs.195471	6-phosphofructo	PGAM, 6PF2K, TM.	2.7
80	407633	NM_007069	Hs.37189	similar to rat	TM,SS	2.6
οU	419216	AU076718	Hs.164021		IL8,TM,SS	2.6
	422363 401644	T55979	Hs.115474	replication fac	TM	2.6
	417479	AI057052	Hs.133554	ĖSTs	zi-czh2,tm, card,tm,	26
				2015	CONTRACTOR OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE	2.6



	426514	BE616633	Hs.301122	h		
	400289	X07820	Hs.2258	bone morphogene matrix metallop	TGF-beta,TGFb_propeptide,TM,SS	2.6
	418478	U38945	Hs.1174	cyclin-dependen	hemopexin, SS ank, TM, SS	2.6 2.6
-	421246	AW582962	Hs.300961	ESTs, Highly si	PolyA_pol_TM,	26
5	428048	AA705745	Hs.185070	ESTs	AMP-binding,TM,	2.6
	452092	8E245374	Hs.27842	hypothetical pr	Acyltransferase,TM,SS	2.6
	440052 452401	A1633744	Hs.195648	ESTs	PAC,TM,SS	2.6
	451813	NM_007115 NM_016117	Hs.29352 Hs.27182	tumor necrosis	Xink,CUB,TM,SS	26
10	410889	X91662	H3.66744	phospholipase A twist (Drosophi	WD40,.SS HLH,TM	26
	422063	BE156476		ab:QV0-HT0368-0	SS	26 26
	418250	U29926	Hs.83918	adenosine monop	A_deaminase,TM,	26
	437641	AA811452	Hs.291911	ESTs .	TM	2.6
15	452571	W31518	Hs.34665	ESTs	TM	2.6
13	411984	NM_005419	Hs.72988	signal transduc	SH2,STAT,,SS	26
	426427 445848	M86699 AA774824	Hs.169840 Hs.13377	TTK protein kin	pkinase,TM,	2.6
	420022	AA256253	Hs.120617	Homo sapiens of ESTs	TM SS	2.6
	451418	8E387790	Hs.26369	hypothetical pr	TM	2.6 2.6
20	428953	AA306610	Hs.194676	DKFZP434C013 pr	arf,TNFR_c6,DEAD,Stathmin,TMLSS	2.6
	424008	R02740	Hs.137555	putative chemok	7tm_1,TM,	2.6
	417863	AB000450	Hs.82771	vaccinia relate	pkinase,TM,SS	2.6
	436961	AW375974	Hs.158704	ESTs	TM	2.5
25	413670 421928	AB000115 AF013758	Hs.75470 Hs.109643	hypothetical pr	TM	2.5
	439963	AW247529	Hs.6793	polyadenylate b platelel-activa	SS BAE AN MAC how obligates The	2.5
	426711	AA383471	Hs.180669	conserved gene	PAF-AH,HMG_box,pkinase,TM, TM	25 25
	422631	BE218919	Hs.118793	hypothetical pr	TM	25
20	417866	AW067903	Hs.82772	collagen, type	TSPN,Collagen,COLFL,SS	25
30	416975	NM_004131	Hs.1051	granzyme B (gra	trypsin,,SS	25
	415947	U04045	Hs.78934	mutS (E. coli)	Muts_c, Muts_n, TM,	2.5
	454678 426572	AW813089	U- 430000	gb:RC3-ST0188-2	TPR,Ribosomal_S5,TM,SS	2.5
	428264	AB037783 AA424839	Hs.170623 Hs.98484	hypothetical pr	PH,FYVE,TM,	· 25
35	444478	W07318	Hs.240	ESTs. Weakly si M-phase phospho	TM kinesin,,SS	2.5
	442295	AJ827248	Hs.224398	Homo sapiens cD	Collagen, COLFI, vwc, TM, SS	2.5 2.5
	410094	BE147897	Hs.58593	general transcr	TFIIF_beta,TM,	24
	413998	AW103807	Hs.243933	ESTs	TPR,TM,SS	2.4
40	412281	AI810054	Hs.14119	ESTs	Ribosomal_S7e,TM,	2.4
40	446852	AW451643	Hs.257479	ESTs, Weakly si	TM	2.4
	408915 442991	NM_016651	Hs.48950	heptacellular c	TM,SS	2.4
	410193	BE281238 AJ132592	Hs.8886 Hs.59757	hypothetical pr	TM	2.4
	410664	NM_006033	Hs.65370	zinc finger pro lipase, endothe	zI-C2H2,TM, Ribosomal_L22,fipase,PLAT,TM,SS	2.4
45	423453	AW450737	Hs.128791	CGI-09 protein	Granin,COP-OH_P_transf,TM,	2.4 2.4
	411598	BE336654	Hs.70937	H3 histone fami	histone,,SS	24
	429663	M68874	Hs.211587	phospholipase A	C2,PLA2_B,TM,	2.4
	428242	H55709	Hs.2250	leukemia inhibi	LIF_OSM,,SS	2.4
50	419559 419839	Y07828 U24577	Hs.91096 Hs.93304	ring finger pro	zf-C3HC4.zf-B_box,TM,	24
-	402819	OZ4377	115.53304	phospholipase A	SS IDD TA	2.4
	431457	NM_012211	Hs.256297	integrin, alpha	IBR,TM, FG-GAP,vwa,TM,SS	2.4 2.4
	443683	BE241717	Hs.9676	uncharacterized	DUF157,TM	24
55	422158	L10343	Hs.112341	protease inhibi	wapSS	2.4
55	423217	NM_000094	Hs.1640	collagen, type	fn3,Collagen,Kunitz_BPTI,vwa,.SS	2.4
	408321 419086	AW405882 NM_000216	Hs.44205	cortistatin	TM	2.4
	427722	AK000123	Hs.89591 Hs.180479	Kalimann syndro hypothetical pr	fn3,wap,,SS	24
	405454	AMOUNES	115.100-13	hypothisucal pr	PH,,SS TM	24
60	422168	AA586894	Hs.112408	S100 calcium-bi	efhand,TM,	2.4 2.3
	421462	AF016495	Hs.104624	aquaporin 9	MIP,TM.	2.3
	403416	A1744626	Hs.301506	ESTs. Highly si	SS	2.3
	448988	Y09763	Hs.22785	gamma-aminobuty	neur_chan,TM,SS	2.3
65	423198 419926	M81933 AW900992	Hs.1634	cell division c	Rhodanese,,SS	2.3
05.	429992	AL050053	Hs.93796 Hs.227397	DKFZP588D2223 p	SS	2.3
	446232	AI281848	Hs.165547	Homo sapiens mR ESTs	ha,YM,SS	2.3
	422493	AW474183	Hs.233816	ESTs	7tm_3,TM, TM	2.3
70	407047	X65965		gb:H.sapiens SO	sodfe,TM,	23 23
70	411096	U80034	Hs.68583	mitochondrial i	Peptidase_M3,	2.3
	426457	AW894667	Hs.169965	chimerin (chima	DAG_PE-bind,RhoGAP,TM,	23
	446545	AJ431798	Hs.164192	ESTs. Weakly si	TM	2.3
	422094 421933	AF129535 R98881	Hs.272027	F-box only prot	TM	23
75	430001	A1580056	Hs.109655 Hs.98992	sex comb on mid	SAMTM	2.3
. •	420802	U22376	Hs.1334	ESTs v-myb avian mye	TM TM	2.3
	402053		. 10. 1007	toute enen mile	gpdh,,SS	2.3 2.3
	432743	A1146966	Hs.101656	ESTs	SS SS	2.3 2.3
80	433409	AI278802	Hs.25661	ESTs	PWWP.PHD,bromodomain,TM,	23
OU	408330	AW182602	Hs.249954	ESTs	TM,SS	23
	407807 435972	AL031427 AA284679	Hs.40094	Human DNA seque	T4_deiodinase,TM,	2.3
	433730	AK002135	Hs.25640 Hs.3542	claudin 3 hypothetical pr	PMP22_Claudin,TM,SS	2.3
			122346	"Thousand he	TM,SS	2.3

	414839	X63692	Hs.77462	DNA (cytosine-5	zf-CXXC,BAH,TM,SS	23
	438192	AI859065	Hs.16808	ESTs, Weakly si	TM.SS	23
	415339	NM_015156	Hs.78398	KIAA0071 protei	ELM2,TM,	2.3
5	449539 450956	W80363 AW193531	Hs.58446	ESTs	pkinase, Furin-like, Recep_L_domain, TM, SS	22
,	430335	D80007	Hs.205647 Hs.239499	ESTs, Moderatel	pkinase,TM,SS	2.2
	417849	AW291587	Hs.82733	KIAA0185 protei nidogen 2	S1,TM,	2.2
	412326	R07566	Hs.73817	small inducible	EGF,tdl_recept_b,thyroglobulin_1,TM,SS tL8,,SS	2.2 2.2
	408349	BE546947	Hs.44276	homeo box C10	homeobox,TM,	2.2
10	424704	AI263293	Hs.152096	cytochrome P450	p450_SS	2.2
	409632	W74001	Hs.55279	serine (or cyst	serpin,TM,	2.2
	415323	BE269352	Hs.949	neutrophil cyto	SH3, TPR, TM,	2.2
	417531	NM_003157	Hs.1087	serine/threamin	pkinase,TM,	22
16	403137				mm,TM,SS	2.2
15	428479	Y00272	Hs.184572	cell division c	pkinase,TM,SS	2.2
	430200	BE613337	Hs.234896	geminin	TM,SS	2.2
	425390 408380	AI092634	Hs.156114	protein tyrosin	ig,Optods_neuropep,TM,SS	22
	422424	AF123050 AI186431	Hs.44532 Hs.116577	diubiquitin	ubiquitin,7tm_3.ANF_receptor.sushi,7tm_1,TM,	2.2
20	400298	AA032279	Hs.61635	prostate differ six transmembre	TGF-beta,,\$\$	2.2
	411571	AA122393	Hs.70811	hypothetical pr	TM SS	2.2
	412802	U41518	Hs.74602	aquaporin 1 (ch	MIP,TM,	2.2 2.2
	414761	AU077228	Hs.77256	enhancer of zes	SET.TM.	2.2
0.5	408432	AW195262		gb:xn67b05.x1 N	TMSS	22
25	429568	AI088691	Hs.208414	Homo sepiens mR	mito_carr,TM,	22
	425300	AW601773	Hs.270259	ESTs	TM	2.2
	439653	AW021103	Hs.6631	hypothetical pr	TM,SS	2.2
	426827	AW067805	Hs.172665	methylenetetrah	THF_DHG_CYH,FTHFS,TM,	2.2
30	444514 425322	A)682905	Hs.270431	ESTs. Wealdy si	cNMP_binding.TM,SS	2.2
50	421662	U63630 NM_014141-	Hs.155637	protein kinase.	MCM,TM,	2.2
	438788	AA825716	Hs.106552	cell recognitio	laminin_G,TM,SS	2.2
	429058	AF138863	Hs.194827	gb:od29e10.s1 N	ank,death,RHD,TM,	22
	423104	AJ005273	Hs.123647	hypothetical pr antigenic deter	TM TM	2.2
35	410406	AI969703	Hs.301842	ESTa	FGGY,TM,	2.2
	421379	Y15221	Hs.103982	small inducible	IL8.TM.SS	2.2 2.2
	422809	AK001379	Hs.121028	hypothetical pr	IQ.TM.	2.2
	418049	AA211467	Hs.190488	hypothetical pr	TM	2.2
40	436209	AW850417	Hs.254020	ESTs, Moderater	TM,SS	2.2
40	408042	AL049233	Hs.42244	Homo sapiens mR	TM	2.2
	425692	090041	Hs.155956	N-acetyltransfe	Acetyltransf2,TM,	2.2
	409665 428157	NM_006731	Hs.55777	Fukuyama type c	SS	2.2
	410480	AJ738719 R97457	Hs.298668	ESTs	hexokinase,TM,	2.2
45	429732	U20158	Hs.63984 Hs.2488	cadherin 13, H-	cadherin,TM,SS	22
	414747	U30872	Hs.77204	lymphocyte cyto centromere prot	SH2,TM, SS	2.2
	425843	BE313280	Hs. 159627	death associate	TM	2.2
	445299	AI910382	Hs.118727	Homo sapiens cD	HLH,TM,	2.2 2.1
	436251	BE515065	Hs.5092	nucleolar prote	Nop,TM,SS	2.1
50	430066	AI929659	Hs.237825	signal recognit	TPR.\$\$	2.1
	427528	AU077143	Hs.179565	minichromosome	MCM,TM,SS	2.1
	448089	AI467945	Hs.173696	ESTs	TM,SS	21
	428728	NM_016625	Hs.191381	hypothetical pr	TM	2.1
55	409929 405264	R38772	Hs.172619	KIAA1106 protei	TM	2.1
55	445625	BE246743	Hs.288529	Hama andres - O	SS	2.1
	408949	AF189011	Hs.49163	Homo sapiens cD putative ribonu	TM	21
	424513	BE385864	Hs.149894	mitochondrial t	Ribonuclease_3,TM,\$S	2.1
	433683	AI817723	Hs.22678	hypothetical pr	GTP_EFTU,IF2,TM, SS	2.1
60	442952	AJ743261	Hs.131860	ESTs	TM	2.1
	432378	AI493048	Hs.146133	ESTs	TM	21 21
	417979	AU077284	Hs.83081	GTP cyclohydrol	TM.SS	21
	433849	BE465884	Hs.280728	ESTs	SS	21
65	437928	NM_005476	Hs.5920	UDP-N-acetylglu	ROK, Epimerase_2, TM,	2.1
05	403055				filament, TM, SS	2.1
	432840	AK001403	Hs.279521	hypothetical pr	TM	21
	418994	AA296520	Hs.89546	selectin E (end	EGF, lectin_c.sushi, TM, SS	2.1
	440908 417621	AI915225	Hs. 126735	ESTs	TM	2.1
70	436895	AV654694 AF037335	Hs.82316 Hs.5338	interferon-indu carbonic anhydr	TM	2.1
	408420	NM_006915			carb_anhydrase,TM,SS	21
	434064	AL049045	Hs.299481 Hs.180758	Homo sapiens mR hypothetical pr	TM codhain TM SS	2.1
	404076		1007 30	- in provious pr	cadherin,TM,SS RmaAD,TM,	2.1
	422515	AW500470	Hs.117950	multifunctional	AIRC,SAICAR_synLTM,	2.1
75	445867	AF272663	Hs.13405	gephyrin	MoCF_biosynth_TM,	21
	441021	AW578716	Hs.7644	H1 histone fami	finker_histone, TM,	2.1 2.1
	446595	T57448	Hs.15467	hypothetical pr	TMSS	21
	417515	L24203	Hs.82237	ataxia-telangle	zf-B_box.,SS	21
80	412429	AV650262	Hs.75765	GRO2 oncogene	ILB,TM,SS	21
80	449207	AL044222	Hs.23255	nucleoporin 155	TM,SS	21
	412095	AI624707	Hs.5921	Homo sapiens cD	TMLSS	2.1
	400861	AA431599	Un 40030-		pkinasa,TM,	2.1
	440591	WW 1223	Hs.132799	Homo saplens cD	ТМ	2.1



	442104	L20971	Hs.168	phosphodiestera	PDEase,TM,	21
	446921	AB012113	Hs.16530	small inducible	ILB,,SS	2.1
	446051	BE048061	Hs.153315	ESTs ·	Reprolysin, Pep_M128_propep,TM,SS	2.1
5.	422675	BE018517	Hs.119140	eukaryotic tran	eIF-Sa,TM,	2.1
٦.	425170	AU077315	Hs.154970	transcription (	TM	21
	453751	R36762	Hs.101282	Homo sapiens mR	TM	21
	426283	NM_003937	Hs.169139	kynureninase (L	TM	2.1
	417874	BE616160	Hs.82829	protein tyrosin	Y_phosphatase,TM,	2.1
10	449555	AW450288	Hs.195390	ESTs	TM	2.1
10	439699	AF085534	Hs.187561	ESTs, Moderatel	TM	2.1
	427413	BE547647	Hs.177781	superoxide dism	sodfe,TM,	2.1
	407802	D84145	Hs.39913	novel RGD-conta	hexapep,TM,SS	2.0
	446035	NM_006558	Hs.13565	Sam68-like phos	TM	20
16	406981	S71129	Hs.296844	Acetylchofinest	COesterase,TM,SS	2.0
15	432343	NM_002960	Hs.2961	S100 calcium-bi	S_100,efhand,TM,SS	2.0
•	414890	BE281095	Hs.77573	uridine phospho	PNP_UDP_1,TM,SS	2.0
	423019	A1840185	Hs.225816	ESTs	SS	20
	422278	AF072873	Hs.114218	trizzled (Droso	Fz,Frizzled,TM,SS	2.0
20	405545				ABC_tran_ABC_membrane,TM,SS	20
20	446237	AW270515	Hs.149596	EST8	6ZIP.TM.	20
	428074	BE387770	Hs.182378	colony stimulat	SS	2.0
	423430	AF112481	Hs.128501	RAD54, S. cerev	SNF2_N,helicase_C,TM,	20
	435767	H73505	Hs.117874	ESTs	Pepiidase_S8,P,TM,	20
~~	432945	AL043683	Hs.271357	ESTs. Wealtly si	PK_SS	20
25	404170				sodfe,TM,	2.0
	422610	AF153820	Hs.1547	potassium inwar	IRKTM	2.0
	417933	X02308	Hs.82952	thymidylate syn	thymidylat_synt,.SS	2.0
	441384	AA447849	Hs.288660	protease, serin	TM	2.0
• •	414020	NM_002984	Hs.75703	small inducible	ILB,,SS	2.0 .
30	427674	NM_003528	Hs.2178	H29 histone fam	histone,TM,SS	2.0
	435425	H16263	Hs.31416	ESTs	TM	2.0
	429782	NM_005754	Hs.220689	Ras-GTPase-acti	rm,NTF2,,SS	2.0
	417366	BE185289	Hs.1076	small proline-r	Cornifin, TM,	2.0
2.0	426746	J03626	Hs.2057	uridine monopho	Pribosyltran, OMPdecase, TM,	2.0
35	432677	NM_0044B2	Hs.278611	UDP-N-acetyl-al	Glycos_transf_2,Ricin_B_tectin,TM,	2.0
				•		
	TABLE 43					
	Pkey:	Uniq	ue Eos probes	et identifier number		
4.0	CAT numb	ber: Gene	cluster numb	er		
40	Accession	Cool	ank accession	a aumhara		
				i ildiideia		
		i. Gent	~~ ~~~~	i numbers		
	Pkey	CAT number	Accession	in numbers		
	Pkgy 408432	CAT number 1058667_1	Accession	R27868 AW811262		
	Pkey	CAT number	Accession AW195262	R27868 AW811262		
.45	Pkey 408432 411560 422063	CAT number 1058667_1	Accession AW195262 AW851186	R27868 AW811262 AW996987 BE143456	6475 AA302839	
.45	Pkey 408432 411560	CAT number 1058667_1 1249443_1	Accession AW195262 AW851186 BE1564761	R27868 AW811262 AW996987 BE143456 BE156473 BE156474 BE15		
.45	Pkey 408432 411560 422063	CAT number 1058667_1 1249443_1 210852_1	Accession AW195262 AW851186 BE1564761 Al803103 A	R27868 AW811262 AW996987 BE143456 BE156473 BE156474 BE15 J885143 AW470793 AW450	6475 AA302839 0703 AU090784 AW271587 AW236950 AW242783	
.45	Pkey 408432 411560 422063 422285	CAT number 1058667_1 1249443_1 210852_1 214669_1	Accession AW195262 AW851186 BE156476 I AI803103 A AW856665	R27868 AW811262 AW996987 BE143456 BE156473 BE156474 BE15 1885143 AW470793 AW450 AA315006 AW954733		
	Pkey 408432 411560 422063 422285 422689	CAT number 1058667_1 1249443_1 210852_1 214669_1 219896_1	Accession AW195262 AW851186 BE1564761 AI803103 A AW856665 AA331908	R27868 AW811262 AW996987 BE143456 BE156473 BE156474 BE15 1885143 AW470793 AW450 AA315006 AW954733 AA312484		
.45	Pkey 408432 411560 422063 422285 422689 423871	CAT number 1058667_1 1249443_1 210852_1 214669_1 219896_1 232749_1	Accession AW195262 AW851186 BE1564761 AI803103 A AW856665 AA331908	R27868 AW811262 AW996887 BE143456 BE156473 BE156474 BE15 I885143 AW470793 AW450 AA315006 AW954733 AA322484 AW978859 AA828841		
	Pkey 408432 411560 422063 422285 422689 423871 438788	CAT number 1058667_1 1249443_1 210852_1 214669_1 219896_1 232749_1 465159_1	Accession AW195262 AW851186 BE1564761 AI803103 A AW856665 AA331908	R27868 AW811262 AW996987 BE143456 BE156473 BE156474 BE15 J885143 AW470793 AW450 AA315006 AW954733 AA312484 AW978859 AA828841 AW758356 M86124		
	Pkey 408432 411560 422063 422285 422689 423871 438788 454456 454678	CAT number 1058667_1 1249443_1 210852_1 214669_1 212689_1 232749_1 465159_1 1207088_1 1228915_1	Accession AW195262 AW851186 BE1564761 AI803103 A AW856685 AA331906 AA825716 AW850984	R27868 AW811262 AW996987 BE143456 BE156473 BE156474 BE15 J885143 AW470793 AW450 AA315006 AW954733 AA312484 AW978859 AA828841 AW758356 M86124		
	Pkey 408432 411560 422063 42285 422689 423871 438788 454456	CAT number 1058667_1 1249443_1 210852_1 214669_1 212689_1 232749_1 465159_1 1207088_1 1228915_1	Accession AW195262 AW851186 BE1564761 AI803103 A AW856685 AA331906 AA825716 AW850984	R27868 AW811262 AW996987 BE143456 BE156473 BE156474 BE15 J885143 AW470793 AW450 AA315006 AW954733 AA312484 AW978859 AA828841 AW758356 M86124		
50	Pkey 408432 411560 422063 422285 422689 423871 438788 454456 454678	CAT number 1058667_1 1249443_1 210852_1 214869_1 232749_1 465159_1 1207088_1 1228915_1 3C:	Accession AW195262 AW851186 BE1564761 AI803103 A AW853665 AA331906 AA825716 AW850884 AW813089	R27868 AW811262 AW996987 BE143456 BE156473 BE156474 BE15 B85143 AW420793 AW450 AA315006 AW954733 AA312484 AW978859 AA828841 AW752836 M86124 W28102		
	Pkey 408432 411560 422063 422285 422689 423871 438788 454456 454678	CAT number 1058667_1 1249443_1 210852_1 214669_1 219996_1 455159_1 1207088_1 1228915_1 3C: Unique num Sequence :	Accession AW195262 AW851186 BE156476 ( AI803103 A AW856665 AA331996 ( AA825716 - AW850984 AW813089	R27868 AW811262 AW996987 BE143456 BE156473 BE156474 BE15 B85143 AW470793 AW450 AA315006 AW954733 AA312484 AW978859 AA828841 AW752836 M86124 W28102 Mding to an Eos probeset digit numbers in this column	0703 Al090784 AW271587 AW235950 AW242783	t gl." refers to the publication entitled "The DNA sequence of
50	Pkey 408432 411560 422063 422685 422689 423871 438788 454456 454678 TABLE 4: Pkey:	CAT number 1058667_1 1249443_1 210852_1 214669_1 219896_1 232749_1 465159_1 1207088_1 1228915_1 3C: Unique num Sequence : human chro	Accession AW195262 AW851186 BE 156476; Al803103 A AW856685 AA331905 A AW859384 AW813089 https://doi.org/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.100	R27868 AW811262 AW996987 BE143456 BE156473 BE156474 BE15 J885143 AW470793 AW450 AA315006 AW954733 AA312484 AW978859 AA828841 AW752836 M86124 W28102 Mding to an Eos probeset digit numbers in this column	0703 Al090784 AW271587 AW236950 AW242783 n are Genbank Identifier (GI) numbers. "Dunham, e re 402489-495.	t al." refers to the publication entitled "The ONA sequence of
50	Pkey 408432 411560 422063 422063 422689 423871 438788 454456 454678 TABLE 45 Pkey: Ref:	CAT number 1058667_1 1249443_1 210852_1 214669_1 2132749_1 455159_1 1207088_1 1228915_1 3C:  Unique num Sequence : human chrit Indicates D	Accession AW195262 AW851186 BE156476 AI803103 A AW856665 AA331906 AA855716 AW85084 AW813089 AW813089 AW813089 AW813089 AW813089	R27868 AW811262 AW996987 BE143456 BE156473 BE156474 BE15 1885143 AW470793 AW450 AA315006 AW954733 AA312484 AW978859 AA828841 AW752836 M86124 W28102 Inding to an Eos probeset digil numbers in this column Dunham, et al. (1999) Natur unblick exons were predicti	0703 Al090784 AW271587 AW236950 AW242783 n are Genbank Identifier (GI) numbers. "Dunham, e re 402489-495.	tal." refers to the publication entitled "The DNA sequence of
50	Pkey 408432 411560 422063 422063 422689 423871 438788 454456 454678 TABLE 45 Pkey: Ref:	CAT number 1058667_1 1249443_1 210852_1 214669_1 2132749_1 455159_1 1207088_1 1228915_1 3C:  Unique num Sequence : human chrit Indicates D	Accession AW195262 AW851186 BE156476 AI803103 A AW856665 AA331906 AA855716 AW85084 AW813089 AW813089 AW813089 AW813089 AW813089	R27868 AW811262 AW996987 BE143456 BE156473 BE156474 BE15 1885143 AW470793 AW450 AA315006 AW954733 AA312484 AW978859 AA828841 AW752836 M86124 W28102 Inding to an Eos probeset digil numbers in this column Dunham, et al. (1999) Natur unblick exons were predicti	0703 Al090784 AW271587 AW236950 AW242783 n are Genbank Identifier (GI) numbers. "Dunham, e re 402489-495.	t al." refers to the publication entitled "The DNA sequence of
50	Pkey 408432 411560 422063 422063 422689 423871 438788 454456 454678 TABLE 45 Pkey: Ref:	CAT number 1058667_1 1249443_1 210852_1 214669_1 2132749_1 455159_1 1207088_1 1228915_1 3C:  Unique num Sequence : human chrit Indicates D	Accession AW195262 AW851186 BE156476 AI803103 A AW856665 AA331906 AA855716 AW85084 AW813089 AW813089 AW813089 AW813089 AW813089	R27868 AW811262 AW996987 BE143456 BE156473 BE156474 BE15 J885143 AW470793 AW450 AA315006 AW954733 AA312484 AW978859 AA828841 AW752836 M86124 W28102 Mding to an Eos probeset digit numbers in this column	0703 Al090784 AW271587 AW236950 AW242783 n are Genbank Identifier (GI) numbers. "Dunham, e re 402489-495.	t al." refers to the publication entitled "The ONA sequence of
50	Pkey 408432 411560 422083 422083 422689 423871 438788 454456 454678 TABLE 4! Pkey; Ref: Strand: NL positio	CAT number 1058667_1 1249443_1 210852_1 214669_1 2132749_1 455159_1 1207088_1 1228915_1 3C:  Unique num Sequence : human chrit Indicates D	Accession AW195262 AW851186 BE156476 AI803103 A AW856665 AA331906 AA855716 AW85084 AW813089 AW813089 AW813089 AW813089 AW813089	R27868 AW811262 AW996987 BE143456 BE156473 BE156474 BE15 1885143 AW470793 AW450 AA315006 AW954733 AA312484 AW978859 AA828841 AW752836 M86124 W28102 Adding to an Eos probeset digil numbers in this column Dunham, et al. (1999) Natur unblick exons were predicti	0703 Al090784 AW271587 AW236950 AW242783 n are Genbank Identifier (GI) numbers. "Dunham, e re 402489-495.	t al." refers to the publication entitled "The DNA sequence of
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50 55 60 65	Pkey 408432 411560 422063 422265 422669 423871 438788 454456 454678 TABLE 4: Pkey: Ref: Strand: NL positic 401644 401747 402053 402819 403055 403137 40376 404170 405454 405454	CAT number 1058667_1 1249443_1 210852_1 214669_1 214669_1 232749_1 1455159_1 1207088_1 1228915_1 1307088_1 1228915_1 1016128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 11406128150 1140612815	Accession AW195262 AW851186 BE1564761 AI803103 A AW856665 AA311906 AA825716 AW850984 AW813089  The correspondence of the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the followi	R27868 AW811262 AW996987 BE143456 BE156473 BE156474 BE15 BE5143 AW470793 AW450 AA315006 AW954733 AA332484 AW978859 AA828841 AW752836 M86124 W28102 Adding to an Eos probeset digit numbers in this column Dunham, et al. (1999) Natur n which exons were predictions of predicted exons. ML position 163855-164016 82655-83959 118598-118816,119119- 131932,132451-132575, 62703-63179 29217-29422 109532-110225 92349-92572,92958-93( 1414-1513,1624-1756) 3848-3967 168836-169248 28556-28684 133807-134053	n are Genbank Identifier (GI) numbers. **Ounham, e g 402-489-495. ed. -119244,119609-119761,120422-120990,130161-13	30381,130468-130593,131097-131258,131866-

TABLE 44A: ABOUT 314 GENES DOWN-REGULATED IN STOMACH CANCER
Table 44A lists about 314 genes significantly down-regulated in stomach cancer compared to normal stomach. These were selected as for Table 42A, except that the numerator and denominator were switched.

Pkey:

ExAccn:

Unique Ecs probeset identifier number

ExAccn:

Unique Ecs probeset identifier number

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Unique number:

Unique number:

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	Unigeno Ti R1:		ena gane title of turnor to norm	nal tissue	
_	Pkey	ExAcon	UnigenelD	Unigene Title	RI
5	412859	NM_000705	Hs.813	ATPase, H+fK+ exchanging, beta polypepti	0.01
	415447	297171	Hs.78454	myocilin, trabecular meshwork inducible	0.05
	427469	AA403084	Hs.269347	ESTs	0.05
	407486 428602	S69741	11- 400000	gb:hSCG-3=stomach cancer gane-3 (oncogen	0.06
10	402761	AL137479 BE387621	Hs. 186655 Hs. 108809	Homo sapiens mRNA; cDNA DKFZp434M0223 (1	0.06
	443547	AW271273	Hs.23767	chaperonin containing TCP1, subunit 7 (e	0.07
	430130	AL137311	Hs.234074	Homo sapiens cDNA FLJ12666 ffs, clone NT Homo sapiens mRNA; cDNA DKFZp761G02121 (	0.07
	435473	N53650	Hs.260881	ESTs	0.07
	455826	BE144228		gb:MR0-HT0165-140200-009-d04 HT0165 Homp	0.07 0.07
15	402015				0.07
	430664	AW969834		gb:EST381912 MAGE resequences, MAGK Homo	0.09
	444515	AW204908	Hs.169979	ESTs	0.09
	429201	X03178	Hs.198246	group-specific component (vitamin D bind	0.10
20	434424 450940	AI811202 AI744943	Hs.125365	Homo sapiens cDNA: FLJ23523 ffs, clone L	0.10
	400811	AF219139	Hs.300744 Hs.87726	ESTs, Moderately similar to ALU7_HUMAN A	0.10
	424596	AB020639	Hs.151017	KIAA0154 protein; ADP-ribosylation facto estrogen-related receptor gamma	0.10
	403670			monder were of receiping designs	0.11 0.11
25	410234	NM_003837	Hs.61255	fructose-1,6-bisphosphatase 2	0.11
25	407462	AJ252011		gb:Homo sapiens partial mRNA for amilori	0.13
	405110				0.13
	402760 408947	A1 000003	Ha 40443		0.13
	413724	AL080093 AA131466	Hs.49117 Hs.23767	Homo sepiens mRNA; cDNA DKFZp564N1662 (f	0.13
30	431514	AW972383	15.23/0/	Home sepiens cDNA FLJ12666 fls, clone NT	0.14
	451103	R52804	Hs.25956	gb:EST384454 MAGE resequences, MAGL Homo DKFZP564D206 protein	0.14
	452033	AW273741	Hs.246977	ESTs	0.14 0.16
	440058	AJ932662	Hs.164073	ESTs	0.16
25	405645				0.17
35	429093	NM_000253	Hs.195799	microsomal triglyceride transfer protein	0.17
	445627 425679	AW818475	Hs.7363	EST _B	0.19
	417296	X05997 L36196	Hs.159177 Hs.81884	lipase, gastric	0.19
	443537	013305	Hs.203	suffotransferase family, cytosolic, 2A, cholecystokinin B receptor	0.19
40	435654	AW139612	Hs.131041	ESTs	0.20
	406326			20.0	0.20 0.20
	454120	AB032990	Hs.40719	hypothetical protein KIAA1164	0.20
	455541	AW993005		gb:RC2-BN0032-160200-013-d04 BN0032 Homo	0.21
45	453989	M63962	Hs.36992	ATPase, H+/K+ exchanging, alpha polypept	0.23
7.7	407261 451062	L03172 AL110125	He Benen	gb:Homo sapiens cell-type T-cell immunog	0.23
	429350	AI754634	Hs.25910 Hs.131987	Homo sapiens mRNA; cDNA DKFZp564C1416 (1 ESTs	0.23
	411021	F00055	Hs.172004	itin	0.23
	441212	AW242447	Hs.146182	ESTs, Wealty similar to lactase phlorizi	0.24 0.24
50	450572	A1700863	Hs.202494	Homo sapiens cONA FL113245 fis, clone OV	0.25
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fls, clone PL	0.26
	421562	AA530994	Hs.105803	ghrelin precursor	0.26
	457432 418421	NM_005136 R58620	Hs.268538	potassium voltage-gated channel, lsk-rel	0.26
55	424104	AA669515	Hs.85050 Hs.144950	phospholamban ESTs	0.26
	422582	AA312660	113.144330	gb:EST 183335 Jurket T-cells VI Homo sapi	0.26
	417332	AW972717	Hs.288462	Homo sapiens cONA: FLJ21511 fis, clone C	0.26 0.27
	432440	X63597	Hs.2996	sucrase-isomaltase	0.27
60	448520	AB002387	Hs.21355	doublecortin and CaM kinase-like 1	0.28
vv	401989 452528	AA742457	No one one		0.28
	412569	H63789	Hs.291479 Hs.296288	ESTs	0.28
	434779	AF153815	Hs.50151	ESTs, Weakly similar to KIAA0638 protein potassium inwardly-rectifying channel, s	0.28
	406255		. 12.90151	potession inwarply-recorying criarines, a	0.28
65	419293	AA746282	Hs.255659	EST ₈	0.29 0.29
	428649	AL045716	Hs.188228	Homo sapiens cDNA FLJ11003 ffs, clone PL	0.29
	410036	R57171	Hs.57975	calsequestrin 2, cardiac muscle	0.29
	414502	AL133721	Hs.224680	ESTs	0.29
70	432113 413808	AA935065 J00287	Hs.152385	ESTs	0.29
	451406	AI694320	Hs.182183 Hs.6295	celdesmon 1 ESTs Worth similar in 717748 honothad	0.29
	434745	AW974445	Hs.185155	ESTs, Weakly similar to T17248 hypotheti ESTs, Weakly similar to HuEMAP (H.sapien	0.29
	420444	AI905985	Hs.111805	ESTs Treaty surmar to received (resamen	0.30 0.30
76	445200	AA084460	Hs.12409	somatostatin	0.30
75	415314	N88802	Hs.5422	glycoprotein M6B	0.30
	427019	AA001732	Hs.173233	hypothetical protein FLI10970	0.30
	431152	AW970998	Lb 374345	gb:EST383083 MAGE resequences, MAGK Homo	0.30
	432306 401775	Y18207	Hs.274315	protein phosphatase 1, regulatory (inhib	0.31
80	440059	AW467335	Hs.257676	ESTs	0.31
	436089	AA804957	Hs.119840	ESTs	0.31 0.31
	447071	AW236867	Hs.244376	ESTs	0.31
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	0.32



	423958	AF098277	Hs.136529	solute carrier family 23 (nucleobase tra	0.32
	445487	AI806287	Hs.201217	ESTs	0.32
	421296	NM_002668	Hs.103253	perilipin	0.32
_	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 28	0.33
5	449916	T50525	Hs.299221	ESTs	0.33
	446393	AW014174	Hs.151707	ESTs	0.33
	445632	AI333565	Hs.159073	diacylglycerol kinase, eta	0.33
	428070	T63918	Hs.182313	retinol-binding protein 2, cellular	0.33
	421451	AA291377	Hs.50831	ESTs Control 2, Control	0.33
10	405817	74451511	13.50001	2013	0.33
. •	454790	AW820852		ANDCO CT0001 100000 014 440 070004 44	
				gb:RC2-ST0301-120200-011-f12 ST0301 Homo	0.33
	413679	BE156765		gb:RC1-HT0370-120100-012-c09 HT0370 Homo	0.34
	404121				0.34
16	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	0.34
15	413079	BE064382		gb:RC4-8T0310-110300-015-c12 BT0310 Homo	0.34
	403059				0.35
	458987	AW750067	Hs_205386	ESTs	0.35
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	0.35
	423371	AU076819	Hs.1650	solute carrier family 26, member 3	0.35
20	424765	AA428211	Hs.284256	hypothetical protein FLJ 14033 similar to	0.35
	451818	AI819018		gb:ts54f01.x1 NOI_CGAP_Kid8 Homo sagiens	0.35
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	0.35
	405742				0.35
	403429				0.35
25	443622	AI911527	Hs.11805	ESTs .	0.36
	404973			2013	0.36
	444567	AV654020	Hs.184261	ECTs Mankly similar to sudalius has II	
	412228	AW503785	Hs.73792	ESTs, Weakly similar to putative type II	0.36
	407110	AA018042		complement component (3d/Epstein Barr vi	0.36
30			Hs.95078	ESTs	0.36
30	411671	BE049094	Hs.278567	ESTs	0.36
	430800	NM_000805	Hs.2681	gastrin	0.36
	454560	AW807281		gb:MR4-\$T0062-240300-003-g01 \$T0062 Homo	0.36
	444536	AJ161068	Hs.14780	ESTs	0.36
~ ~	454042	H22570	Hs.172572	hypothetical protein FLJ20093	0.37
35	444102	AV647953	Hs.282379	ESTs	0.37
	424122	AA335593	Hs.116147	ESTs	0.37
	452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	0.37
	436277	R88520	Hs.120917	ESTs	0.37
	456350	BE246762	Hs.89499	arachidonate 5-lipoxygenase	0.37
40	451027	AW519204	Hs.40808	ESTs	0.37
• •	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	0.38
	410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	0.38
	436802	N34486	Hs.170504	ESTs	
	448142	AJ521768	Hs.164586	ESTS	0.38
45	442378	R54033			0.38
73			Hs.21245	EST8	0.38
	446406	AI553681	Hs.25248	ESTs	0.38
	455753	BE075124		gb:PM1-BT0585-110200-003-h02 BT0585 Homo	0.38
	424903	T26477	Hs.22883	ESTs, Weakly similar to ALU8_HUMAN ALU S	0.38
60	406714	AJ219304	Hs.283108	hemoglobin, gamma G	0.39
50	434340	AI193043	Hs.128685	ESTs	0.39
	406036				0.39
	431078	U82827	Hs.249195	homeo bax A13	0.39
	457663	AW371946	Hs.116119	ESTa	0.39
	451880	AJ821032	Hs.209387	ESTs	0.39
55	419219	AW583139	Hs.89717	carboxypeptidase A2 (pancreatic)	0.39
	446414	W93246	Hs.59187	ESTs	0.39
	442317	Al915599	Hs.129225	ESTs	0.39
	447261	NM_006691		lymphatic vessel endothelial hyaluronan	0.39
	439569	AW602166	Hs.222399	CEGP1 protein	0.39
60	433485	AJ493076	Hs.78183	aldo-keto reductase family 1, member C1	0.40
	432753	NM_014075		PRO0593 protein	0.40
	420200	AI271429	Hs.88142	ESTs	
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DXFZp434P228 (fr	0.40
	453950	AA156998	Hs.211568		0.40
65	407408	AF054830	PIS.211300	eukaryotic translation Initiation factor	0.40
UJ	410732	AW984328		gb:Homo sapiens interleutin-1 type I rec	0.40
			11-001000	gb:PM3-HN0010-050400-001-h12 HN0010 Homo	0.40
	458272	AI797360	Hs.264899	ESTs. Weakly similar to ALU3_HUMAN ALU S	0.40
	401514	AF147188		gb:AF147186 Homo sapiens library (Schere	0.40
70	436363	AA843926	Hs.124434	ESTs	0.40
70	434445	Al349306	Hs.11782	ESTs	0.40
	413272	AA127923	Hs.293256	ESTs	0.40
	409681	N51508	Hs.143718	ESTs	0.40
	454554	AW847505		gb:RC0-CT0210-280999-021-c10 CT0210 Homo	0.40
	450891	AI743118	Hs.238914	ESTs, Wealdy similar to neurogulin-4 sho	0.40
75	452078	AA022620	Hs.52170	ESTs	0.41
-	419278	AU076799	Hs.1247	apolipoprotein A-IV	0.41
	433637	AW024214	Hs.135405	ESTS	0.41
	449923	BE258051	110.100700		
	416982	J05401	Hs.80691	gb:601111034F1 NIH_MGC_16 Homo sapiens c	0.41
80	453139	AA330620		creatine kinase, mitochondrial 2 (sarcom	0.41
30	408614		Hs.240559	ESTs	0.41
		AL137698	Hs.46531	Horno sapiens mRNA; cDNA DKFZp434C1915 (f	0.41
	437931	A1249468	Hs.145274	ESTs	0.41
	402759				0.41

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	450888	AW021446	Hs.80714	<b>ESTs</b>	0.41
	417318	AW953937	Hs.12891	ESTs	0.41
	407244 424884	M10014 AW299437	Hs.75431 Hs.225717	fibrinogen, gamma polypeptide ESTs	0.41
5	439024	R96696	Hs.35598	ESTs	0.41 0.42
	423732	AF058056	Hs.132183	solute carrier family 16 (monocarboxylic	0.42
	409300	AA126190		gb:zm78f03.r1 Stratagene neuroepithelium	0.42
	444237	AA336878	Hs.9842	Human DNA sequence from clone RP4-788L20	0.42
10	425860 447021	L29339 Al356564	Hs.1964 Hs.161406	solute carrier family 5 (sodium/glucose ESTs	0.42
	422270	AF114494	Hs.114062	protein tyrosine phosphatase-like (profi	0.42 0.42
	407850	AW086230	Hs.244912	ESTs	0.42
	449884	AI673110	Hs.222195	ESTs	0.42
15	436327	AA813075	Hs.120181	ESTs	0.42
13	415972 400917	H11438	Hs.260201	ESTs	0.42
	435309	AW089050	Hs.187993	ESTs	0.43 0.43
	424410	W79027	Hs.271762	ESTs	0.43
20	445577	N40696	Hs.146077	ESTs	0.43
20	411069 440286	AL133092 U29589	Hs.68055	hypothetical protein DKFZp434l0428	0.43
	451123	A1927224	Hs.7138 Hs.213480	cholinergic receptor, muscarinic 3 ESTs	0.43 0.43
	457151	AW206116	Hs.253538	ESTs	0.43
26	459185	AI908222		gb:RC-BT165-300399-020 BT165 Homo sapien	0.43
25	411607	AW853498		gb:RC1-CT0252-170200-025-h02 CT0252 Homo	0.43
	424815 429704	AA347287 AA584440	Hs.104573 Hs.185812	ESTs SET-	0.43
	411067	AI681006	Hs.301543	ESTs ESTs	0.43 0.43
20	430172	AA468591	Hs.161889	ESTs	0.43
30	435124	AA725362	Hs.120456	ESTs	0.43
	445966 443741	L17330	Hs.280	pre-T/NK cell associated protein	0.43
	416275	AW451759 H42823	Hs.145420 Hs.155742	ESTs	0.43
	451138	W92287	Hs.40268	glyoxylate reductase/hydroxypyruvate red ESTs	0.44 0.44
35	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	0.44
	426730	AL040738		gb:DKFZp43481615_r1 434 (synonym; htes3)	0.44
	410066 427965	AL117664 D00306	Hs.58419	DKFZP586L2024 protein	0.44
	418026	BE379727	Hs.183864 Hs.83213	elastase 38 fatty acid binding protein 4, adipocyte	0.44
40	408479	BE047329	Hs.144483	ESTs	0.44 0.44
	457994	AW136239	Hs.132922	ESTs	0.44
	435564	AF210652	Hs.16614	5(3)-deoxyribonucleotidase (dNT-2); nucl	0.45
	435869 434399	AF255910 AAB78845	Hs.54650 Hs.125769	vascular endothelial junction-associated	0.45
45	415797	AI291896	Hs.72800	ESTs ESTs	0.45 0.45
	430264	AA470519	1.5.12000	gb:nc71f10.s1 NCI_CGAP_Pr1 Homo sapiens	0.45
	409435	AI810721	Hs.95424	ESTs	0.45
	433542	AA598869	Hs.173770	ESTs	0.45
50	455400 412047	AW936342 AA934589	Hs.49695	gb:QV4-DT0021-281299-070-h12 DT0021 Homo ESTs	0.45
•	443948	T56148	Hs.9997	Homo sepiens mRNA full length insert cDN	0.45 0.45
	450307	AW450336	Hs.201783	ESTs	0.45
	434500	AF143877	Hs.215047	Homo sapiens clone fMAGE:113431 mRNA seq	0.45
55	420460 450752	AA262331 AA012986	Hs.135503 Hs.60466	ESTs	0.45
-	418138	AA213626	Hs.136204	ESTs EST	0.45 0.45
	441088	AA916546	Hs.126546	ESTs	0.46
	410990	AW812929		gb:RC3-ST0186-250200-018-c05 ST0186 Homo	0.46
60	438211 434349	T08401	14. 2004	gb:EST06292 Infant Brain, Bento Soares H	0.46
oo	409824	NM_015678 AW501063	Hs.3821	neurobeachin	0.46 0.46
	403279			gb:UI-HF-BP0p-aiz-c-01-0-UI.r1 NIH_MGC_5	0.46
	434882	AW974752	Hs.269497	ESTs	0.46
65	404529				0.46
05	427393 454651	AB029018 AW812091	Hs.177635	KIAA1095 protein	0.46
	401992	A11012031		gb:RC4-ST0173-191099-032-b04 ST0173 Homo	0.46 0.46
	457275	AA463422	Hs.209431	ESTs	0.46
70	403710				0.46
70	419728	L36861	Hs.92858	guanylate cyclase activator 1A (retina)	0.46
	401075 421387	AF059566	Hs.103983	solute envise family & facility indide	0.46
	453404	AA035446	Hs.261224	solute carrier family 5 (sodium lodide s ESTs	0.46 0.48
76	407208	T10695	Hs.102948	enigma (LIM domain protein)	0.46
75	440681	AW449696	Hs.166547	ESTs	0.46
	454208 402466	AW810279		gb:MR4-ST0125-151299-029-809 ST0125 Homo	0,47
	429996	N90822	Hs.48969	ESTs	0.47 0.47
00	403680				0.47
80	428151	AA422028		gb:zv26g06.r1 Soares_NhHMPu_S1 Homo sapi	0.47
	410495 402851	N95428		gb:zb80d09.s1 Soares_senescent_fibroblas	0.47
	438421	AAB06907	Hs.194451	ESTs .	0.47
				_010	0.47

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	454661	BE244138		gb:TCBAP1E1218 Pediatric pre-8 cell acut	0.47
	408753	AJ337192	Hs.47438	SH3 domain binding glutamic acid-rich pr	0.47
	409106 413199	AW337854	Hs.177386	ESTs	0.47
5	442799	M62843 AL564739	Hs.75236 Hs.68505	ELAV (embryonic lethal, abnormal vision, ESTs	0.47
•	457955	AI208986	Hs.143945	ESTs	0.47 0.47
	458147	AW752597	18.17070	gbdL3-CT0214-161299-045-B06 CT0214 Horno	0.47
	407938	AA905097	Hs.85050	phospholamban	0.47
	414141	BE255083		gb:601111390F1 NIH_MGC_16 Homo sapiens c	0.47
10	448869	AI792798	Hs.12496	ESTs	0.47
	400749				0.47
	458745	AW207347	Hs.211101	ESTs	0.48
	418437	AA771738	Hs.295351	ESTs	0.48
15	452285 430369	AJ358570 AA477631	Hs.123933	ESTs ESTs	0.48
13	453572	AA382590	Hs.119484 Hs.31848	== -	0.48
	455175	AW993247	15.31040	ESTs, Weakly similar to hypothetical pro gb:RC2-BN0033-180200-014-h09 BN0033 Homo	0.48 0.48
	445765	AV655102	Hs.117266	ESTs	0.48
	400322	AF045576	Hs.247758	offactory receptor, family 5, subfamily	0.48
20	412526	M90366	Hs.73982	zona pellucida glycoprotein 2 (sperm rec	0.48
	407986	U32659	Hs.41724	Interleukin 17 (cytotoxic T-lymphocyte-a	0.48
	455479	AW948312		gb:RC0-MT0015-280300-021-h04 MT0015 Homo	0.48
	450308	AI692571	Hs.201681	ESTs	0.48
25	411149	N68715	Hs.269128	ESTs	0.48
23	453982	AW014252	Hs.252837	ESTs	0.48
	410971 410839	AW812258 NM_006849	Hs.66581	gb:RC0-ST0174-191099-031-b02 ST0174 Homo	0.48
	421553	AA536080	Hs.97302	protein disuffide isomerase ESTs	0.48 0.48
	442376	W95588	Hs.129982	Homo sapiens cDNA FLJ12228 fs, clone MA	0.48
30	454754	AW819191	1.3.123302	gb:CM1-ST0283-071299-061-d08 ST0283 Homo	0.48
-	447858	AW080339	Hs.211911	ESTs	0.49
	422639	AI929377	Hs.173724	creatine kinase, brain	0.49
	402449				0.49
26	420440	NM_002407	Hs.97644	mammaglobin 2	0.49
35	435056	AW023337	Hs.5422	glycoprotein M6B	0.49
	419543 407033	AA244170	Hs.188719	ESTs	0.49
	437468	U78628 AA457619		gb:Human leukemia inhibitory factor rece gb:aa89d11.r1 Stratagene fetal retina 93	0.49
	412639	AW961284	Hs.296235	ESTs	0.49 0.49
40	406109	A11501204	113.230233	2318	0.49
	404519				0.49
	410285	AA083609		gb:zm63d05.r1 Stratagene fibroblast (937	0.49
	406014			•	0.49
46	400938				0.49
45	414290	AI568801	Hs.71721	ESTa	0.49
	432433	AW014734	Hs.157969	ESTs	0.49
	405273 454738	BE072139			0.49
	414383	BE279406		gb:PM1-BT0533-291299-002-b05 BT0533 Homo	0.49
50	445911	AI985987	Hs.145645	gb:601157981F1 NIH_MGC_21 Homo sapiens c ESTs, Moderately similar to ALU1_HUMAN A	0.49 0.49
	451241	AI767545	Hs.209572	ESTs	0.49
	428336	AA503115	Hs.183752	microseminoprotein, beta-	0.49
	418310	AA814100	Hs.86693	ESTs	0.49
	452152	AL046755	Hs.28219	protein phosphatase 2 (formerly 2A), reg	0.49
55	454869	AW836004		gb:PM0-LT0019-170200-001-d11 LT0019 Homo	0.49
	400332	\$66407	Hs.248032	FLT4	0.49
	425280	U31519	Hs.1872	phosphoenolpyruvata carboxykinasa 1 (sol	0.49
	408221 440179	AA912183	Hs.47447	ESTs	0.49
60	425360	AI990151 BE547704	Hs.125904	ESTs	0.50
00	406600	DE.OHI I (H		gb:601076309F1 NIH_MGC_12 Homo sapiens c	0.50 0.50
	418594	A1732083	Hs.187619	ESTs	0.50
	432128	AA127221	Hs.117037	ESTs	0.50
	458611	A1268407	Hs.211458	ESTs	0.50
65	426495	NM_001151	Hs.2043	solute carrier family 25 (mitochondrial	0.50
	441068	AA913897	Hs.233559	ESTs	0.50
	428108	AA421452	Hs.164851	ESTs	0.50
	400803	*******			0.50
70	439996	AA916565	Hs.221675	ESTs	0.50
70	TABLE 4	AR-			
	Pkey:		ique Eos probeset	identifier number	
	CAT nur		ne cluster number		
	Accessio			ession numbers	
75					
	Pkey	CAT numbe	r Accession		
	409300	111676_1		074486 AA074707 AA070059 AA084885	
	409824	1155499_1		W503034 AW501523	
80	410285	119128_1		1083790 AA112048	
30	410495 410732	1205826_1 1218556_1		040 AW751366 H81987 W994323 AW994346 AM994330 D69437 AW994333 AM7700	007 41400 4224
	410732	1218556_1		W984322 AW984318 AW984330 R58427 AW984332 AW7998 WB12252 AW812261 AW812263 AW812285 AW812277 AW8	
	410990	1228649_1	AW812929 A	W812779 AW813088	

	411607	1251251_1	AW853498 A	W853442 AW853590 AW853433 AW853592
	413079	1348528_1	BE064382 BI	E064387 BE064385 BE064381 BE153367 BE153366 BE153401 BE153385 BE064372
	413679	1382784_1		E156770 BE156767 BE156769 BE156803 BE156802 BE156804 BE156853 BE156780 BE156836 BE156792 BE156834 BE156779
				E156833 BE156844 BE156831 BE156849 BE156797 BE156784 BE156801 BE156843 BE156793 BE156852
5	414141	1420715_1	BE255083 BI	
9	414383			
		1440279_1	BE 279406 BI	
	422582	218132_1	AA312660 A	
	425360	250631_1	BE547704 A	
10	426730	271055_1	AL040738 A	<b>\383683</b>
10	428151	287658_1	AA422028 W	79191
	430264	315008_1	AA470519 B	E303010 BE302954 BE384120
	430664	321423_1		A528493 AA483165 AW969842
	431152	328675_1		W971004 AA574217 AA493538
	431514	334213_1		VA506335 AI077445
15	437468	43743_1	AA457619 A	
	438211	45225_1	T08401 2839	
	449923			
	451818	81926_1		45/58 AA004732 BE255126
		887271_1		5492 W27615
20	454206	1050848_1		E146684 BE146693 BE146694 BE146679 AW810472 AW810208 AW810356 AW810193 AW178838 AW178837 AW178857 AW810515
20				W810514 AW810441 AW810358 AW178852 AW810359 AW810322 AW810327 AW810211 AW178835 AW810635 AW810288 AW810263
				W810443 AW810198 AW810321 AW810265 AW810567 AW810447 AW810328 AW810513 BE146674 AW810257 AW810185 AW810281
			AW810258 E	3E062400 AW810323 AW810293 BE145652 AW810516 BE146689 AW810289 AW810566 AW810636 AW178842 BE062434 BE146653
			AW810536 A	
0.0	454554	1223842_1	AW847505 A	NW811792 BE061442 BE061433 AW847506 AW806999 AW806996 BE061436 BE061430 BE142460 BE146499 AW806994 AW809156
25			AW806991 A	AW814082 AW806992 BE061669 AW807002 BE146659 AW806995 AW807000 AW845743 AW845747 AW847504 BE142458 BE061431
				W847507 BE14650 BE142470 AW814096 AW807012 BE061438 AW807011 AW806993 BE142465 BE142459 BE142462 AW854330
			AW854331 E	BE061434 BE061731 BE142464 AW847501 AW807001 BE142463 AW811800 BE061437 AW811802 BE061440 AW806997 AW806998
			BE061745 B	
	454560	1223940_1		AW807092 AW807425 AW807330 AW807174 AW807171 AW807274 AW807278 AW807367
30	454651	1228069_1		W812228 AW812106 AW938581 AW812080
	454661	1228527_1		E244727 AW812636 AW812647
	454738	1232449_1		
	454754			E157977 BE157974 AW857974 AW817778
	454154	1233580_1		AW819252 AW819183 AW819175 AW819177 AW819188 AW819180 BE158470 AW819242 AW819269 AW819244 AW819190 AW819265
35	45 4700	4004250 4		AW819246 BE152602 AW819249 AW819251 AW819263 AW819194
رد	454790	1234752_1		AW820773 AW821088
	454869	1238137_1		AW836087 AW836163 AW836162 AW836085 AW836084 AW836079 AW836083 AW836082 AW836086 AW836088 AW836166 AW836164
				AW836078 AW836161 AW862135 AW836165 AW836003
	455175	1257335_1	AW993247	
40	455400	1288135_1	AW936342	
40	455479	1293163_1	AW948312	AW948286 AW948289 AW948297 AW948279 AW948295
	455541	1323705_1	AW993005	AW993285 AW993290
	455753	1356070_1	BE075124 8	BE075229 BE075278
	455826	1373392_1	BE144228 E	3E144291
	458147	488021_1		AW848781 AW849062 AW848490 AW752699 AW752604 AW752700
45	459185	922823_1		I908224 AI908217
	TABLE 44	IC:		
	Pkey:		tue number cor	responding to an Eos probeset
	Ref;	Seo	VENCE SOUTCE	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The ONA
50		sec	sence of huma	n chromosome 22' Dunham, et al. (1999) Nature 402:489-495.
	Strand:			nd from which exons were predicted.
	Nt_positio			e positions of predicted exons.
			Coles Houseons	b positions of production discuss.
	Pkey	Ref	Strand	
55	400749	7331445		All naciliae
,,	400803			Ni_position
			Minus	9162-9293
		8567875	Minus Minus	9162-9293 18267-19088
	400917	8567875 7283186	Minus Minus Minus	9162-9293 18267-19088 173258-173631
	400917 400938	8567875 7283186 7652890	Minus Minus Minus Minus	9162-9293 18267-19088 173258-173631 92074-92423
60	400917 400938 401075	8567875 7283186 7652890 3687273	Minus Minus Minus Minus Plus	9162-9293 18267-19088 173258-173631 92074-92423 81218-81395
60	400917 400938 401075 401514	8567875 7283186 7652890 3687273 7622355	Minus Minus Minus Minus Plus Plus	9162-9293 18267-19088 173258-173631 92074-92423 81218-81395 93224-93292-94913-95065,95163-95334
60	400917 400938 401075 401514 401775	8567875 7283186 7652890 3687273 7622355 9966311	Minus Minus Minus Minus Plus Plus Minus	9162-9293 18267-19088 173258-173631 92074-92423 81218-81395 93224-93292-94913-95065,95163-95334 110228-110340
60	400917 400938 401075 401514 401775 401989	8567875 7283186 7652890 3687273 7622355 9966311 4309964	Minus Minus Minus Minus Plus Plus Minus Minus	9162-9293 18267-19088 173258-173631 92074-92423 81218-81395 93224-93292-94913-95065,95163-95334
60	400917 400938 401075 401514 401775 401989 401992	8567875 7283186 7652890 3687273 7622355 9966311 4309964 4153858	Minus Minus Minus Minus Plus Plus Minus	9162-9293 18267-19088 173258-173631 92074-92423 81218-81395 93224-93292-94913-95065,95163-95334 110228-110340
	400917 400938 401075 401514 401775 401989 401992 402015	8567875 7283186 7652890 3687273 7622355 9966311 4309964	Minus Minus Minus Minus Plus Plus Minus Minus	9162-9293 18267-19088 173258-173631 92074-92423 81218-81395 93224-93292-94913-95065,95163-95334 110228-110340 118611-118821
60 65	400917 400938 401075 401514 401775 401989 401992 402015 402449	8567875 7283186 7652890 3687273 7622355 9966311 4309964 4153858	Minus Minus Minus Minus Plus Plus Plus Minus Minus Minus Plus	9162-9293 18267-19088 173258-173631 92074-92423 81218-81395 93224-93292-94913-95065,95163-95334 110228-110340 118611-118821 31452-31649
	400917 400938 401075 401514 401775 401989 401992 402015	8567875 7283186 7652890 3687273 7622355 9966311 4309964 4153858 7417802	Minus Minus Minus Minus Plus Plus Minus Minus Minus Minus Plus Minus Plus Minus	9162-9293 18267-19088 173258-173631 92074-92423 81218-81395 93224-93292-94913-95065,95163-95334 110228-110340 118611-118821 31452-31649 43791-49043,50038-50205,51630-51672,54448-54565,55933-56073
	400917 400938 401075 401514 401775 401989 401992 402015 402449	8567875 7283186 7652890 3687273 7622355 9966311 4309964 4153858 7417802 9796674 9796919	Minus Minus Minus Minus Plus Plus Minus Minus Minus Minus Minus Plus Minus Plus Minus Plus Plus	9162-9293 18267-18088 173258-173631 92074-92423 81218-81395 93224-93292,94913-95065,95163-95334 110228-110340 118611-118821 31452-31649 48791-49043,50038-50205,51630-51672,54448-54565,55933-56073 59867-60039,62588-62828,63465-63623,64923-65108 57659-57866,58839-58908
	400917 400938 401075 401514 401775 401989 401992 402015 402449 402466 402759	8567875 7283186 7652890 3687273 7622355 9966311 4309964 4153858 7417882 9796674 9796919 9213869	Minus Minus Minus Minus Pius Pius Pius Minus Minus Pius Minus Pius Pius Pius Pius Pius Pius	9162-9293 18267-19088 173258-173631 92074-92423 81218-81395 93224-93292, 94913-95065, 95163-95334 110228-110340 118611-118821 31452-31649 48791-49043,50038-50205, 51530-51672, 54448-54565, 55933-56073 59867-60039, 62288-628, 63465-63623, 64923-65108 57659-57666, 58839-58908 134177-134281
65	400917 400938 401075 401514 401775 401989 401992 402015 402449 402466	8567875 7283186 7283186 7652890 3687273 7622355 9966311 4309964 4153858 7417802 9796674 9796919 9213869 9213869	Minus Minus Minus Minus Plus Minus Minus Plus Minus Plus Plus Plus Plus Plus	9162-9293 18267-19088 173258-173631 92074-92423 81218-81395 93224-93292-94913-95065,95163-95334 110228-110340 118611-118821 31452-31649 48791-49043,50038-50205,51530-51672,54448-54565,55933-56073 59867-60039,62588-62828,63465-63623,64923-65108 57659-57866,58839-58908 134117-134281 136829-135952,137336-137521
65	400917 400938 401075 401575 4019775 401989 401992 402015 402449 402456 402759 402760 402851	8567875 7283186 7652890 3687273 7622355 9966311 4309964 4153858 7417882 9796674 9796919 9213869 9213869 9650753	Minus Minus Minus Minus Minus Plus Plus Minus Minus Plus Minus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	9162-9293 18267-19088 173258-173631 92074-92423 81218-81395 93224-93292,94913-95065,95163-95334 110228-110340 118611-118821 31452-31649 48791-49043,50038-50205,51530-51672,54448-54565,55933-56073 59867-60039,62588-62828,63465-63623,64923-65108 57659-57866,58839-58908 134177-134281 136828-136952,137336-137521 63022-63136,63883-63783
	400917 400938 401075 401514 401775 401989 401992 402015 402449 402456 402759 402760 402851 403059	8567875 7283186 7652890 3687273 7622355 9966311 4309964 4153858 7417802 9796674 9766919 9213869 9213869 9213869 9250753 8954192	Minus Minus Minus Minus Pius Minus Minus Pius Pius Pius Pius Pius Pius Minus Pius Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Mi	9162-9293 18267-19088 173258-173631 92074-92423 81218-81395 93224-93292, 94913-95065, 95163-95334 110228-110340 118611-118821 31452-31649 48791-49043,50038-50205, 51530-51672, 54448-54565, 55933-56073 95867-60039, 62588-628, 63465-63623, 64923-65108 57659-57666, 58839-58908 134117-134281 136829-136952, 137336-137521 63022-83136, 63683-83783
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65	400917 400938 401075 401514 401775 401989 401992 402015 402466 402759 402759 402750 402851 403059 403279	8567875 7283186 7652890 3687273 7622355 9966311 4309964 4153858 7417802 9796674 9796919 9213869 9213869 9650753 8954192 8072597 9719566	Minus Minus Minus Minus Minus Plus Plus Minus Minus Plus Minus Plus Minus Plus Plus Plus Plus Plus Minus Plus Plus Minus Plus Minus Plus Minus Plus Minus Minus Plus Minus Minus Minus Minus Minus Minus Minus Minus Minus	9162-9293 18267-19088 173258-173631 92074-92423 81218-81395 93224-93292,94913-95065,95163-95334 110228-110340 118611-118821 31452-31649 48791-49043,50038-50205,51530-51672,54448-54565,55933-56073 59867-60039,62588-62828,63465-63623,64923-65108 57659-57866,58839-58908 134117-134281 136829-136952,137336-137521 63022-63136,63683-63783 69553-69702 162569-162768,163918-164168 52789-52917
65 70	400917 400938 401075 401514 401775 401989 401992 402015 402449 402456 402759 402760 402851 403059 403279 403429 403429	8567875 7283186 7652890 3687273 7622355 9966311 4309964 4153858 7417802 9796674 9796919 9213869 9213869 9213869 9250753 8954192 8072597 9719566 7259739	Minus Minus Minus Minus Minus Pius Minus Minus Minus Pius Minus Pius Pius Pius Pius Pius Minus Pius Minus Pius Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus	9162-9293 18267-19088 173258-173631 92074-92423 81218-81395 93224-93292, 94913-95065, 95163-95334 110228-110340 118611-118821 31452-31649 48791-49043,50038-50205, 51530-51672, 54448-54565, 55933-56073 93867-60039, 622588-6228, 63465-63623, 64923-65108 57659-57665, 58639-58908 134117-134281 136829-135952, 137336-137521 63022-83136, 63683-83783 69553-69702 162569-162768, 163318-164168 52789-52917 88377-88537
65 70	400917 400938 401075 401514 401775 401992 402015 402449 402469 402759 402760 402859 403279 403429 403680	8567875 7283186 7652890 3687273 7622355 9966311 4309964 4153858 417802 9796674 9796919 9213869 9650753 8954192 8072597 9719566 7259739 7331517	Minus Minus Minus Minus Minus Plus Plus Minus Minus Plus Minus Plus Minus Plus Minus Plus Plus Plus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus	9162-9293 18267-19088 173258-173631 92074-92423 81218-81395 93224-93292-94913-95065,95163-95334 110228-110340 118611-118821 31452-31649 48791-49043,50038-50205,51530-51672,54448-54565,55933-56073 98867-600799,62588-62928,63465-63623,64923-65108 57659-57866,58839-58908 134177-134281 138629-1389522,137336-137521 63022-83136,63683-83783 69553-69702 162569-162768,1633918-164168 52789-52917 88377-88537 157184-157415
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65 70	400917 400938 401075 401514 401775 401989 401992 402015 402049 402750 402851 4030279 40369 403710 40380 403710 404519	8567875 7283186 7652890 3687273 7622355 9966311 4309964 4153858 417802 9796674 9796919 9213869 9650753 8954192 8072597 9719566 7259739 7331517 6437516 9796219 8152000	Minus Minus Minus Minus Minus Plus Plus Minus Plus Minus Plus Plus Plus Plus Minus Plus Plus Minus Plus Minus Plus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Plus Minus Plus Minus Plus Plus Plus	9162-9293 18267-19088 173258-173631 92074-92423 81218-81395 93224-93292-94913-95065,95163-95334 110228-110340 118611-118821 31452-31649 48791-49043,50038-50205,51530-51672,54448-54565,55933-56073 59867-60039,62588-562878,63465-63623,64923-65108 57659-57866,58839-58908 134177-134281 138629-1385952,137336-137521 63022-83136,63683-63783 69553-69702 162569-162768,163918-164168 52789-52917 88377-88537 157184-157415 27413-28978 59256-59401 12817-13000
65 70	400917 400937 401514 401775 401981 401992 402015 40245 402466 402759 402466 402759 403670 403851 403670 403870 403870 404629	8567875 7283186 7652890 3687273 7622355 9966311 4309964 4153858 7417802 9796674 9796919 9213869 9213869 9213869 9250753 8954192 8072597 9719566 7259739 731517 6437516 9796219 8152000 9796665	Minus Minus Minus Minus Minus Pius Pius Minus Minus Pius Pius Minus Pius Pius Pius Minus Pius Pius Minus Pius Minus Pius Minus Pius Minus Pius Minus Pius Minus Pius Minus Pius Minus Pius Pius Pius Pius Pius Pius Pius Pi	9162-9293 18267-19088 173258-173631 92074-92423 81218-81395 93224-93292,94913-95065,95163-95334 110228-110340 118611-118821 31452-31649 48791-49043,90038-50205,51530-51672,54448-54565,55933-56073 59867-69039,62588-62828,63465-63623,64923-65108 57659-57866,58839-58908 134117-134281 136829-136952,137336-137521 63022-63136,63683-63783 69553-69702 162569-162768,163918-164168 52785-52917 88377-88537 157184-157415 27413-28978 59256-59401 12817-13000 55584-55796
65 70 75	400917 400938 401075 401514 401755 401989 401992 402015 402449 402469 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 402750 40	8567875 7283186 7652890 3687273 762235 9966311 4309964 4153858 7417802 9796674 9796919 9213869 9213869 9213869 9213869 72597 9719566 7259739 7331517 6437516 9796219 8152000 97966665 3213020	Minus Minus Minus Minus Pius Pius Minus Minus Pius Minus Pius Pius Pius Pius Minus Pius Pius Pius Minus Pius Pius Pius Pius Pius Pius Pius Pi	9162-9293 18267-19088 173258-173631 92074-92423 81218-81395 93224-93292_94913-95065,95163-95334 110228-110340 118611-118821 31452-31649 48791-49043,50038-50205,51530-51672_54448-54565,55933-56073 95867-60039,622888-6228,63465-63623,64923-65108 57659-57666,58839-58908 134117-134281 136829-135952_137336-137521 63022-83136,63683-83783 69553-63702 162569-162768,163918-164168 52789-52917 88377-88537 157184-157415 27413-28978 59256-59401 12817-13000 55584-55796 101602-102591
65 70	400917 400938 401075 401514 401775 401989 401992 402015 402449 402466 402750 402851 4030279 403429 403670 403710 404629 404629 404629 404629 404629 404629 404629	8567875 7283186 7652890 3687273 7622355 9966311 4309964 4153858 4417802 9796674 9796919 9213869 9650753 8954192 8072597 9719566 7259739 7331517 6437516 9796219 8152000 9796665 3213020 8095688	Minus Minus Minus Minus Minus Plus Plus Minus Plus Minus Plus Minus Plus Plus Minus Plus Minus Plus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Plus Plus Plus Plus Plus Plus Plus Pl	9162-9293 18267-19088 173258-173631 92074-92423 81218-81395 93224-93292-94913-95065,95163-95334 110228-110340 118611-118821 31452-31649 48791-49043,50038-50205,51530-51672,54448-54565,55933-56073 58867-60039,62588-56288,63465-63623,64923-65108 57659-57866,58839-58908 134177-134281 136829-136952,137336-137521 63022-83136,63683-63783 69553-69702 162569-162768,163918-164168 52789-52917 88377-88537 157184-157415 27413-28978 59256-59401 12617-13000 55584-55796 101602-102591 118340-119100
65 70 75	400917 400937 401514 401775 401918 401992 402015 402045 402456 402759 402769 403279 403279 403279 403279 403279 40329 403710 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 404121 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412 40412	8567875 7283186 7652890 3687273 7622355 9966311 4309964 4153858 7417802 9796674 9796919 9213869 9213869 9213869 9213869 9250753 8954192 8072597 979566 7259739 7331517 6437516 9796219 8152000 9796665 3213020 8096888 4156137	Minus Minus Minus Minus Minus Pius Minus Minus Minus Pius Minus Pius Minus Pius Pius Minus Pius Minus Pius Minus Pius Minus Pius Minus Pius Minus Pius Minus Pius Minus Pius Minus Pius Pius Pius Pius Pius Pius Pius Pi	9162-9293 18267-19088 173258-173631 92074-92423 81218-81395 93224-93292,94913-95065,95163-95334 110228-110340 118611-118821 31452-31649 48791-49043,50038-50205,51530-51672,54448-54565,55933-56073 59867-60039,62588-52828,63485-63623,64923-65108 57659-57866,58839-58908 134177-134281 136829-136952,137336-137521 63022-63136,63883-63783 69553-69702 162569-162768,163918-164168 52789-52917 88377-88537 157184-157415 27413-28978 59256-59401 12817-13000 55584-55796 101602-102591 118940-119100 98141-98754
65 70 75	400917 400938 401075 401514 401775 401989 401992 402015 402449 402466 402750 402851 4030279 403429 403670 403710 404629 404629 404629 404629 404629 404629 404629	8567875 7283186 7652890 3687273 7622355 9966311 4309964 4153858 4417802 9796674 9796919 9213869 9650753 8954192 8072597 9719566 7259739 7331517 6437516 9796219 8152000 9796665 3213020 8095688	Minus Minus Minus Minus Minus Plus Plus Minus Plus Minus Plus Minus Plus Plus Minus Plus Minus Plus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Plus Plus Plus Plus Plus Plus Plus Pl	9162-9293 18267-19088 173258-173631 92074-92423 81218-81395 93224-93292-94913-95065,95163-95334 110228-110340 118611-118821 31452-31649 48791-49043,50038-50205,51530-51672,54448-54565,55933-56073 58867-60039,62588-56288,63465-63623,64923-65108 57659-57866,58839-58908 134177-134281 138629-138592,137336-137521 63022-83136,63683-63783 69553-69702 162569-162768,163918-164168 52789-52917 88377-88537 157184-157415 27413-28978 59256-59401 12617-13000 55584-55796 101602-102591 118340-119100

	405817	4071056	Plus	19914-20112,25655-25810
	405014	6758904	Minus	23738-24076
	406036	6758919	Plus	17942-18163
_	406109	9127147	Minus	58328-58485
5	406255	7417729	Plus	2959-3200
	406326	9212385	Plus	84508-84655
	406600	8248616	Minus	36296-36610

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TABLE 45A: ABOUT 947 GENES UP-REGULATED IN STOMACH CANCER COMPARED TO NORMAL ADULT TISSUES

Table 45A lists about 947 genes up-regulated in stomach cancer compared to normal adult tissues. These were selected from 59680 probesets on the Aflymetrix/Eos Hu/O3

GeneChip array such that the radio of "average" stomach cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" stomach cancer level was set to
the 90th percentile amongst various atomach cancers. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to
remove gene-specific background levets of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and
the denominator before the ratio was availuated.

Play:

Unique Eos probeset identifier number

Exemplar Accession number, Genbank accession number

Uniquene Tide:

Unique Tide:

Unique agene title

Ratio of stomach cancer compared to normal stomach

15

20

	Pkey	ExAccn	UnigenetD	Unigene Title	R1
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (intensitial	66.80
~ ~	411243	AB039886	Hs.69319	CA11	61.16
25	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	42.36
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	35.80
	425679	X05997	Hs.159177	lipase, gastric	28.34
	409041	AB033025	Hs.50081	KIAA1199 protein	26.91
20	452121	NM_004081	Hs.70936	deleted in azoospermia	26.22
30	403776			NA	25.00
	444783	AK001468	Hs.62180	anillin (Orosophila Scraps homolog), act	23.90
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	23.90
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	23.35
35	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	22_26
22	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	21.06
	415989	AI267700	Hs.317584	ESTs	20.72
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	19.84
	452401	NM_007115	Hs.29352	humor necrosis factor, alpha-Induced pro	15.50
40	438639 426427	AI278360 M86699	Hs.31409	ESTs	15.16
40	449032	AA045573	Hs.169840 Hs.22900	TTK protein kinase	14.54
	443211	AJ128388	Hs.143655	nuclear factor (erythroid-derived 2)-lik ESTs	14.26
	421470	R27496	Hs.1378	annexin A3	14.22
	400792	AA635062	Hs.50094	T. 1777-117	13.96
45	424086	Al351010	Hs.102267	Homo sapiens mRNA; cDNA DKFZp43400515 (1 hysyl oxidase	13.94
1.5	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	13.73 13.38
	409757	NM_001898	Hs.123114	cystatin SN	13.33
	447033	Al357412	Hs.157601	ESTs	13.20
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	12.80
50	420159	AI572490	Hs.99785	Homo sapiens cONA: FLJ21245 fis, clone C	12.66
• •	432596	AJ224741	Hs.278461	matriin 3	12.64
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	12.46
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	12.32
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	12.18
55	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	11.74
	442660	AW138174	Hs.130651	ESTs	11.73
	441693	AA384573	Hs.7943	RPB5-mediating protein	11.16
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	11.08
<b>~</b>	414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fis, clone HE	10.90
60	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	10.48
	443715	AI583187	Hs.9700	cyclin E1	10.44
	420900		Hs.44269	ESTs	10.38
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazotes 1	10.36
65	415076	NM_000857	Hs.77890	guanytata cyclase 1, soluble, beta 3	10.20
03	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	10.18
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	10.14
	414422	AA147224	Hs.337232	ESTs	10.12
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	10.02
70	414972	BE263782	Hs.77695	KIAA0008 gene product	10.02
70	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	9.80
	428365	AA295331	Hs.183861	Homo sepiens cDNA FLJ20042 fis, clone CO	9.72
	416661 400195	AA634543 NA	Hs.79440	IGF-II mRNA-binding protein 3	9.68
	418738	AW388533	Un CCOO	NA	9.66
75	420170	U43374	Hs.6682	solute carrier family 7, (cationic amino	9.64
, ,	414259	W44633	Hs.95631	Human normal keratinocyte mRNA	9.60
	417517	AF001176	Hs.301296 Hs.82238	Homo sapiens cDNA: FLJ23131 fis, clone L	9.58
	446998	N99013	Hs.16762	POP4 (processing of precursor , S. cerev	9.34
	429486	AF155827	Hs.203963	Homo sapiens mRNA; cDNA DKFZp56482062 (f hypothetical protein FLJ 10339	9.26 9.16
80	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	9.16 8.95
	431810	X67155	Hs.270845	kinesin-like 5 (mitotic kinesin-like pro	8.93 8.84
	419261	X07876	Hs.89791	wingless-type MMTV integration site tami	8.80
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	8.78
				The same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the sa	5.75

	424834	A V004 433	41- 459400		
	413268	AK001432 AL039079	Hs.153408 Hs.75256	Homo sapiens cDNA FLJ 10570 fts, clone NT	8.69
	417801	AA417383	Hs.82582	regulator of G-protein signating 1 integrin, beta-like 1 (with EGF-like rep	8.68
	452461	N78223	Hs.108106	transcription factor	8.68
5	425916	NM 006786	Hs.162200	urotensin 2	8.68 8.64
	422805	AA435989	Hs.121017	H2A histone family, member A	8.54
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophiim)-l	8.52
	441377	BE218239	Hs.202656	ESTs	8.41
10	445891	AW391342	Hs.199460	ESTs	8.31
10	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	8.30
	439521	A1808955	Hs.58248	ESTs	8.30
	425087	R62424	Hs.126059	ESTs	9.28
	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	8.22
15	441795	N58115	Hs.21137	AD024 protein	8.02
13	427878	C05766	Hs.181022	CGI-07 protein	8.00
	413583 407853	AL120806 AA338797	Hs.5888 Hs.40499	ESTs	7.98
	426269	H15302	Hs.168950	dickkopf (Xenopus laevis) homolog 1 Homo sapiens mRNA; cDNA DKFZp566A1046 (f	7.98
	404996	*********	113.100300	NA	7.97 7.96
20	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	7.96
	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	7.94
	417655	AA780791	Hs.14014	hypothetical protein FLJ14813	7.92
	452838	U65011	Hs.30743	preferentially expressed antigen in meta	7.91
25	418895	AA894638	Hs.14600	ESTs	7.90
25	446155	AI553695	Hs.159422	Homo saplens cDNA FLJ13997 fis, clone Y7	7.86
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; Human selen	7.82
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	7.80
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (b	7.72
30	418763 447289	AK000219 AW247017	Hs.88367	hypothetical protein FLJ20212	7.70
50	443354	AW970672	Hs.36978 Hs.9247	melanoma antigen, family A, 3	7.70
	427718	A1798680	Hs.25933	protein kinase, AMP-activated, atpha 1 c ESTs	7.69
	434032	AW009951	Hs.206892	ESTs	7.66 7.60
	427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35kD, Ze	7.58
35	450480	X82125	Hs.25040	zinc finger protein 239	7.51
	418678	NM_001327	Hs.167379	cancer/testis antigen	7.49
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	7.44
	452705	H49805	Hs.246005	ESTs	7.36
40	443846	AI085198	Hs.164226	ESTs	7.32
40	425420	BE536911	Hs.234545	hypothetical protein NUF2R	7.30
	420617	AK001652	Hs.99423	ATP-dependent RNA helicase	7.28
	421155	H87879	Hs.102267	lysyl oxidase	7.24
	450715 447254	AJ266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	7.24
45	435473	NM_004153 NS3550	Hs.17908	origin recognition complex, subunit 1 (y	7.22
75	413293	AL047483	Hs.260881 Hs.302498	ESTs	7.20
	449347	AV649748	Hs.295901	GTP-binding protein homologous to Saccha KIAA0493 protein	7.14
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	7.11
	408908	BE296227	Hs.250822	serine/threonine kinase 15	7.11 7.11
50	408660	AA525775	Hs.292523	ESTs, Moderately similar to PC4259 ferri	7.10
	453688	AW381270	Hs.194110	hypothetical protein PRO2730	7.02
	426890	AA393167	Hs.41294	ESTs	6.98
	404440			NA	6.97
55	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	6.96
55	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	6.95
	413833	Z15005	Hs.75573	centromere protein E (312kD)	6.94
	426249	F05422	Hs.168352	nucleoporin-like protein 1	6.94
	441421 400298	AA356792 AA032279	Hs.334824 Hs.61635	hypothetical protein FLJ14825	6.92
60	423903	M57765	Hs.1721	six transmembrane epithelial antigen of interleukin 11	6.85
	431041	AA490967	Hs.197955	KIAA0704 protein	6.84 6.74
	417256	U94332	Hs.81791	tumor necrosis factor receptor superfami	6.74
	426921	AA037145	Hs.172865	cleavage stimulation factor, 3 pre-RNA,	6.70
65	407771	AL138272	Hs.62713	ESTs	6.69
65	433393	AF038564	Hs.98074	itchy (mouse homolog) E3 ubiquitin prote	6.66
	407162	N63855	Hs.142634	zinc finger protein	6.64
	411343	U77949	Hs.69563	CDC6 (cell division cycle 6, S. cerevisi	6.64
	427920	Z11502	Hs.181107	annexin A13	6.59
70	450159	AJ702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	6.58
, 0	427401	U20582	Hs.2149	actin like protein	6.55
	447102 431806	BE167434 AF186114	Hs.98471	ESTs, Weakly similar to T18712 hypotheti	6.54
	435159	AF186114 AA668879	Hs.270737	tumor necrosis factor (ligand) superfami	6.54
	440209	H05049	Hs.116649 Hs.22269	ESTs	6.54
75	418134	AA397769	Hs.86617	neurexin 3 ESTs	6.54
	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	6.50
	434894	AW977850	Hs.23856	hypothetical protein MGCS297	6.47
	422505	AL120862	Hs.124165	ESTs	6.40 6.34
00	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	6.32
80	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	6.31
	408380	AF123050	Hs.44532	dlublquitin	6.31
	420218	AW958037	Hs.286	ribosomal protein L4	6.29
	405817	NA		NA	6.28

	406747	AI925153	H- 217402	manuia A2	
	448743	A8032962	Hs.217493 Hs.21896	annexin A2 KIAA1138 protein	5.24 5.24
	434636	AA083764	Hs.6101	hypothetical protein MGC3178	6.20
-	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	6.17
5	412661	N32860	Hs.24611	ESTs. Weakly similar to 154374 gene NF2	6.17
	401644 423248	AA380177	Hs.125845	NA ribulose-5-phosphate-3-epimerase	6.16
	427335	AA448542	Hs.251677	G antigen 78	6.13 6.12
	450375	AA009647	Hs.8850	a disintegrin and metafloproteinase doma	6.07
10	422420	U03398	Hs. 1524	tumor necrosis factor (ligand) superfami	6.06
	419752 413573	AA249573 A1733859	Hs.152618 Hs.149089	ESTs, Moderately similar to ZN91_HUMAN 2	6.06
	408758	NM_003686	Hs.47504	ESTs exonuclease 1	6.06 6.02
	444188	Al393165	Hs.699	peptidylprolyl isomerase B (cyclophilin	6.02
15	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	6.00
	446364 418939	AB006624	Hs.14912	KIAA0286 protein	5.98
	424639	AW630603 AI917494	Hs.89497 Hs.9812	tamin B1 Homo sapiens cDNA FLJ14388 ffs, clone HE	5.90 5.88
	434377	AW137148	Hs.306593	Homo sepiens cDNA FLJ11382 fis, clone HE	5.86
20	419863	AW952691	Hs.93485	Homo sepiens mRNA; cDNA DKFZp761D191 (fr	5.84
	430849	AI940727	Hs.270556	ESTs, Highly similar to AF156779 1 ASB-4	5.82
	428822 448776	W28418 BE302464	Hs.30715 Hs.30057	potassium voltage-gated channel, lsk-rel MRS2 (S. cerevisiae)-like, magnesium hom	5.80 5.74
	442957	AI949952	Hs.49397	ESTs	5.72
25	444577	AI207721	Hs.11393	RAD51 (S. cerevisiae) homolog C	5.72
	424565	AW102723	Hs.75295	guanytate cyclase 1, soluble, alpha 3	5.71
	433330 428618	AW207084 AA885360	Hs.132816 Hs.160199	hypothetical protein MGC14801 NADPH oxidase, EF hand calcium-binding d	5.68 5.68
	432867	AW016936	Hs.233364	ESTs	5.64
30	412140	AA219691	Hs.73625	RAB6 Interacting, kinesin-like (rabkines	5.63
	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	5.62
	418379 434551	AA218940 BE387162	Hs.137516 Hs.280858	fidgetin-like 1	5.57
	442353	BE379594	Hs.49136	ESTs, Highly similar to A35661 DNA excis ESTs, Moderately similar to ALU7_HUMAN A	5.57 5.56
35	427386	AW836261	Hs.337717	ESTs	5.54
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	5.52
	428479 449370	Y00272 AK002114	Hs.184572 Hs.23495	cell division cycle 2, G1 to S and G2 to hypothetical protein FLJ11252	5.51
	431118	BE264901	Hs.250502	carbonic anhydrase VIII	5.50 5.50
40	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	5.50
	453931	AL121278	Hs.25144	ESTs	5.49
	409044 436291	A1129586 BE568452	Hs.33033 Hs.5101	hypothetical protein FLJ14623	5.48
	448336	R53848	Hs.44976	protein regulator of cytokinesis 1 ESTs	5.45 5.44
45	454018	AW016892	Hs.100855	ESTs	5.42
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	5.42
	412246 432193	AI160873 AA372264	Hs.69233 Hs.273193	zinc finger protein	5.40
	437319	BE410958	Hs.56406	hypothetical protein FLJ10706 Homo sapiens cDNA FLJ13549 fis, clone PL	5.40 5.40
50	427660	AI741320	Hs.114121	Homo sepiens cDNA: FLJ23228 fis, clone C	5.40
	452862	AW378065	Hs.8687	ESTs	5.38
	409327 412811	L41162 H06382	Hs.53563 Hs.21400	collagen, type IX, alpha 3 ESTs	5.36 5.34
	448390	AL035414	Hs.21068	hypothetical protein	5.32
55	428187	AI687303	Hs.285529	G protein-coupled receptor 49	5.30
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	5.29
	434265 407811	AAB46811 AW190902	Hs.130554 Hs.40098	Homo sapiens cDNA: FLJ23089 fis, clone L	5.28
	446638	AL133063	Hs.15783	cysteine knot superfamily 1, BMP antagon Homo sapiens mRNA; cDNA DKFZp434P1115 (F	5.27 5.26
60	444743	AAD45648	Hs.301957	nudix (nucleoside diphosphate linked mol	5.25
	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, ty	5.24
	452150 432865	W42490 AJ753709	Hs.260844 Hs.152484	ESTs ESTs, Wealdy similar to I38022 hypotheti	5.24 5.24
	453382	AA709285	Hs.5997	hypothetical protein FLJ13078	5.22
65	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	5.22
	426518	Z43039	Hs.170198	KIAA0009 gene product	5.22
	453884 429625	AA355925 AA455568	Hs.36232 Hs.193814	KIAA0185 gene product	5.20
	413472	BE242870	Hs.75379	ESTs solute carrier family 1 (glial high affi	5.20 5.20
70	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	5.19
	444059	R69743	Hs.116774	integrin, alpha 1	5.18
	409432 412719	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	5.17
	444342	AW016610 NM_014398	Hs.129911 Hs.10887	ESTs similar to hysosome-associated membrane	5.15 5.14
75	425739	T19016	Hs.159410		5.12
	452198	AI097560	Hs.61210	ESTs, Weakly similar to 138022 hypotheti	5.12
	445657	AW612141	Hs.279575		5.10
	434699 424296	AA643687 Al631874	Hs.149425 Hs.155140		5.09
80	441645	AI222279	Hs.201555		5.08 5.06
	412723	AA648459	Hs.335951	hypothetical protein AF301222	5.06
	448811	AI590371	Hs.174759	ESTs	5.05
	447342	Al199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	5.04

	411835	U29343	Hs.72550	hyaluronan-mediated motitity receptor (R	5.04
	421373 448991	AA808229 AW771565	Hs.167771 Hs.189594	ESTS	5.04
	429370	C19097	Hs.89709	ESTs ghtamate-cysteine ligase, modifier subu	5.02
5	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	5.00 4.98
	405770			NA NA	4.96
	421110	AJ250717	Hs.1355	cathepsin E	4.96
	452588	AA889120	Hs.110637	homeo box A10	4.92
10	433159 420952	AB035898	Hs.150587	kinesin-like protein 2	4.91
10	408321	AA282067 AW405882	Hs.88972 Hs.44205	ESTs, Moderately similar to A46010 X-lin	4.88
	441801	AW242799	Hs.86366	cortistatin ESTs	4.87 4.84
	450568	AL050078	Hs.25159	Homo sapiens cONA FLJ10784 fis, clone NT	4.83
	452909	NM_015368	Hs.30985	pannexin 1	4.82
15	409799	D11928	Hs.76845	phosphoserine phosphatase-like	4.82
	451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens	4.80
	417158 418203	AL133117 X54942	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	4.80
	418994	AA296520	Hs.83758 Hs.89546	CDC28 protein kinase 2	4.80
20	436982	AB018305	Hs.5378	selectin E (endothelial adhesion molecul spondin 1, (f-spondin) extracellular mat	4.78 4.78
	432874	W94322	Hs.279651	melanoma inhibitory activity	4.78
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	4.78
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PL	4.77
25	442980	AA857025	Hs.8878	kinesin-like 1	4.76
2.5	432437 414869	W07088 AA157291	Hs.293685 Hs.21479	ESTs white work is 4	4.76
	446254	BE179829	Hs.179852	ubinuclein 1 Homo sapiens cDNA FLJ12832 fis, clone NT	4.74 4.74
	418380	AA425473	Hs.84429	KIAA0971 protein	4.74
20	419343	AA456245	Hs.85603	down-regulated by Ctnnb1, a	4.74
30	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	4.72
	425813	AA364136	Hs.210553	hypothetical protein DKFZp7611172	4.71
	425071 412733	NM_013989 AA984472	Hs.154424 Hs.74554	delodinase, iodothyronine, type (1	4.71
	444325	AW152618	Hs.16757	KIAA0080 protein ESTs	4.68
35	407638	AJ404572	Hs.334483	hypothetical protein FLJ23571	4,66 4,66
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	4.66
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	4.64
	449448	D60730	Hs.57471	ESTs	4.62
40	409732 432415	NM_016122	Hs.58148	NY-REN-58 antigen	4.62
70	421987	T16971 Al133161	Hs.289014 Hs.285131	ESTs, Weakly similar to A43932 musin 2 p	4.62
	430217	N47863	Hs.336901	CGI-101 protein ribosomal protein S24	4.60
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	4.58 4.57
46	425932	M81650	Hs.1968	semenogelin I	4.57
45	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	4.56
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	4.55
	451254 422426	AI571016 W79117	Hs.172967	ESTs	4.54
	439483	T69980	Hs.58559 Hs.58323	ESTs Homo sapiens cDNA FLJ11613 fis, clone HE	4,54
50	435420	AI928513	Hs.59203	ESTs	4.53 4.53
	447519	U48258	Hs.339665	ESTs	4.52
	424176	AL137273	Hs.142307	hypothetical protein	4.52
	414812	X72755	Hs.77367	monokine induced by gamma interferors	4.51
55	438069 450096	N80701 AI682088	Hs.33790	ESTs	4.50
23	438159	Z83947	Hs.79375	holocarboxylase synthetase (blotin-[prop	4.50
	433925	Al183551	Hs.26481	gb:H.sapiens mRNA; clone CD 117 S8B/26 protein	4.50 4.48
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	4.48
40	433384	AI021992	Hs.124244	ESTs	4.47
60	421863	AI952677	Hs.108972	Homo sepiens mRNA; cDNA DKFZp434P228 (fr	4.47
	453941 423401	U39817	Hs.36820	Bloom syndrome	4.45
	430510	NM_001992 AW162916	Hs.128087 Hs.241576	coagulation factor (I (thrombin) recepto	4.44
	424084	A1940675	Hs.20914	hypothetical protein PRO2577 hypothetical protein FLJ23056	4.43
65	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	4,42
	417956	AA210704	Hs.190465	ESTs	4.42
	449433	AJ672096	Hs.9012	ESTs, Wealty similar to \$26650 DNA-bindi	4.42
	421477	A1904743	Hs.104650	hypothetical protein FLJ10292	4.42
70	406687 451813	M31126 NM_016117	Hs.272620	pregnancy specific beta-1-glycoprotein 9	4.41
, ,	415091	AL044872	Hs.27182 Hs.77910	phospholipase A2-activating protein	4.41
	425142	AW954397	Hs.154762	3-hydroxy-3-methylglutaryl-Coenzyme A sy HTV-1 rev binding protein 2	4.40 4.40
	441720	A1346487	Hs.28739	ESTs	4.40
75	409683	U33317	Hs.711	defensin, alpha 6, Paneth cell-specific	4.39
75	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	4.38
	430044	AA464510	Hs.152812	ES7s	4.37
	436246 409582	AW450963 R27430	Hs.119991	ESTS	4.37
	453652	AW009640	Hs.271565 Hs.28368	ESTs ESTs, Moderately similar to \$65657 alpha	4.37
80	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	4.35 4.34
	448692	AW013907	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	4.34
	409459	D86407	Hs.54481	low density tipoprotein receptor-related	4.34
	442470	AW273860	Hs.5759	ESTs	4.33

	441894	AA134329	Hs.24170	Homo sapiens, clone IMAGE:3685398, mRNA,	4.32
	422867	L32137	Hs. 1584	cartilage ofigomeric matrix protein (pse	4.31
	436396	A1683487	Hs.152213	wingless-type MMTV integration site fami	4.31
5	433397 417576	AW079768	Hs.134880	ESTs, Wealdy similar to unnamed protein	4.30
•	413278	AA339449 BE563085	Hs.82285 Hs.833	phosphoribosytglycinamide formyltransfer	4.29
	451592	AI805416	Hs.213897	interferon-stimulated protein, 15 kDa ESTs	4.29 4.28
	453900	AW003582	Hs.226414	ESTs. Wealthy similar to ALUS_HUMAN ALU S	4.28
	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	4.26
10	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	4.26
	428389	AW135714	Hs.283127	ESTs, Weakly similar to T19201 hypotheti	4.24
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	4.23
	409913	BE243842	Hs.283077	centrosomal P4.1-associated protein; unc	4.22
15	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4.21
IJ	445640 422232	AW969626 D43945	Hs.31704	ESTs, Wealdy similar to KIAAD227 [H.sapi	4.20
	442655	AW027457	Hs.113274 Hs.30323	transcription factor EC ESTs, Wealdy similar to B34087 hypotheti	4.18 4.18
	444381	BE387335	Hs.283713	ESTs, Wealdy similar to S64054 hypotheti	4.16
	434217	AW014795	Hs.23349	ESTs	4.16
20	413384	NM_000401	Hs.75334	exostoses (multiple) 2	4.14
	407768	AW002841	Hs.29475	ESTS	4.14
	419168	AJ338132	Hs.33718	Homo sapiens cONA FLJ12641 ffs, clone NT	4.13
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	4.12
25	443691 409640	AI081724	Hs.17267	ESTs	4.12
23	438176	U78722 AW138970	Hs.55481 Hs.122113	zinc finger protein 165 ESTs	4.12
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	4.10 4.10
	419606	AW294795	Hs.198529	ESTs	4.08
	452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	4.08
30	414152	NM_003248	Hs.75774	thrombospondin 4	4.08
	418688	T85017	Hs.1192	KIAA0074 protein	4.07
	404253			NA	4.06
	421741	AK001879	Hs.107527	hypothetical protein FLJ11017	4.06
35	428218 428858	AA424266 AA436760	Hs.123642	EphA3	4.06
23	428336	AA503115	Hs.183752	gb:zv67d11.r1 Soares_total_fetus_Nb2HF8_ microseminoprotein, beta-	4.06
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	4.05 4.04
	421841	AA908197	Hs.108850	MAK-related kinase	4.04
40	451177	AI969716	Hs.13034	ESTs	4.04
40	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	4.04
	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	4.03
	424634	NM_003613	Hs.151407	cartilage Intermediate tayer protein, nu	4.02
	438777 423343	AA825487	Hs.142179	ESTs	4.02
45	425788	AA324643 BE466417	Hs.246106 Hs.231899	ESTs	4.02
75	409928	AL137163	Hs.57549	ESTs, Wealdy similar to rab3 effector-5 hypothetical protein dJ47384	4.02 4.01
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	4.01
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	4.00
60	433225	AW816515	Hs.173540	ATPase, Class V, type 100	4.00
50	411765	H43346		gb:yp09a04.r1 Soares breast 3NbHBst Homo	4.00
	452022	AW072330	Hs.293875	ESTs	4.00
	451806	NM_003729	Hs.27076	RNA 3-terminal phosphate cyclase	3.99
	423541 414132	AA296922 AI801235	Hs.129778 Hs.48480	gastrointestinal peptide	3.99
55	452453	At902519	F18.4040U	ESTs gb:QV-B7009-101198-051 B7009 Homo sapien	3.99
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.98 3.98
	430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypotheti	3.98
	453160	AI263307	Hs.239884	H28 histone family, member L	3.97
60	417235	AA810278	Hs.24250	ESTs	3.96
UU	425398	AL049689	Hs.156369	hypothetical protein similar to tenascin	3.95
	414136 436608	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	3.94
	431753	AA628980 X76029	Hs.192371 Hs.2841	down syndrome critical region protein DS	3.94
	453161	AA628608	Hs.61656	neuromedin U ESTs	3.94 3.94
65	454821	AW833504	. 4.0.030	gb:0V4-TT0008-091199-025-f03 TT0008 Homo	3.94
	427961	AW293165	Hs.143134	ESTs	3.94
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	3.93
	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	3.93
70	418396	A1765805	Hs.26691	ESTa	3.92
, 0	451411 445885	AAD17492	Hs.135655	EST	3.92
	407698	A1734009 AA058900	Hs.127699 Hs.32646		3.92
	442896	R37725	Hs.261108	hypothetical protein FLJ21901 ESTs	3.91
	433361	AW469373	Hs.300141	ribosomal protein L39	3.90 3.90
75	419926	AW900992	Hs.93796	OKF2P586O2223 protein	3.89
	413775	AW409934	Hs.75528	nucleolar GTPase	3.88
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	3.86
	428549	AA430064	Hs.220929	Homo sepiens cDNA FLJ14369 fis, clone HE	3.86
80	456120	AA535244	Hs.78305	RAB2, member RAS oncogene family	3.86
50	452194 421247	A1594413 BE391727	Hs.332649 Hs.102910		3.85
	417720	AA205625	Hs.208067		3.85
	418811	AK001407	Hs.88663	hypothetical protein FLJ10545	3.85 3.84
				**	3.04

	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	3.84
	421246	AW582962	Hs.102897	CGI-47 protein	3.83
	407366 428698	AF026942 AA852773	Hs.334838	gb:Homo sapiens cig33 mRNA, partial sequ KAA1866 protein	3.83
5	435202	AI971313	Hs.170204	KIAA0551 protein	3.82 3.82
•	454074	R63503	Hs.28419	ESTs	3.82
	448917	AI683598	Hs.201615	ESTs	3.82
	410507	AA355288	Hs.40834	transitional epithelia response protein	3.82
• •	452571	W31518	Hs.34665	EST\$	3.82
10	445663	AJ247343	Hs.149232	ESTs	3.82
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ 12280 fis, clone MA	3.80
	423025	AA831267	Hs.12244	hypothetical protein FLJ20097	3.80
	425656 407168	AB018284 R45175	Hs.158688	KIAA0741 gene product	3.80
15	403422	NA NA	Hs.117183	ESTs NA	3.79
1.	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	3.79 3.79
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	3.79
	457325	AA744550	Hs.136345	ESTs	3.78
••	433800	AI034361	Hs.135150	tung type-I cell membrane-associated gly	3.77
20	428865	BE544095	Hs.164960	Bartl-like homeobox 1	3.76
	424188	AW954552	Hs.142634	zinc finger protein	3.75
	424638	AJ472106	Hs.49303	Homo saplens cDNA FLJ11663 fis, clone HE	3.75
	451099 448105	R52795 AW591433	Hs.25954 Hs.298241	interleukin 13 receptor, alpha 2	3.75
25	452785	AL359942	Hs.296434	Transmembrane protease, serine 3 erythroid differentiation and denucleati	. 3.74 3.74
	459000	AA903705	Hs.4190	Homo sepiens cDNA: FLJ23269 fs, clone C	3.74
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	3.73
	409632	W74001	Hs.55279	serina (or cysteine) proteinase inhibito	3.73
20	414883	AA926960	Hs.334883	CDC28 protein kinase 1	3.73
30	415064	AA159804	Hs.149305	hypothetical protein MGC2603	3.72
	432198	AI475306	Hs.50458	ESTs	3.72
	458194	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	3.72
	415263 408296	AA948033 AL117452	Hs.130853 Hs.44155	ESTS	3.71
35	408460	AA054726	Hs.285574	DKFZP586G1517 protein ESTs	3.71 3.71
	437496	AA452378	Hs.170144	Homo saplens mRNA; cDNA DKFZp547J125 (tr	3.70
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	3.68
	432021	AA524470	Hs.58753	ESTs	3.68
40	420092	AA814043	Hs.88045	ESTs	3.68
40	414923	AW445008	Hs.77637	homeo box A4	3.68
	429432	AI578059	Hs.202676	synaptonemal complex protein 2	3.68
	435496 430544	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	3.67
	432542	AA481066 AW083920	Hs.105153 Hs.16098	Homo sapiens, clone IMAGE:3461987, mRNA, claudin 2	3.67
45	410782	AW504860	Hs.288836	hypothetical protein FLJ12673	3.67 3.66
	421106	AA877124	Hs.172844	ESTs	3.64
	439107	AL046134	Hs.13944	adrenergic, beta, receptor kinase 2	3.64
	418735	N48769	Hs.44609	ESTs	3.64
50	411598	BE336654	Hs.70937	H3 histone family, member A	3.63
50	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase 8	3.63
	438411 429774	AW67#352 AI522215	Hs.50883	gb:ba63c07.y1 NIH_MGC_12 Homo sapiens c0	3.63
	448844	AI581519	Hs.177164	KIAA1804 protein ESTs	3.62 3.61
	402473	AB033035	Hs.51965	KIAA1209 protein	3.61
55	44 1085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 ffs, clone NT	3.61
	429534	AW976987	Hs.163327	ESTs, Weakly similar to 2109260A B cell	3.60
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.60
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	3.59
60	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.59
00	451381 428664	BE241831 AK001666	Hs.172330 Hs.189095	hypothetical protein MGC2705	3.58
	424345	AK001380	Hs.145479	similar to SALL1 (sal (Drosophila)-like Homo sapiens cDNA FLJ10518 (is, clone NT	3.58 3.58
	440717	AA904527	Hs.42207	ESTs	3.58
	450698	W31489	Hs.95044	ESTs. Weakly similar to 138022 hypotheti	3.58
65	423675	AI990509	Hs.131342	small inducible cylokine subfamily A [Cy	3.58
	424882	AJ379461	Hs.153636	far upstream element (FUSE) binding prot	3.57
	410784	AW803201		gb:IL2-UM0077-070500-080-E08 UM0077 Homo	3.55
	41 1096	U80034	Hs.68583	mitochondrial intermediate peptidase	3.55
70	430294 439225	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.54
. 0	429183	AA192669 AB014604	Hs.45032 Hs.197955	ESTS VIA 60704 contrin	3.54
	419948	AB041035	Hs.93847	KIAA0704 protein NADPH coidase 4	3.54 3.53
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.52
	408556	U49516	Hs.46362	5-hydroxytryptamine (serotonin) receptor	3.52
75	417048	AI088775	Hs.55498	geranyigeranyi diphosphate synthase 1	3.52
	432101	AI918950	Hs.123642	EphA3	3.52
	419216	AU076718	Hs.164021	, , ,	3.51
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	3.51
80	422093 404765	AF151852 NA	Hs.111449		3.50
-0	441513	AW014567	Hs.112420	NA ESTs	3.50 3.50
	444301	AK000136	Hs.10760	asporin (LRR class 1)	3.50
	417315	A1080042	Hs.336901		3.50
				•	<b></b>



	407182	**313661	H- 030457	FRI	
	443204	AA312551 AW205878	Hs.230157 Hs.29643	ESTs Homo sapiens cDNA FLJ13103 fs, clone NT	3.49 3.49
	432289	AI860145	Hs.55118	ESTs	3.49
_	453644	AJ813444	Hs.42197	ESTS	3.48
5	427986	N45214	Hs.282387	Homo saplens cDNA: FLJ21837 fis, clone H	3.48
	405466			NA	3.48
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	3.48
	430357 418428	AW976789 Y12490	Hs.165607 · Hs.85092	ESTs thyroid hormone receptor interactor 11	3.46
10	422260	AA315993	Hs.105484	regenerating gene type IV	3.46 3.46
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	3.45
	451403	AA885569	Hs.40919	Homo saplens cDNA FLJ14511 fis, clone NT	3.46
	406117			NA	3.46
15	458242	BE299588	Hs.28465	Homo sepiens cDNA: FLJ21859 fis, clone H	3.46
13	408562 440105	AI436323 AA694010	Hs.31141	Homo sepiens mRNA for KIAA1568 protein,	3.45
	443767	BE562136	Hs.6932 Hs.9736	Homo sapiens clone 23809 mRNA sequence proteasome (prosome, macropain) 26S subu	3.45 3.45
	426320	W47595	Hs.169300	transforming growth factor, beta 2	3.45
~~	444478	W07318	Hs.240	M-phase phosphoprotein 1	3.45
20	425904	AI805990	Hs.82238	POP4 (processing of precursor, S. cerev	3.44
	416702	AA186428	Hs.85591	ESTs	3.44
	448668 410004	AJ560305 AJ298027	Hs.199852 Hs.5057	ESTs	3.42 3.42
	428771	AB028992	Hs.193143	carboxypeptidase D KIAA1069 protein	3.42
25	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.42
	429628	H09604	Hs.13268	ESTS	3.40
	448816	AB033052	Hs.22151	KIAA1226 protein	3.40
	456032 439635	AW957446	Hs.301711	ESTs	3.39
30	414275	AA477288 AW970254	Hs.94891 Hs.889	hypothetical protein FLJ22729 Charot-Leyden crystal protein	3.39 3.38
50	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	3.38
	416057	AI927382	Hs.29857	ESTs	3.38
	430704	AW813091	Hs.335799	ESTs	3.38
35	423600	A1633559	Hs.310359	ESTs	3.38
33	453891 430178	AB037751	Hs.36353	Homo sapiens mRNA full length Insert cDN	3.38
	417791	AW449612 AW965339	Hs.152475 Hs.111471	ESTs ESTs	3.37 3.37
	408867	AA437199	Hs.656	cell division cycle 25C	3.37
40	449802	AW901804	Hs_23984	hypothetical protein FLJ20147	3.37
40	457003	S78234	Hs.172405	cell division cycle 27	3.36
	458076	R80061	Hs.164478	hypothetical protein FLJ21939 similar to	3.36
	436203 418782	BE384982 AJ792648	Hs.5076 Hs.14665	Homo sapiens cDNA: FLJ22128 fis, clone H ESTs	3.36 3.34
	449722	BE280074	Hs.23960	cyclin B1	3.34
45	447984	AI457263	Hs.37244	ESTs	3.34
	451103	R52804	Hs.25956	DKFZP564D206 protein	3.34
	408812	BE397160	Hs.254763	ESTs, Wealty similar to A42442 integrin	3.34
	448305 418849	AA625207 AW474547	Hs.264915 Hs.53565	Homo sapiens CDNA FLJ12908 fis, clone NT	3.34
50	450531	AW301032	Hs.203800	Homo sapiens PIG-M mRNA for mannosyttran ESTs	3.33 3.32
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	3.32
	416530	U62801	Hs.79361	katilkrein 6 (neurosin, zyme)	3.31
	425746	NM_001701	Hs.159440	bile acid Coenzyme A: amino acid N-acylt	3.30
55	421037 430388	A1684808 AA356923	Hs.197653	ESTs	3.30
55	433132	AB026264	Hs.240770 Hs.284245	nuclear cap binding protein subunit 2, 2 hypothetical protein IMPACT	3.30 3.30
	447078	AW885727	Hs.301570	ESTs	3.30
	402408	NA		NA .	3.29
60	437044	AL035864	Hs.69517	cONA for differentially expressed CO16 g	3.29
OU	423126 446223	AA322245	Hs.290165	ESTs	3.28
	451917	8E300091 AW391351	Hs.119699 Hs.50820	hypothetical protein FLJ12969 Homo sapiens unknown mRNA	3.27 3.27
	419335	AW960146	Hs.284137	hypothetical protein FLJ 12888	3.26
	411078	AJ222020	Hs.182364		3.26
65	419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mi	3.26
	427119	AW880562	Hs.114574	ESTs	3.26
	400250 429044	NA Al261490	Hs.145527	NA ESTs	3.26
	451050	AW937420	Hs.69662	ESTs	3.25 3.24
70	447425	AI963747	Hs.18573	acylphosphatase 1, erythrocyte (common)	3.24
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	3.23
	416565	AW000960	Hs.44970	endoplasmic reticulum resident protein 5	3.22
	442028	A1239437	Hs.48945	ESTs	3.22
75	409110 418926	AA191493 AA232658	Hs.48778 Hs.105794	niban protein	3.22
	408353	BE439838	Hs.44298	UDP-glucose:glycoprotein glucosyttransfe mitochondrial ribosomal protein S17	3.22 3.21
	445417	AK001058	Hs.12680	Homo sepiens cDNA FLJ10196 fis, clone HE	3.20
	442979	AW440782	Hs.174743	ESTS	3.20
80	439292	AA090421	Hs.5555	hypothetical protein MGC5347	3.20
οU	440953	A1683036	Hs.124135		3.20
	447020 451181	T27308 Al796330	Hs.16986 Hs.207461	hypothetical protein FLJ11046 ESTs	3.20
	422809	AK001379	Hs.121028		3.19 3.19
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	411573	AB029000	Hs.70823	KIAA1077 protein	3.19
	424539 443179	L02911 AJ928402	Hs.150402 Hs.6933	activin A receptor, type I hypothetical protein FLJ 12684	3.18 3.18
_	452545	N31940	Hs.14434	ESTs. Weakly similar to 138022 hypotheti	3.18
5	433024	AA573847	Hs.26549	KIAA1708 protein	3.18
	414737	Al160386	Hs.125087	ESTs	3.18
	444230 419741	H95537 NM_007019	Hs.146067 Hs.93002	ESTs ubiquitin carrier protein E2-C	3.18
	428945	AW192803	Hs.98974	ESTs, Wealty similar to \$65824 reverse t	3.17 3.17
10	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	3.17
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.17
	443598 413518	AW499970 BE145907	Hs.14822	ESTs, Weakly similar to 178885 serine/th	3.16
	434389	AA971235	Hs.128098	gb:MR0-HT0208-221299-204-e12 HT0208 Homo ESTs	3.16 3.16
15	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Horno	3.15
	432158	W33165	Hs.22983	UDP-glucose:glycoprotein glucosyltransfe	3.15
	453331 410286	AI240665 AI739159	Hs.6895 Hs.61898	ESTa DKFZP586N2124 protein	3.15
	408687	AL110280	Hs.301152	Homo sapiens mRNA; cDNA DKFZp434F053 (fr	3.14 3.14
20	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	3.14
	419078	M93119	Hs.89584	insulinoma-associated 1	3.14
	414080 451525	AA135257 AW001757	Hs.47783 Hs.14005	B aggressive lymphoma gene ESTs	3.14
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.13 3.13
25	433183	AF231338	Hs.222024	transcription factor BMAL2	3.12
	424783	AA913909	Hs.153088	TATA box binding protein (TBP)-essociate	3.12
	413170 437181	BE068819 Al306615	Hs.125343	gb:MR0-BT0374-220300-001-b03 BT0374 Homo	3.12
	442991	BE281238	Hs.8886	ESTs, Weakly similar to KIAA0758 protein hypothetical protein FLJ20424	3.12 3.11
30	453867	AI929383	Hs.33032	hypothetical protein DKFZp434N185	3.11
		- AAB11452	Hs.291911	ESTs	3.10
	428651 427927	AF196478 AI879165	Hs.188401 Hs.2227	annexin A10 CCAAT/enhancer binding protein (C/EBP),	3.09
	419196	AF110908	Hs.297660	TNF receptor-associated factor 3	3.09 3.09
35	414569	AF109298	Hs.118258	prostate cancer associated protein 1	3.09
	408633	AW963372	Hs.46677	PRO2000 protein	3.09
	403381 444619	BE538082	Hs.8172	NA ESTE Madagestale similar to A 450 to V lin	3.08
	422363	T55979	Hs.115474	ESTs, Moderately similar to A46010 X-lin replication factor C (activator 1) 3 (38	3.08 3.08
40	434138	AA625804		gb:zu86h01.s1 Soares_testis_NHT Homo sap	3.07
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	3.07
	436556 427043	AI364997 AA397679	Hs.7572 Hs.3991	ESTs ESTs	3.07
	443055	AV653742	Hs.15536	hypothetical protein DKFZp761J139	3.06 3.06
45	419229	AI827237	Hs.282884	ESTs	3.05
	414718	H95348	Hs.107987	ESTs	3.05
	439737 448587	AI751438 AI539652	Hs.41271 Hs.28338	Homo sapiens mRNA full length insert cDN KIAA1546 protein	3.05
	448595	AB014544	Hs.21572	KIAA0644 gene product	3.04 3.04
50	407201	N31998	Hs.164256	hypothetical protein FLJ20657	3.04
	423065	R96158	Hs.267130	Homo sapiens, clone MGC:5406, mRNA, comp	3.04
	431980 416198	AA523696 H27332	Hs.324507 Hs.99598	hypothetical protein FLJ20986	3.04
	429410	X98494	Hs.201676	hypothetical protein MGC5338 M-phase phosphopratein 10 (U3 small nucl	3.04 3.04
55	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	3.03
	441031	AJ110684	Hs.7645	fibrinogen, 8 beta polypeptide	3.03
	446142 402167	AJ754693	Hs.145968	ESTs NA	3.02
<i>c</i> ^	402299			NA NA	3.02 3.02
60	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	3.02
	419910 424001	AA662913 W67883	Hs.190173	ESTs, Westly similar to A46010 X-linked	3.02
	413930	W86153	Hs.137476 Hs.75618	paternally expressed 10 RAB11A, member RAS oncogene family	3.01 3.01
<i>C</i>	439924	AJ985897	Hs.125293	ESTs	3.01
65	414343	AL036166	Hs.323378	coated vesicle membrane protein	3.01
	432201 445845	AI538613 AI261870	Hs.298241	Transmembrane protease, serine 3	3.00
	420727	H75701	Hs.145555 Hs.99886	ESTs complement component 4-binding protein,	3.00
70	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	3.00 3.00
70	403637	NA		NA	3.00
	410947	AK000305	Hs.67055	hypothetical protein FLJ20298	3.00
	413430 423575	R22479 C18863	Hs.167073 Hs.163443	Home sepiens cONA FLI13047 fis, clone NT	3.00
-	426711	AA383471	Hs.180669	Homo saplens cDNA FLJ11576 fis, clone HE conserved gene amplified in osteosarcoma	2.99 2.99
75	442204	A1635450	Hs.21914	ESTs	2.98
	429682	NM_006306	Hs.211602		2.98
	419227 447233	BE537383 AW246333	Hs.89739 Hs.17901	cholinergic receptor, nicotinic, beta po	2.97
00	441826	AW503603	Hs.129915	Homo sapiens, clone iMAGE:3937015, mRNA, phosphotriesterase related	2.97 2.97
80	433404	T32982	Hs.102720	ESTS	2.96
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	2.96
	423880 411750	8E278111 BE562298	Hs.134200		2.96
		0000000	Hs.71827	KIAA0112 protein; homolog of yeast ribos	2.96

	408155	AB014528	Hs.43133	KIAA0528 gene product	2.96
	424131 451250	AA335714 AA491275	Hs.199665 Hs.236940	ESTs hypothetical protein FLJ12542	2.96
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	2.96 2.96
5	447829	AI433029	Hs.164104	ESTs .	2.95
	410561	BE\$40255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	2.95
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cONA A430	295
	452693	179153	Hs.48589	zinc finger protein 228	2.95
10	407742 421430	AF186252 AW207555	Hs.38084 Hs.97093	sulfotransferase family, cytosofic, 1C, Homo sapiens cDNA: FLJ23004 fis, clone L	2.94 2.94
	407995	AI094748	Ha.100134	hypothetical protein FLJ 12787	294
	413281	AA861271	Hs.222024	transcription factor BMAL2	294
	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.94
1.5	441020	W79283	Hs.35962	ESTs	294
15	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	294
	420005 412530	AW271106 AA766268	Hs.133294 Hs.266273	EST8	2.93 2.93
	435602	AF217515	Hs.283532	hypothetical protein FLJ13346 uncharacterized bone marrow protein BM03	293
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fts, clone NT	293
20	443341	AW631480	Hs.8688	ESTS	2.92
	435481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	2.92
	410144	W07189	Hs.68185	ESTs, Wealthy similar to ARL3_HUMAN ADP-R	2.92
	434450 450402	S78564 BE218027	Hs.87 Hs.89969	retinoblastoma-like 1 (p107) ESTs	2.92 2.92
25	422026	U80736	Hs.110826	trinucleotide repeat containing 9	2.92
	421562	AA530994	Hs.334471	ghrelin precursor	2.92
	410434	AF051152	Hs.63868	toli-like receptor 2	2.92
	422665	AJ011812	Hs.119018	transcription factor NRF	2.91
30	428966 412416	AF059214	Hs.194687	cholesterol 25-hydroxylase	2.90
20	446232	AI628253 AI281848	Hs.22580 Hs.194691	alkylgtycerone phosphate synthase retinoic acid induced 3	2.90 2.90
	454600	AW810001	113.154051	gb:MR4-ST0124-270300-005-b11 ST0124 Homo	2.90
	438018	AKD01160	Hs.5999	hypothetical protein FLJ 10298	2.90
25	433252	AB040957	Hs.151343	KIAA1524 protein	2.90
35	444355	BE383686	Hs.191621	ESTs, Moderately similar to ALUS_HUMAN A	2.90
	443054 421308	AI745185	Hs.8939	yes-essociated protein 65 kDa	2.89
	411643	AA687322 A1924519	Hs.192843 Hs.192570	leucine zipper protein FKSG14 hypothetical protein FL/J22028	2.89 2.89
	419559	Y07828	Hs.91096	ring tinger protein	2.89
40	433527	AW235613	Hs.133020	ESTs	2.68
	426274	D38122	Hs.2007	turnor necrosis factor (ligand) superfami	2.88
	406182	NA		NA	2.88
	432731 429274	R31178	Hs.287820	fibronectin 1	2.88
45	418216	A/379772 AA662240	Hs.99206 Hs.283099	ESTs AF15q14 protein	2.87 2.87
	410168	AK001376	Hs.59346	hypothetical protein FLJ10514	2.86
	452665	AW839326	Hs.330414	ESTs, Moderately similar to \$65657 atpha	2.86
	424696	BE439547	Hs.151903	GrpE-like protein cochaperone	2.86
50	410174	AA306007	Hs.59461	DKFZP434C245 protein	2.85
30	443640 432912	A/872643 BE007371	Hs.134218 Hs.200313	ESTs ESTs	2.85 2.85
	431611	U58766	Hs.264428	tissue specific transplantation entigen	2.85
	446565	D13757	Hs.311	phosphoribosyl pyrophosphate amidotransi	2.85
	424770	AA425562	Hs.11065	Homo sapiens HDCME13P mRNA, partial cds	2.84
55	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	2.84
	403639 451110	NA A1955040	Hs.265398	NA	2.84
	416185	AW975861	Hs.47367	ESTs, Wealdy similar to transformation-r KIAA1785 protein	2.84 2.84
	444565	BE613126	Hs.47783	B aggressive lymphoma gene	2.83
60	423441	R68649	Hs.278359	absent in metanoma 1 like	283
	450584	AA040403	Hs.60371	ESTs	283
	420191 425599	AW003565 AW366745	Hs.192323	Home sapiens mRNA for FLJ00057 protein,	2.83
	424408	A1754813	Hs.214140 Hs.146428	ESTs, Weakly similar to ALU1_HUMAN ALU S collagen, type V, alpha 1	2.83 2.83
65	448769	N66037	Hs.38173	ESTs	2.82
	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	2.82
	435347	AW014873	Hs.116963	ESTs	2.82
	438435	AA807142	Hs.42194	hypothetical protein FLI22649 similar to	2.82
70	427687	AW003867	Hs.1570	histamine receptor H1	2.82
, 0	426951 427970	AA393636 AA418187	Hs.97454 Hs.330515	ESTs ESTs	2.82 2.82
	442577	AA292998	Hs.163900		2.82
	441016	AW138653	Hs.25845	ESTs	2.81
75	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.81
75	417160	N76497	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	281
	409346	AL162066	Hs.54320	hypothetical protein DKFZp762D096	281
	410407 407137	X66839 T97307	Hs.63287	carbonic anhydrase IX gb:ye53h05.s1 Soares fetal liver spleen	2.81 2.81
	435849	BE305242	Hs.16098	daudin 2	2.80
80	426695	AW118191	Hs.112729		2.80
	428301	AW628666	Hs.98440	ESTs, Wealdy similar to I38022 hypotheti	2.80
	420759	T11832	Hs.127797		2.80
	421341	AJ243212	Hs.279611	deleted in malignant brain tumors 1	2.80

	419423	D26488	Hs.90315	KIAA0007 protein	2.79
	452355 425826	N54926 U97698	Hs.29202 Hs.159593	G protein-coupled receptor 34	2.79
	457465	AW301344	Hs.122908	mucin 6, gastric DNA replication factor	2.79 2.79
5	426472	BE246138	Hs.30853	ESTs	2.79
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.78
	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1, c	2.78
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	2.78
10	423430 410011	AF112481 AB020641	Hs.128501 Hs.57856	RAD54, S. cerevisiae, homolog of, B PFTAIRE protein kinase 1	2.78 2.78
	453700	AB009426	Hs.560	apolipoprotein B mRNA editing enzyme, ca	2.78
	431250	BE264549	Hs.251377	taxol resistance associated gene 3	2.77
	414043	AL521210	Hs.97977	ESTS	2.77
15	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.77
13	439223 425956	AW238299 M60828	Hs.250618 Hs.164568	UL16 binding protein 2	2.76
	437612	AA827715	Hs.105153	fibroblast growth factor 7 (kerafinocyte Homo sapiens, clone IMAGE:3461987, mRNA,	2.76 2.76
	426119	W94997	Hs.189917	ESTs	2.76
20	459574	AI741122	Hs.101810		2.76
20	442339	BE299668	Hs.227591	ESTs. Weakly similar to 1901303A Leu zip	2.76
	414334 418217	AA824298 AI910647	Hs.21331 Hs.13442	hypothetical protein FLJ 10036 ESTs	2.76
	420022	AA256253	Hs.120817	ESTS	2.76 2.76
	408243	Y00787	Hs.624	Interleukin 8	2.75
25	421346	Z34277	Hs.103707	apomucin	2.75
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.75
	425773 449611	N21279 AI970394	Hs.237749 Hs.197075	ESTs ESTs	275
	424827	AI057094	Hs.96867	Homo sapiens cDNA: FLJ23155 fis, clone L	274 274
30	448621	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S	274
	428523	AW974540	Hs.98626	ESTs	2.73
	410839	NM_006849	Hs.66581	protein disuffide isomerase	2.73
	437380 424641	AL359577 AB001106	Hs.112198 Hs.151413	Homo sapiens mRNA; cDNA DKFZp547M073 (tr glia maturation factor, beta	2.73
35	431708	A1698136	Hs. 108873	ESTs	2.73 2.73
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed prot	2.73
	441790	AW294909	Hs.132208	ESTs	2.73
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	2.73
40	409506 423482	NM_006153 BE280172	Hs.54589 Hs.129228	NCK adaptor protein 1	2.73
	417015	M83772	Hs.80876	galactokinase 2 flavin containing monooxygenase 3	2.73 2.72
	448165	NM_005591	Hs.202379	meiotic recombination (S. cerevisiae) 11	2.72
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 (H	2.72
45	447803	BE620578	Hs.30858	ESTs, Weakly similar to \$65657 alpha-1C-	2.72
7.7	429703 448796	T93154 AA147829	Hs.28705 Hs.301431	ESTs	2.72
	410902	AW809665	113.30 143 1	endothefial zinc finger protein induced gb:MR4-ST0124-261099-015-g07 ST0124 Homo	2.72 2.72
	424745	AA214618	Hs.152759	activator of S phase kinase	2.72
50	454469	AW792775		gb:CM0-UM0001-010300-258-g10 UM0001 Homo	2.72
50	458632	AI744445	Hs.167073	Homo sepiens cDNA FLJ13047 fis, clone NT	2.72
	452012 422109	AA307703 \$73265	Hs.279766 Hs.1473	kinesin family member 4A gastrin-releasing peptide	2.72
	438008	AA775026	Hs.203802	ESTs	2.72 2.72
	420552	AK000492	Hs.98806	hypothetical protein	271
55	427038	NM_014633	Hs.173288	KIAA0155 gene product	2.71
	409239 425371	AA740875	Hs.44307 Hs.155981	ESTs, Moderately similar to 138022 hypot	2.71
	439857	D49441 AA847194	Hs.232002	mesothelin ESTs	2.71 2.71
	455309	AW894017		gb:RC4-NN0027-150400-012-g04 NN0027 Harmo	2.71
60	439580	AF086401	Hs.293847	ESTs, Moderately similar to \$65657 alpha	2.70
	437257	AJ283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	2.70
	435039 438796	AW043921 W67821	Hs.130526	ESTs	2.70
	407013	U35637	Hs.109590	genethonin 1 gb:Human nebulin mRNA, partial cds	2.70 2.70
65	445413	AA151342	Hs.12677	CGI-147 protein	270
	418416	U11700	Hs.84999	ATPase, Cu↔ transporting, beta polypept	2.70
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	2.69
	448045 441858	AJ297436	Hs.20166	prostate stem cell antigen	2.69
70	441008	A1400276 A1627826	Hs.183485 Hs.209109	ESTs ESTs	2.69 2.69
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.69
	427617	D42063	Hs.199179	RAN binding protein 2	2.69
	414518	AI204600	Hs.96978	hypothetical protein MGC10764	2.69
75	441350	AB020690 AA236233	Hs.7782	paraneoplastic antigen MA2	2.58
	419310 445279	R41900	Hs.188716 Hs.22245	ESTs ESTs	2.68 2.68
	439741	BE379646	Hs.6904	Homo saplens mRNA full length insert cDN	2.68
	446692	Z44514	Hs.156829	Homo sapiens mRNA for KIAA1763 protein,	2.68
80	449300	AI656959	Hs.222165		2.68
OU.	444585 444384	AW170015 BE174527	Hs.6594 Hs.11065	ESTs Homo sapiens HDCME13P mRNA, partial cds	2.68
	448104	AI674818	Hs.316433		2.68 2.67
	446839	BE091926	Hs.16244	mitnic spindle colled-coil related prot	2.67



	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	2.67
	418971	AA360392	Hs.87113	ESTs	2.66
	446152 441553	AI292036 AA281219	Hs.150028 Hs.121296	ESTs ESTs	2.66 2.66
5	403548	74401213	10.12.200	NA .	2.66
	452699	AW295390	Hs.213062	ESTs	2.66
	449532 453985	W74653 N44545	Hs.271593 Hs.251865	ESTs, Moderately similar to A47582 B-cel ESTs	2.66 2.65
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	2.65
10	409446	AI561173	Hs.67688	ESTs	2.65
	422094 445462	AF129535 AA378776	Hs.272027 Hs.288649	F-box only protein 5 hypothetical protein MGC3077	2.65 2.64
	432670	AA806536	Hs.291841	ESTs	2.64
15	418634	AK000064	Hs.86905	ATPase, H+ transporting, lysosomal (vacu	2.64
13	453528 442117	AW243307 AW664964	Hs.83937 Hs.128899	hypothetical protein ESTs	2.64 2.64
	416248	H99169	Hs.23450	mitochondrial ribosomal protein \$25	2.64
	414531 423268	AW970130 BE386898	Hs.65408 Hs.131162	ESTS Woods similar to ALLIE LUMANUALLE	2.64 2.64
20	413597	AW302885	Hs.117183	ESTs, Weakly similar to ALU5_HUMAN ALU S ESTs	2.63
	445031	AJ271704	Hs. 18987	Homo sapiens BAC done RP11-505D17 from	2.63
	450142 436304	AW207469 AA339622	Hs.24485 Hs.108887	chondroitin sulfate proteoglycan 6 (barna ESTs	2.63 2.63
	439832	TB1829	Hs.14870	Horno sapiens, Similar to hect domain and	263
25	449207	AL044222	Hs.23255	nucleoporin 155kD	2.62
	416111 414747	AA033813 U30872	Hs.79018 Hs.77204	chromatin assembly factor 1, subunit A ( centromere protein F (350/400kD, mitosin	2.62 2.62
	423811	AW299598	Hs.50895	homeo box C4	2.62
30	439474 417218	A1824060	Hs.211501	ESTs	2.62
30	408031	AA005247 AA081395	Hs.285754 Hs.42173	met proto-oncogene (hepatocyte growth fa Homo sapiens cDNA FLJ10366 fis, clone NT	2.62 2.62
	442821	BE391929	Hs.8752	transmembrane protein 4	2.62
	418245 447917	AA088767 AL048037	Hs.83883 Hs.164588	transmembrane, prostate androgen induced	2.62
35	424840	D79987	Hs.153479	ESTs, Moderately similar to neuronal thr extra spindle poles, S. cerevisiae, homo	2.61 2.61
	443268	AI800271	Hs.129445	hypothetical protein FLJ12498	261
	403056 433037	R58624 NM_014158	Hs.2186 Hs.279938	eukanyotic translation elongation factor HSPC067 protein	2.61 2.61
	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein	2.60
40	426181	AA371422	Hs.334371	hypothetical protein MGC13096	2.60
	414853 457233	U31116 Al355009	Hs.77501 Hs.221698	sarcoglycan, beta (43kD dystrophin-assoc ESTs	2.60 2.60
	416049	AJ970536	Hs.16603	hypothetical protein FLJ 13163	2.60
45	418946	A1798841	Hs.164526	ESTs	2.60
73	441891 443742	AW129145 AW627805	Hs.128076 Hs.145421	ESTs ESTs	2.60 2.60
	433868	AA612960	Hs.337300	ESTs	2.60
	442717 444542	R88362 Al161293	Hs.180591 Hs.280380	ESTs, Wealdy similar to T23976 hypotheti	2.59
50	452940	AA029722	Hs.2173	aminopeptidase fucosyltransferase 4 (atpha (1,3) fucosy	2.59 2.59
	429170	NM_001394		dual specificity phosphatase 4	2.59
	417531 401458	NM_003157	Hs.1087	serine/threonine kinase 2 NA	2. <del>5</del> 9 2.58
	436016	AA806465	Hs.121536	Human DNA sequence from clone RP11-472E5	2.58
55	430980	AW971904	Hs.122164	diaphanous (Drosophila, homolog) 3	2.58
	441581 435693	BE551408 Al033134	Hs.127196 Hs.119887	ESTs	2.58 2.58
	431814	BE256242	Hs.270847	delta-tubulin ·	2.58
60	446269 422765	AW263155 AW409701	Hs.14559	hypothetical protein FLJ10540	2.58
-	456999	AA319798	Hs.1578 Hs.298581	baculoviral IAP repeat-containing 5 (sur eutkaryotic translation elongation factor	2.58 2.58
	425234	AW152225	Hs.165909	ESTs, Weakly similar to 138022 hypotheti	2.58
	434423 425782	NM_006769 U66468	Hs.3844 Hs.159525	LIM domain only 4 cell growth regulatory with EF-hand doma	2.57 2.57
65	433929	Al375499	Hs.27379	ESTs	2.57
	414907	X90725	Hs.77597	polo (Drosophia)-like kinase	2.57
	411789 435627	AF245505 W88774	Hs.72157 Hs.118370	DKFZP5641922 protein ESTs	2.57 2.57
70	432168	AK000563	Hs.272805	hypothetical protein FLJ20556	2.57
70	432375 424057	BE536069	Hs.2962	S100 calcium-binding protein P	2.57
	424315	A1339874 AW614850	Hs.126593 Hs.193384		2.57 2.57
	435663	AI023707	Hs.134273	ESTs	2.56
75	439277 427747	R80051 AW411425	Hs.164478 Hs.180655		2.56 2.56
. •	438182	AW342140	Hs.182545		2.56
	421102	AI470093	Hs.283085	protocadherin beta 6	2.56
	445725 448243	AK000956 AW369771	Hs.13209 Hs.52620	hypothetical protein FLJ10094 integrin, beta 8	2.56 2.56
80	442881	AI023175	Hs.167022	ESTs	2.56
	422165 425843	AL041199 RE313300	Hs.1481	histidine decarboxytase	2.56
	448569	BE313280 BE382657	Hs.159627 Hs.21486	death associated protein 3 signal transducer and activator of trans	2.56 2.55

	440000				
	416806 438113	NM_000288	Hs.79993	peroxisomal biogenesis factor 7	2.55
	413374	AJ467908	Hs.8882	ESTs	2.55
	448275	NM_001034 BE514434	Hs.75319 Hs.20830	ribonucleotide reductase M2 polypeptide kinesin-like 2	2.55
5	419987	NM_005014	Hs.94070	osteomodulin	2.55 2.55
	439929	S73205		gb:insulin activator factor (human, pane	2.55
	452240	AI591147	Hs.61232	ESTs	2.55
	417806	AIB67277	Hs.183733	ESTs	255
10	421482	AL135462	Hs.104715	inversin	2.55
10	456884	AA054679	Hs.155150	ribonuclease P (14kD)	2.55
	442961	BE614474	Hs.289074	F-box only protein 22	2.55
	411274 419359	NM_002776	Hs.69423	kallikrein 10	2.55
	448666	AL043202 NM_014953	Hs.90073 Hs.323346	chromosome segregation 1 (yeast homolog) KIAA1008 protein	2.54
15	428911	Z43848	Hs.194478	Homo sapiens mRNA; cDNA DKFZp43401572 (f	2.54 2.54
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	254
	430733	AW975920	Hs.283361	ESTs	2.54
	421184	NM_003616	Hs.102456	survival of motor neuron protein interac	2.54
20	435361	A1168596	Hs.117117	ESTs .	2.54
20	452833	BE559681	Hs.30736	KIAA0124 protein	2.54
	422330 424962	D30783	Hs.115263	epiregulin	2.54
	430264	NM_012288 AA470519	Hs.153954	TRAM-like protein	254
	447178	AW594641	Hs.192417	gb:nc71f10.s1 NCI_CGAP_Pr1 Homo saplens ESTs	253
25	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	2.53 2.53
	433571	AA765256	Hs.135191	ESTs, Wealty similar to unnamed protein	2.53
	419449	H18417	Hs.57483	Homo sapiens cDNA FLJ14294 fis, clone PL	2.53
	448019	AW947164	Hs.195641	ESTs, Moderately similar to 138022 hypot	253
30	409435	AI810721	Hs.95424	ESTs	2.52
30	417900 431385	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	2.52
	422314	BE178536 K01900	Hs.11090 Hs.73890	membrane-spanning 4-domains, subfamily A interferon, aloha 8	2.52
	441343	AJ970348	Hs.132230	ESTs	2.52
	417185	NM_002484	Hs.81469	nucleotide binding protein 1 (E.coli Min	2.52 2.52
35	401747	•		NA	2.52
	448526	AB028946	Hs.21361	KIAA1023 protein	2.52
	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	2.52
	413627	BE182082	Hs.246973	ESTs	2.51
40	441285 446921	NM_002374 AB012113	Hs.167 Hs.16530	microtubule-associated protein 2	2.51
• • •	429357	AA779725	Hs. 164589	smal) inducible cytokine subfamily A (Cy ESTs	2.51 2.51
	443171	BE281128	Hs.9030	TONDU	2.50
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	2.50
45	420795	AA323037	Hs.128645	sorting nexin 16	2.50
45	448582	AI538880	Hs.94812	ESTs	2.50
	445459	AJ478829	Hs.158465	likely ortholog of mouse putative IKK re	2.50
	423909 414315	AJ223183 Z24878	Hs.135194	immunoglobutin superfamily, member 6	2.50
	407568	AA740964	Hs.62699	gb:HSB65D052 STRATAGENE Human skeletal m ESTs	2.50
50	453911	AW503857	Hs.4007	Sarcolemmal-associated protein	2.50 2.50
	431571	AW500486	Hs.180610	splicing factor proline/glutamine rich (	2.50
	433843	AW021423	Hs.112819	ESTS	2.50
	456254	T19844		gb:B711F Heart Homo sapiens cDNA clone 8	2.50
55	403137 425895	A1260404	11- 151100	NA .	2.50
"	418612	AI269484 AB037788	Hs.161427 Hs.224961	zinc finger protein 215	2.50
	1.00/2	70007700	113.224301	cleavage and polyadenylation specific fa	2.50
	TABLE 45	<b>58</b> :			
60	Pkey:		e Eos probes	set identifier number	
60	CAT num		cluster numb		
	Accession	i: Genz	ank accession	numbers	
	Pkey	CAT Number	Accessions		
	410784	1221005_1		BE079700 BE062940	
65	410902	1226078_1		AW810108 AW809781 AW809844	
	411765	125700_1		248302 AA095182	
	413170	1351880_1		BE068821 BE068825	
	413516	1374595_1	BE145907 I	BE145796 BE145803 BE145851 BE145923 BE145812	BE145809 BE145852 BE145856
70	414315 428858	143512_1		494098 F13654 AA494040 AA143127	
70	430264	296453_1 315008_1		AW237453 BE327496 N47347 N56967 BE303010 BE302954 BE384120	
	431322	331543_1		AAS03009 AAS02998 AAS02989 AAS02805 T92188	
	434138	380572_1	AA625804	AW418787 AW074833 AI675842 AI393368	
	436411	419334_1	AW674352	AA715374 225205	
75	438159	451062	Z83947		
	439929	480591	S73205		
	451105	859083_1		W880941 AW880937	
	452453 454469	918300_1 1213727_1		1902518 A1902516 DE072509 AW702059	
80	454600	1226077_1	AW810001	BE072509 AW792958 AW810092 AW810170 AWR09884 AWR09564 AW910	353 AW810428 AW810209 AW810429 AW810154 AW810168 AW809786 AW810006
			AW809672	AW809694 AW810552 AW810345 AW810432 AW809	>>> ATTO 10428 AYTO 10203 AYYS 10923 AWYS 10154 AWS 10168 AWS 09786 AWS 10066
	454821	1238365_1	AW833504	AW833751 AW833493 AW833341	
	455309	1278153_1		AW893956 AW894032	

	456254	1699246_1	T19844 T11	755 T11830 T20136 T11957 R45834 R45828 R	5595				
	TABLE 45								
5	Pkey: Ref:	Sequ	vence source.	nber corresponding to an Eos probeset source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA flumnan chromosome 22" Dunham, et al. (1999) Nature 402-489-495.					
	Strand: ML_positio	ITIQXC	zaes una soa	les DNA strand from which exons were predicted.  les nucleobde positions of predicted exons.					
10	_								
10	Pkey	Ref	Strand	Nt_position					
	401458	9187886	Plus	76485-77597					
	401644	8576138	Plus	82655-83959					
	401747	9789672	Minus	118596-118816,119119-119244,119609-1197	1,120422-120990,130161-130381 130	M6R.130693 131007.131360 434066			
15				131932,132451-132575,133580-134011		P-100-10000,101001-101230,131000-			
13	402167	8571795	Plus	109122-110357					
	402299	6693370	Plus	23367-25175					
	402408	9796239	Minus	110326-110491					
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,9394	-94072 94591.94749 95214.95222				
20	403381	9438267	Minus	26009-26178					
20	403422	9665041	Minus	151169-151561					
	403548	8081591	Minus	38760-39352					
	403637	8671936	Minus	142647-142771,145531-145762					
	403639	8871948	Plus	113234-113326,115186-115287,119649-1197	6				
25	403778	7770611	Minus	1414-1513,1624-1756	_				
25	404253	9367202	Minus	55675-56055					
	404440	7528051	Ptus	80430-81581					
	404766	7882612	Minus	158681-158882,160838-160973					
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055	40674.42351-42450				
30	405466	7767904	Minus	04438-04675					
30	405770	2735037	Plus	61057-62075					
	405817 406117	4071056	Plus	19914-20112,25655-25810					
	405182	9142932 5923650	Plus	54304-54584					
	400102	3323030	Minus	28256-28935	•				
35									
	TARI F 46	A- AROUT 1303	CENECIDE	ECIMATED BUOTONIA CAMPAGA CAMPAGA	····				
	TABLE 46A: ABOUT 1303 GENES UP-REGULATED IN STOMACH CANCER COMPARED TO NORMAL STOMACH Table 46A 63bs about 1303 genes up-regulated in stomach cancer compared to normal stomach. These were selected as for Table 45A except using non-malignant stomach specimens in determining the denominator value and the ratio was found nor constructives.								
	specimens	In determinion	the denominat	or value and the ratio was equal to or greater that	mach. These were selected as for Tar	ble 45A except using non-malignant stomach			
	Pkey:			or Agron gard to Lander. Of Identifier until Land Mass edinal to or Greater tha	5.0.				
40	ExAcon:	Exen	nniar Arressin	n number, Genbank accession number					
	Unigenati	): Unio	ene number	minutes, Gentpank accession number					
	Unigene T		ene gene tide						
	R1:	Ratio	of tumor to no	ormal body tissue					
4 5									
45	Pkey	ExAcon	UnigenelD	Unigene Title	R1				
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	80.50				
	414152	NM_003248	Hs.75774	thrombospondin 4	70.52				
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	65.30				
50	428698	AA852773	Hs.334838	KIAA1866 protein	61.90				
50	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	50.60				
	409041	AB033025	Hs.50081	KIAA1199 protein	44.50				
	452281	T93500	Hs.28792	Homo sapiens cONA FLJ11041 fis, clone PL	41.10				
	452862 427585	AW378065	Hs.8687	ESTs	33.50				
55	424834	D31152 AK001432	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	32.10				
-	428398	A1249368	Hs.153408	Homo sapiens cDNA FLJ 10570 fis, clone NT	26.90				
	409757		Hs.98558	ESTS	26.40				
	403776	NM_001898	Hs.123114	cystatin SN	25.48				
	427674	NM_003528	Hs.2178	NA N2C Notice of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of the Park of t	24.90				
60	419968	X04430	Hs.93913	H2B histone family, member Q	23.80				
	427108	AB028976	Hs.173571	interleutrin 6 (interferon, beta 2) KIAA 1053 protein	23.10				
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	21.76				
	400419	AF084545		NA	20.70				
	415989	AI267700	Hs.317584	ESTs	20.40				
65	432101	AI918950	Hs.123642	EphA3	19.80				
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecul	19.70				
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	19.00				
	412652	AI801777	Hs.6774	ESTs	18.40 18.20				
70	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	17.71				
70	422168	AA586894	Hs.112408	\$100 calcium-binding protein A7 (psorias	17.38				
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	17.36				
	437446	AA788946	Hs.16869	ESTs, Moderately similar to CA1C RAT COL	17.00				
	440594	AW445167	Hs.126036	ESTs	17.00				
75	430044	AA464510	Hs.152812	ESTs	17.00				
15	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	16.90				
	414737	AI160386	Hs. 125087	ESTs	16.50	•			
	427335	AA448542	Hs.251677	G antigen 78	16.30				
	423453	AW450737	Hs.128791	CGI-09 protein	15.50	•			
80	414569	AF109298	Hs.118258	prostate cancer associated protein 1	15.40				
	401961 434551	NA 0C397163	LL 200027	NA .	15.40				
	432069	8E387162 AW975868	Hs.280858	ESTs, Highly similar to A35661 DNA excis	15.40				
	434699	AA543687	Hs.294100	ESTS	15.30				
	10100	. 410-3001	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	15.30				

	409062 400289	AL157488 X07820	Hs.50150	Homo sapiens mRNA; cDNA DKFZp564B182 (fr	15.30
	415138	C18356	Hs.2258 Hs.295944	matrix metalloproteinase 10 (stromelysin tissue factor pathway inhibitor 2	15.20
	426820	AA436187	Hs.172631	integrin, alpha M (complement component	15.20 15.19
5	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	15.10
	438639	AI278360	Hs.31409	ESTs	15.10
	458997	AW937420	Hs.69662	ESTs	15.00
	432731	R31178	Hs.287820	fibronectin 1	14.90
10	459247 451099	N46243 R52795	Hs.110373	ESTs, Highly similar to T42626 secreted	14.70
10	452242	R50956	Hs.25954 Hs.159993	Interteukin 13 receptor, alpha 2 gycosyttransferase	14.70 14.70
	426427	M86699	Hs.169840	TTK protein kinase	14.50
	439924	AI985897	Hs.125293	ESTs	14,45
	414869	AA157291	Hs.21479	ubinuclein 1	14.40
15	411573	AB029000	Hs.70823	KIAA 1077 protein	14.40
	418593	AI750878	Hs.87409	thrombospondin 1	14.37
	421823 423903	N40850 N57765	Hs.28625 Hs.1721	ESTs interleukin 11	14.30
	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	14.20 14.10
20	447417	AW732858	Hs.143067	KIAA1602 protein	13.96
	416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	13.90
	446392	AF142419	Hs.15020	homolog of mouse quaking QKI (KH domain	13.90
	412863	AA121673	Hs.59757	zinc finger protein 281	13.90
25	449509 440953	AA001615 AI683036	Hs.84561	ESTS	13.80
25	432415	T16971	Hs.124135 Hs.289014	Homo sapiens cDNA FLJ13051 fis, clone NT ESTs, Weakly similar to A43932 mucin 2 p	13.80 13.60
	428769	AW207175	Hs.106771	ESTs	13.60
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	13.41
20	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	13.40
30	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13555 fls, clone PL	13.30
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	13.26
	406972 432368	M32053 AW970244	Hs.162188	gb:Human H19 RNA gene, complete cds.	13.19
	424806	AA382523	Hs.105689	ESTs MSTP031 protein	13.16 13.08
35	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	12.98
-	437789	AJ581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	12.90
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	12.80
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	12.80
40	402363 444301	NA AK000135	11- 40750	NA	12.78
40	416783	AA206186	Hs.10760 Hs.79889	asporin (LRR class 1) monocyte to macrophage differentiation-a	12,76 12.60
	435706	W31254	Hs.7045	GL004 protein	12.50
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	12.50
45	439737	AJ751438	Hs.41271	Homo sapiens mRNA full length insert cDN	12.49
45	405770			NA	12.48
	418678	NM_001327	Hs.167379	cancer/testis antigen	12.45
	414132 410434	AI801235 AF051152	Hs.48480 Hs.63668	ESTs	12.40
	451092	AI207256	Hs.13766	toll-like receptor 2 Homo sapiens mRNA for FLJ00074 protein,	12.30 12.26
50	407891	AA486620	Hs.41135	endomucin-2	12.20
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	12.01
	411213	AA676939	Hs.69285	neuropilin 1	12.00
	436476	· AA326108	Hs.33829	bHLH protein DEC2	12.00
55	413582 449318	AW295647 AW236021	Hs.71331 Hs.78531	hypothetical protein MGC5350	11.90
73	401747	A11230021	NS.70001	Homo sepiens, Similar to RIKEN cONA 5730 NA	11.90 11.88
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	11.84
	432596	AJ224741	Hs.278481	matrilin 3	11.80
60	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	11.73
60	425688	U48361	Hs.159223		11.72
	407938 419948	AA905097	Hs.85050	phospholamban	11.70
	459645	AB041035 AA074346	Hs.93847 Hs.250715	NADPH oxidase 4 ESTs	11.70
	438462	AI624122	Hs.89578	general transcription factor IIH, polype	11.51 11.50
65	434851	AA806164	Hs.116502		11.50
	418699	BE539639	Hs.173030		11.47
	413453	AA129640	Hs.128065	ESTs	11.40
	442028	AI239437	Hs.48945	ESTs	11.40
70	428479 453313	Y00272 BE005771	Hs.184572 Hs.153746		11.39
,,	421633	AF121860	Hs.106260		11.20
	410339	AI916499	Hs.298258		11.20 11.20
	448111	AA053486	Hs.20315	Interferon-Induced protein with tetratri	11.15
76	453857	AL080235	Hs.35851	DKFZP586E1621 protein	11.15
75	430217	N47863	Hs.336901	ribosomal protein S24	11.10
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	11.10
	416530 416854	U62801 H40164	Hs.79361 Hs.80296	kalikrein 6 (neurosin, zyme)	11.06
	447072	D61594	Hs.17279	Purkinje cell protein 4 tyrosytprotein sulfotransferase 1	10.90 10.90
80	424882	AI379461	Hs.153636		10.80
	448693	AW004854	Hs.228320		10.80
	408750	8E294069	Hs.93581	hypothetical protein FLJ10512	10.80
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	10.80



441533 A3484673   441597   41171   41171   41171   41171   41171   41171   41172   41173   41173   41173   41174   41175   41175   41176   41177   41177   41177   41177   41177   41178   41178   41178   41178   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4118   4		436411	AW674352		-b4-62-02 t tmt 1100 1011	
414920 00723 h. 147753 (19)-circ clean-rage system protein H (amrino 10.00 h. 147757 (19197) h. 1485366 (19197) h. 14753 (19197) h. 1485366 (19197) h. 1485366 (19197) h. 14162 (19197) h. 148536 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162 (19197) h. 14162				He 7043	gb:ba63c07.y1 NIH_MGC_12 Homo sapiens cD	10.80
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1977   1987   1989   1988   1942   1987   1988   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   19	_				ESTs	
141412   AWSSA197   Hs. 150942   Horne sapiers cDNA FLJ1439 fs, done HE   10.30   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10.50   10	5				ubiquitin-like 1 (sentrin)	
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405044   Al129586   ks.33033   hypothetical protein FU14823   10.30   43819   AW\$11097   ks.112755   ESTs   10.30   43819   AW\$11097   ks.112755   ESTs   10.30   43819   AW\$11097   ks.112755   ESTs   10.30   43819   AW\$11097   ks.112755   ESTs   10.30   AW\$1766   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682   ks.18682	25					
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	420900	AL045633 BE081050	Hs.44269	ESTs	9.11
	450757 410929	H47233	Hs.31570 Hs.30643	ESTs, Weakly similar to KIAA1324 protein ESTs	9.10
_	427319	AW631495	Hs.27135	B-cell receptor-associated protein BAP29	9.10 9.10
5	443745	AB039670	Hs.9728	ALEX1 protein	9.10
	436574	AW293527	Hs.126465	ESTs	9.10
	407192	AA509200		gb:af12e02.s1 Soares_testis_NHT Homo sap	9.08
	426075 408778	AW513691 AI500519	Hs.270149 Hs.63382	ESTs, Weakly similar to 2109260A B cell	9.07
10	434542	AA769310	Hs.61260	hypothetical protein PRO2714 hypothetical protein FLJ13164	9.03 9.00
••	404440	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	113.512.55	NA	9.00
	407168	R45175	Hs.117183	ESTs	9.00
	451678	AA374181	Hs.26799	DKFZP564D0764 protein	9.00
15	431946 408875	AI018336 NM_015434	Hs.131730	ESTs	8.92
13	409928	AL137163	Hs.48604 Hs.57549	DKFZP434B168 protein hypothetical protein dJ473B4	8.90 8.90
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	8.89
	445029	AF196481	Hs.12256	midline 2	8.86
20	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	8.80
20	409089 419261	NM_014781 X07876	Hs.50421	KIAA0203 gene product	8.80
	418190	N54000	Hs.89791	wingless-type MMTV integration site fami gb:yy99d02.r1 Soares_multiple_sclerosis_	8.80 8.80
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	8.77
0.5	416440	AI823912	Hs.79335	Homo sepiens, Similar to SWI/SHF related	8.76
25	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	8.70
	441031 452234	Al110684	Hs.7645	fibringen, 8 beta polypeptide	8.70
	452822	AW084176 X85689	Hs.223296 Hs.288617	ESTs. Weathy similar to I38022 hypotheti hypothetical protein FLJ22621	8.70 8.70
	430462	AI584156	Hs.105640	Homo sapiens, clone IMAGE:4139775, mRNA,	8.65
30	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	8.65
	412054	W87482	Hs.302209	ESTs	8.64
	450236	AW162998	Hs.24684	KIAA1376 protein	8.63
	418782 452631	AI792648 AI188658	Hs.14665 Hs.87498	ESTs ESTs	8.60 8.60
35	425268	AJB07883	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	8.60
	432014	H56741	Hs.38540	ESTs, Weakly similar to ALU4_HUMAN ALU S	8.60
	440270	NM_015986	Hs.7120	cytokine receptor-like molecule 9	8.60
	414784 426809	NM_000344	Hs.288986	survival of motor neuron 1, telomeric	8.60
40	419704	BE313114 AA429104	Hs.29706 Hs.45057	ESTs ESTs	8.60 8.60
	452909	NM_015368	Hs.30985	pannexin 1	8.60
	432639	AW973785		gb:EST385886 MAGE resequences, MAGM Homo	8.60
	430418	R98852	Hs.36029	heart and neural crest derivatives expre	8.58
45	450480	X82125	Hs.25040	zinc finger protein 239	8.58
73	444984 419086	H15474 NM_000216	Hs.132898 Hs.89591	fatty acid desaturase 1 Kallmann syndrome 1 sequence	8.58 8.57
	430518	AW363687	Hs.82916	chaperonin containing TCP1, subunit 6A (	8.50
	424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family	8.50
50	414061	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic	8.50
50	407894 441079	AJ278313 AW150697	Hs.41143	phosphoinositide-specific phospholipase	8.50
	419354	M62839	Hs.107418 Hs.1252	ESTs apolipoprotein H (beta-2-glycoprotein I)	8.50 8.50
	418618	U66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dy	8.50
<i>5                                    </i>	416565	AW000960	Hs.44970	endoplasmic reticulum resident protein 5	8.50
55	441540	C01367	Hs.127128	ESTs	8.50
	416434 417801	AW163045 AA417383	Hs.79334 Hs.82582	nuclear factor, interleukin 3 regulated integrin, beta-like 1 (with EGF-like rep	8.50
	426855	AL117427	Hs.172778	Homo sapiens mRNA; cDNA DKFZp566P013 (fr	8.50 8.48
60	436515	AJ278111	Hs.195292	putative turnor antigen	8.43
60	416315	AA179483	Hs.73605	ESTs	8.42
	408432 410094	AW195262	Lin COCOC	gb:xn67b05.x1 NCI_CGAP_CML1 Homo sapiens	8.40
	419198	BE147897 AA234938	Hs.58593 Hs.87384	general transcription factor (IF, polype ESTs	8.40 8.36
	448920	AW408009	Hs.22580	alkylghycerone phosphate synthase	8.36
65	410305	AF030409	Hs.62185	solute carrier family 9 (sodium/hydrogen	8.31
	408687	AL110280	Hs.301152	Homo sepiens mRNA; cDNA DKFZp434F053 (fr	8.30
	427707 459060	NM_005578 H89244	Hs.180398	LIM domain-containing preferred transloc	8.30
	451957	A1796320	Hs.303627 Hs.10299	heterogeneous nuclear ribonucleoprotein Horno sapiens cDNA FLJ13545 fis, clone PL	8.30 8.30
70	443977	AL120986	Hs.150627	ESTs, Weakly similar to 138022 hypotheti	8.30
	457997	AA806616	Hs.209523		8.30
	451934	AI540842	Hs.61082	ESTs	8.30
	404335 445073	AW291389	LL 1205C	NA humathadard acetain El 142020	8.30
75	431566	AF176012	Hs.13056 Hs.260720	hypothetical protein FLJ13920  J domain containing protein 1	8.30
	446307	T50083	Hs.9094	ESTs	8.29 8.28
	423928	AA332680		gb:EST36768 Embryo, 8 week t Homo sapien	8.26
	436420	AA443966	Hs.31595	ESTa	8.25
80	426110 442988	NM_002913 AI026130	Hs.166563		8.25
-	402408	NA NA	Hs.131683	ESTs NA	8.25 8.24
	438707	L08239	Hs.5326	amino acid system N transporter 2; porcu	8.23
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Sequency (s	8.22

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	448704	AW080932	Hs.249247	hatamananus nuclear austria stantas ta	0.74
	452682	AA456193	Hs.9071	heterogeneous nuclear protein similar to progesterone membrane binding protein	8.21 8.20
	411984	NM_005419	Hs.72988	Signal transducer and activator of trans	8.20
_	420018	U56387	Hs.94376	proprotein convertase subtilisin/kexin t	8.20
5	437048	AA743240	Hs.91582	ESTS	8.20
	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	8.20
	447066	8E167667	Hs.32163	ESTs	8.20
	425932	M81650	Hs.1968	samenogelin I	8.20
10	431819	AA515995	Hs.152334	ESTs	8.20
10	431810 459702	X67155 AJ204995	Hs.270845	kinesin-like 5 (mitotic kinesin-like pro	8.20
	406687	M31126	Hs.272620	gb:sn03c03.x1 Stratagene schizo brain S1	8.20
	413109	AW389845	Hs.110855	pregnancy specific beta-1-glycoprotein 9 ESTs	8.18 8.17
	424720	M89907	Hs.152292	SW/SNF related, matrix associated, acti	8.16
15	424335	AW021508	Hs.28170	ESTs	8.10
	453096	AW294631	Hs.11325	ESTS	8.10
	427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35kD, Ze	8.10
	457796	AA913389	Hs.126691	ESTs	8.10
20	429340 445165	N35938	Hs.199429	Homo sapiens mRNA; cDNA DKFZp434M2216 (f	8.10
20	418048	AV652831	U- CC044	gb:AV652831 GLC Homo sapiens cDNA clone	8.08
	426269	W49670 H15302	Hs.56044 Hs.168950	ESTS	8.06
	439451	AF086270	Hs.278554	Homo sapiens mRNA; cDNA DKFZp568A1046 (f heterochromatin-like protein 1	8.04
	419559	Y07828	Hs.91096	ring finger protein	8.02 8.02
25	409268	AA625304	Hs.188554	EST8	8.00
	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	8.00
	446977	AW863613	Hs.156798	ESTs	8.00
	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	8.00
30	407013	U35637		gb:Human nebulin mRNA, partial cds	7.99
50	414523 440637	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	7.98
	417076	AW900115 AW973454	Hs.7309 Hs.238442	Homo sapiens clone 23741 mRNA sequence	7.96
	425921	NM_007231	Hs.162211	ESTs, Moderately similar to ALU7_HUMAN A solute carrier family 6 (neurotransmitte	7.95 7.94
	415585	R59946	Hs.184852	KIAA1553 protein	7.94
35	453331	AI240665	Hs.8895	ESTs	7.92
	445527	W39694	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	7.90
	417318	AW953937	Hs.12891	ESTs	7.90
	429393	AA383024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (1	7.90
40	444769	A1191650	Hs.221436	ESTs	7.90
70	444272 425264	A1138596 AA353953	Hs.154619	ESTs	7.90
	412642	BE244598	Hs.20369 Hs.809	ESTs, Weakly similar to gonadotropin ind	7.90
	453765	BE279901	Hs.35091	hepatocyte growth factor (hepapoietin A; hypothetical protein Ft.J10775	7.90 7.90
	421558	AB011125	Hs.105749	KIAA0553 protein	7.90
45	446444	A1743737	Hs.24370	ESTs	7.90
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	7.86
	437237	BE513073		gb:601171435F1 NIH_MGC_15 Homo sapiens c	7.88
	409582	R27430	Hs.271565	ESTs	7.84
50	419235 439620	AW470411 AA838727	Hs.288433	neurotrimin	7.83
50	441690	R81733	Hs.124405 Hs.33106	ESTs, Weakly similar to A46010 X-finked ESTs	7.82
	417735	AA188175	Hs.82506	KIAA1254 protein	7.80 7.80
	441795	N58115	Hs.21137	AD024 protein	7.80
	442992	AJ914699	Hs.13297	ESTs	7.80
55	422554	AA312219	Hs.296338	ESTs	7.80
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; Human selen	7.80
	428627 429228	BE002993	Hs.187660	putative Rab5 GDP/GTP exchange factor ho	7.60
	429399	AI553633 AA452244	Hs.337139	ESTs	7.80
60	438396	AI583487	Hs.16727 Hs.152213	ESTs wingless-type MMTV integration site fami	7.80
	455510	AA422029	Hs.143640	ESTs, Weakly similar to hyperpolarizatio	7.77 7.76
	429396	AW954598	Hs.201626	Homo sapiens clone 25015 mRNA sequence	7.76
	453439	A1572438	Hs.32976	guanine nucleotide binding protein 4	7.75
65	410561	BE540255	Hs.6994	Homo sepiens cDNA: FLJ22044 fis, clone H	7.71
65	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	7.71
	428655	H05769	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp	7.70
	404996	NM_001034	Hs.75319	ribonucleolide reductase M2 polypeptide	7.70
	418947	W52990	Hs.22860	NA For-	7.70
70	427401	U20582	Hs.2149	ESTs actin like protein	7.70 7.70
	410748	BE383816	Hs. 12532	chromosome 1 open reading frame 21	7.70
	426262	A1792141	Hs.196270	folate transportericarrier	7.70
	446955	AW613138	Hs.156747	ESTs	7.70
75	449199	AJ990122	Hs.196988		7.70
13	443212	AW269515	Hs.102500		7.70
	446155	AI553695	Hs.159422		7.70
	427164 452627	AB037721 AJ122843	Hs.173871 Hs.184319		7.70
	452588	AA889120	Hs.110637		7.70
80	451838	AW005866	Hs.193969		7.70 7.67
	422956	BE545072	Hs.122579		7.67 7.66
	451227	R84429	Hs_151944	ESTs, Wealdy similar to high-risk human	7.66
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	7.65

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	43000	000400			
	432695 447476	D63480 BE293466	Hs.278634	KIAA0146 protein	7.63
	447289	AW247017	Hs.20880 Hs.36978	ESTs, Weakly similar to t38022 hypotheti	7.60
_	447505	AL049266	Hs.18724	melanoma antigen, family A, 3 Homo saplens mRNA; cDNA DKFZp564F093 (tr	7.60
5	423065	R96158	Hs.267130	Homo sapiens, clone MGC:5406, mRNA, comp	7.60 7.60
	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	7.60
	450628	AW382884	Hs.204715	ESTs	7.60
	418995	H39599	Hs.294008	ESTs	7.60
10	416402	NM_000715	Hs_1012	complement component 4-binding protein,	7.60
10	405545			NA	7.60
	440866 421281	AI703103	Hs.271360	hypothetical protein MGC16275	7.60
	424534	AI299139 NM_003613	Hs.17517 Hs.151407	EST8	7.60
	421041	N36914	Hs.14691	cartilage intermediate layer protein, nu ESTs, Moderately similar to I38022 hypot	7.60
15	453311	AW104911	Hs.126707	hypothetical protein FLJ11457	7.60 7.54
	453060	AW294092	Hs.21594	hypothetical protein MGC15754	7.50
	417655	AA780791	Hs.14014	hypothetical protein FLJ14813	7.50
	417531	NM_003157	Hs.1087	serine/threonine kinase 2	7.50
20	444099	D87432	Hs.10315	solute carrier family 7 (cationic amino	7.50
20	407853	AA336797	Hs.40499	dickkopf (Xenopus laevis) homolog 1	7.50
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	7.50
	447806 424748	W03816 AA346257	Hs.10432 Hs.134933	ESTs, Wealdy similar to I38022 hypotheti	7.48
	421089	AB037771	Hs.101799	ESTs KIAA1350 protein	7.48
25	444856	AI888057	Hs.12097	ESTs	7.46 7.42
	447425	A1963747	Hs.18573	acylphosphalase 1, erythrocyte (common)	7.41
	418450	R84397	Hs.193651	ESTs, Weakly similar to alternatively sp	7.40
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	7.40
30	437036	AI571514	Hs.133022	ESTs	7.40
20	414680	AA743331	Hs.272572	hemoglobin, alpha 2	7.40
	451815 433577	AW974911 AW007080	Hs.184793 Hs.8817	Homo sapiens cDNA: FLJ21880 fis, clone H	7.40
	453652	AW009640	Hs.28368	ESTs ESTs, Moderately similar to S65657 alpha	7.40
	422665	AJ011812	Hs.119018	transcription factor NRF	7.40 7.40
35	424188	AW954552	Hs.142634	zinc finger protein	7.40
	407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell s3 93	7.40
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	7.40
	452958	AA883929	Hs.40527	ESTs	7.40
40	418763 428279	AK000219 AA425310	Hs.88367	hypothetical protein FLJ20212	7.40
40	449670	F07693	Hs.155766 Hs.23869	ESTs. Weakly similar to A47582 B-cell gr	7.40
	449601	AA461509	Hs.293565	Homo sapiens mRNA; cDNA DKF2p434K2172 (f ESTs, Weakly similar to putative p150 fH	7.40
	438490	AW593272	Hs.301299	ESTs	7.40 7.40
	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	7.40
45	429509	AW614420	Hs.204354	ras homolog gene family, member B	7.38
	433393	AF038564	Hs.98074	itchy (mouse homolog) E3 ubiquitin prote	7.38
	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	7.37
	425773	N21279	Hs.237749	EST8	7.36
50	422755 410566	T25365 AA373210	Hs.119687 Hs.43047	RAN binding protein 8	. 7.36
50	412851	AI826502	Hs.106149	Homo sapiens cONA FLJ13585 fis, clone PL ESTs	7.35
	418661	NM_001949	Hs.1189	EZF transcription factor 3	7.35 7.35
	436246	AW450963	Hs.119991	ESTs	7.34
	433159	AB035898	Hs.150587	kinesin-like protein 2	7.33
55	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	7.32
	453878	AW964440	Hs.19025	DC32	7.31
	414696 402250	AF002020	Hs.76918	Niemann-Pick disease, type C1	7.31
	439039	AV655272 AI656707	Hs.20252	novel Ras family protein	7.31
60	417976	BE565892	Hs.48713 Hs.83077	ESTs interleukin 18 (Interferon-parmma-Inducin	7.30 7.30
-	419438	AA991639	Hs.242413	hypothetical protein DKFZp434K1421	7.30 7.30
	417008	AW673606	Hs.80758	aspartyl-IRNA synthelase	7.30 7.30
	425420	BE536911	Hs.234545	hypothetical protein NUF2R	7.30
65	425889	M57414	Hs.161305	tachyltinin receptor 2	7.29
05	442969	AI025499	Hs.132238	ESTs	7.26
	446360 438022	N42553 AW517524	Hs.267914	homolog of mouse transient receptor pote	7.25
	407183	AA358015	Hs. 135201	NOD2 protein	7.25
	429882	AA278898	Hs.225979	gb:EST66664 Fetal tung III Homo sapiens hypothetical protein similar to small G	7.24
70	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.24 7.22
	400212	NA		NA	7.22 7.20
	431812	AA515902	Hs.130650	ESTs	7.20
	419481	AI879195	Hs.90606	15 kOa selenoprotein	7.20
75	447078	AW885727	Hs.301570	ESTs	7.20
,,	413200	AA127395	Hs.222414	ESTS	7.20
	411750 439901	BE562298 N73885	Hs.71827	KIAA0112 protein; homolog of yeast ribos	7.20
	411815	AA156679	Hs.124169 Hs.125790	ESTS	7.20
•	459279	AW814996	119.163130	leucine-rich repeat-containing 2 gb:MR1-ST0206-170400-024-h09 ST0206 Homo	7.20
80	445263	H57646	Hs.42586	KIAA1560 protein	7.20 7.20
	413801	M62246	Hs.35406	ESTs. Highly similar to unnamed protein	7.20
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	7.20
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.20

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	425202	AW962282	Hs.152049	ESTs, Weakly similar to 138022 hypotheti	7.20
	403764			NA	7.20
	416896	AI752862	Hs.5638	KIAA 1572 protein	7.20
5	416636 428071	N32536 AF212848	Hs.42645 Hs.182339	ESTs ets homologous factor	7.20
•	450142	AW207469	Hs.24485	chondroitin sulfate proteoglycan 6 (bama	7.20 7.18
	451017	BE391847	Hs.181173	hypothetical protein MGC10771	7,17
	409759	N40285	Hs.81182	histamine N-methyltransferase	7.16
10	452448 427951	AW182440 AI826125	Hs.61389 Hs.43546	ESTs, Wealdy similar to unnamed protein	7.16
10	407939	W05608	Hs.312679	ESTs ESTs, Wealdy similar to A49019 dynein he	7.16 7.15
	419457	AA243146	Hs.209334	ESTs, Moderately similar to SZ3A_HUMAN P	7.12
	411769	AI694575	Hs.27207	KIAA0982 protein	7.11
15	430355 419511	NM_006219	Hs.239818 Hs.75113	phospholnosidde-3-kinase, catalytic, be	7.10
	409032	AA429750 AW301807	Hs.297260	general transcription factor IIIA ESTs	7.10 7.10
	424539	L02911	Hs.150402	activin A receptor, type I	7.10
	439221	AA737106	Hs.32250	ESTs, Moderately similar to 178885 serin	7.10
20	430719	AA488988	Hs.293796	ESTs	7.10
20	408020 420218	AA127940 AW958037	Hs.62781 Hs.286	ESTs ribosomal protein L4	7.10 7.10
	443487	AI073491	Hs.269887	ESTs, Highly similar to KPBB_HUMAN PHOSP	7.10 7.10
	414865	AA157155	Hs.274414	hypothetical protein FLJ 14457	7.10
25	428724	AL390128	Hs.191268	KIAA1530 protein	7.10
23	413293 419126	AL047483 AI810144	Hs.302498 Hs.135276	GTP-binding protein hornologous to Saccha ESTs	7.10
	437044	AL035864	Hs.69517	cONA for differentially expressed CO16 g	7.09 7.09
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	7.07
30	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	7.07
30	457019 409697	AA421844 AB018348	Hs.12830 Hs.55947	hypothesical protein KIAA0805 protein	7.07
	400977	NA	113.55541	NA	7.06 7.06
	436668	AA831857	Hs.209071	ESTs	7.03
35	451684	AF216751	Hs.26813	CDA14	7.03
20	404029 448719	AA033627	Hs.21858	NA Innucleotide repeat containing 3	7.02
	445577	N40696	Hs.137084	cytoplasmic polyadenylation element bind	7.02 7.00
	419647	AA348947	Hs.91816	hypothetical protein	7.00
40	442075	AW135928		gb:UI-H-Bi1-adp-d-08-0-UI.s1 NCI_CGAP_Su	7.00
40	429598 450832	AA811257 AW970602	Hs.269710 Hs.105421	ESTs ESTs	7.00
	421389	AA531291	Hs.101064	Homo sapiens cDNA FLJ12777 fis, clone NT	7.00 7.00
	453931	AL121278	Hs.25144	ESTs	7.00
15	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	7.00
45	452979 431696	AW167599	Hs.232282	ESTs	7.00
	413583	AA259068 AL120806	Hs.267819 Hs.5888	protein phosphatase 1, regulatory (inhib ESTs	7.00 7.00
	436758	AW977167	Hs.155272	ESTs	7.00
50	455944	BE160643		gb:PM1-HT0422-291299-002-f03 HT0422 Homo	6.98
50	430302	AL137502	Hs.238679	Rag D protein	6.96
	437613 440524	R19892 R71264	Hs.10267 Hs.16798	MIL1 protein ESTs	6.96
	451047	AB022317	Hs.25887	sema domain, immunoglobulin domain (lg),	6.95 6.93
e e	450377	AB033091	Hs.74313	KIAA1265 protein	6.93
55	457396	Z20964	Hs.323817	OKFZP547E1010 protein	6.93
	417393 414417	R10484 BE299433	Hs.82071 Hs.68533	Cbp/p300-Interacting transactivator, wit KIAA1879 protein	6.92
	412248	AJ160873	Hs.69233	zinc finger protein	6.92 6.90
60	411003	AA181018	Hs.13056	hypothetical protein FLJ13920	6.90
60	413833	Z15005	Hs.75573	centromere protein E (312kD)	6.90
	405696 431689	NA AA305688	Hs.267695	NA LIDO Cal-hotoClobiAo hoto 1.3 polostos de	6.90
	414429	R51494	Hs.71818	UDP-Gal:betaGlcNAc beta 1,3-galactosyttr ESTs	6.90 6.90
	424841	AB001106	Hs.151413	glia maturation factor, beta	6.90
65	418895	AA894638	Hs.14600	ESTs	6.90
	445900 446006	AF070526 NM_004403	Hs.13429 Hs.13530	Homo sapiens clone 24787 mRNA sequence	6.90
	432038	AA524745	Hs.162110	deafness, autosomal dominant 5 ESTs	6.90 6.87
~~	445610	AV659433	Hs.282984		6.86
70	451286	AW139789	Hs.16370	Homo sapiens cDNA FLJ11652 fis, clone HE	6.86
	408915 418934	NM_016651 TB3845	Hs.48950	heptacellular carcinoma novel gene-3 pro	6.85
	435143	R12375	Hs.191116 Hs.194600		6.82 6.82
7.	442660	AW138174	Hs.130651		6.82
75	432729	AK000292	Hs.278732	hypothetical protein FLJ20285	6.81
	435990	AJ015862	Hs.131793	ESTs	6.80
	449062 453688	AJ272268 AW381270	Hs.22958 Hs.194110	calcium channel, voltage-dependent, alph hypothetical protein PRO2730	6.80
	421476	AW953805	Hs.21887	ESTs	6.80 6.80
80	430510	AW162916	Hs.241576	hypothetical protein PRO2577	6.80
	409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp43400515 (I	6.80
	410298 420560	A1693821 AW207748	Hs.182185 Hs.59115	ESTs ESTs	6.80
	-20000	**********	14.33113	2018	6.80

	427752	AA470687	Hs.104772	ESTs .	6.80
	414080 422420	AA135257 U03398	Hs.47783	B aggressive lymphoma gene	6.80
	416913	AW934714	Hs.1524	tumor necrosis factor (figand) superfami	6.80
5	426890	AA393167	Hs.41294	gb:RC1-DT0001-031299-011-a11 DT0001 Homo ESTs	6.80
_	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	6.60 6.80
	413328	Y15723	Hs.75295	guanyiate cyclase 1, soluble, alpha 3	6.79
	437619	AW351491	Hs.334853	hypothetical protein FLJ23544	6.79
10	434267	AI206589	Hs.116243	ESTs	6.79
10	419358	T78763	Hs.90063	neurocalcin delta	6.79
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	6.78
	424925 443184	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant	6.77
	444484	A1538728 AK002126	Hs.131973 Hs.11260	ESTs	6.77
15	429483	AA974832	Hs.128708	hypothetical protein FLJ11264 ESTs	6.77 6.78
	425605	BE544300	Hs.7076	KIAA1705 protein	6.76
	425045	AW953186	Hs.92400	ESTs	6.76
	438776	AW245243	Hs.334368	hypothetical protein MGC11257	6.75
20	458174	AA781530	Hs.127236	hypothetical protein FLJ12879	6.74
20	445129	R39878	Hs.21394	ESTs	6.74
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	6.73
	444442 431240	A1149234 AA496790	Hs.298423 Hs.179481	ESTs, Moderately similar to I54374 gene	6.73
	422109	S73265	Hs.1473	ESTs gastrin-releasing peptide	6.72
25	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	6.70 6.70
	423811	AW299598	Hs.50895	homeo box C4	6.70
	443695	AW204099	Hs.337720	ESTs, Wealdy similar to AF126780 1 retin	6.70
	420686	A1950339	Hs.40782	ESTs	6.70
30	419574	AK001989	Hs.91165	hypothetical protein	6.70
30	418269	AA806113	Hs. 189025	EST8	6.70
	434164 408660	AW207019 AA525775	Hs.148135	serine/threonine kinase 33	6.70
	453370	AJ470523	Hs.292523 Hs.139336	ESTs, Moderately similar to PC4259 ferri ATP-binding cassette, sub-family C (CFTR	6.70
	409506	NM_006153	Hs.54589	NCK adaptor protein 1	6.70 6.70
35	454029	W05150	Hs.37034	homeo box A5	6.70
	413365	AW205188	Hs.124304	Homo sapiens cDNA FLJ14635 fts, clone NT	6.70
	447247	AW369351	Hs.287955	Homo sapiens cONA FLJ13090 fis, clone NT	6.70
	426566	AF131836	Hs.170453	tropomodulin	6.70
40	446261	AA313893	Hs.306219	hypothetical protein FLJ12615 similar to	6.70
70	408547 430458	AA574291 AA479300	Hs.57837	ESTs	6.70
	413627	BE182082	Hs.225706 Hs.246973	ESTs, Wealdy similar to I38022 hypotheti ESTs	6.70
	410498	AA355749	F15.240973	gb:EST64459 Jurkat T-cells VI Homo sapie	6.70 6.70
	434015	AA844518	Hs.300876	hypothetical protein FLJ 13386	6.70
45	453691	H12235	Hs.226505	ESTs	6.68
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	6.68
	415885	D79983	Hs.78894	KIAA0161 gene product	6.68
	405529	AW410458	Hs.5258	chromosome 11 open reading frame2	6.68
50	438242 442643	AW241910 U82756	Hs.122254	ESTs, Wealdy similar to JX0369 collagen	6.68
•	424802	X79201	Hs.8551 Hs.153221	PRP4/STKWD splicing factor synovial sarcoma, translocated to X chro	6.67
	415007	BE244332	Hs.77770	adaptor-related protein complex 3, mu 2	6.67 6.67
	458714	R20916	Hs.202501	ESTs	6.66
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	6.65
55	433260	AB040966	Hs.83575	KIAA1533 protein	6.65
	400268	NA		NA	6.63
	453180 403973	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	6.62
	436862	NA A1821940	Hs.264622	NA ESTe Modernieh eimileete ALLIS MISSAN A	6.60
60	428046	AW812795	Hs.155381	ESTs, Moderately similar to ALU8_HUMAN A ESTs, Moderately similar to I38022 hypot	6.60 6.60
	453387	A1990741	Hs.252809	ESTs	6.60
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	6.60
	418444	AI902899	Hs.8\$155	butyrate response factor 1 (EGF-response	6.60
65	448172	N75276	Hs.135904	ESTs	6.60
C)	409571	AA504249	Hs.187585	ESTs	6.60
	423025	AA831267	Hs.12244	hypothetical protein FLJ20097	6.60
	430701 450373	A1760833 A1915790	Hs.293971 Hs.337282	ESTs	6.60
	419384	AA490866	Hs.39429	ESTs ESTs	6.60
70	429828	AB019494	Hs.225767	IDN3 protein	6.60 6.60
	441761	AJ222880		gb:qp40c06.x1 NCI_CGAP_Co8 Homo sepiens	6.60
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	6.60
	421111	BE299047	Hs.43532	ESTs. Weakly similar to T20177 hypotheti	6.60
75	407424	AF120493		gb:Homo sapiens elastase 1 precursor (EL	6.59
13	412396	AW947895	11. 70075	gb:PM1-MT0010-200300-001-f10 MT0010 Homo	6.57
	416209 406674	AA236776 AA332152	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	6.57
	400860		Hs.288036	tRNA isopentanylpyrophosphata transferas NA	6.57
	457893	AA744292		gb:ny51d05.s1 NCI_CGAP_Pr18 Homo sepiens	6.56 6.55
80	426108	AA622037	Hs. 166468	programmed cell death 5	6.54
	422133	AW612779	Hs.333159	Homo sapiens laryngeal carcinoma related	6.54
	421044	AF061871	Hs.311736	Human DNA sequence from clone RP1-238D15	6.54
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	6.53

	400351	AF060169	Hs.272369	Homo sepiens AS11 protein mRNA, partial	6.52
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	6.52
	410416	BE410072	Hs.63304	protein phosphatase methylesterase-1	6.50
5	419852	AW503756	Hs.286184	hypothetical protein dJ55102.5	6.50
,	419677 431806	N77342 AF186114	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	6.50
	429774	A1522215	Hs.270737 Hs.50883	tumor necrosis factor (ligand) superfami KIAA1804 protein	6.50 6.50
	428228	AA424352	Hs.210586	ESTS	6.50
	418134	AA397769	Hs.86617	ESTs	6.50
10	403859	NA		NA .	6.50
	422704	AA972147	Hs.132275	ESTs	6.50
	416737	AF154335	Hs.79691	LIM domain protein	6.50
	429854	R55508	Hs.99472	ESTs	6.50
15	422672	X12784	Hs.119129	collagen, type IV, alpha 1	6.49
13	453600	BE245211	Hs.119120	E3 ubiquitin ligase SMURF1	6.48
	454835 434603	AW833763 AF147384		gb:QV4-TT0008-130100-077-d10 TT0008 Homo	6.48
	408243	Y00787	Hs.624	gb:Homo sapiens full length insert cDNA Interleukin 8	6.48
	429317	AA831552	Hs.268016	Homo sapiens cDNA: FLJ21243 fs, clone C	6.48 6.47
20	451316	AI770011	Hs.208310	ESTs	6.46
	448339	AL035920	Hs.20938	RNA binding motif, single stranded inter	6.46
	433423	BE407127	Hs.8997	heat shock 70kD protein 1A	6.44
	410358	AW975168	Hs.13337	ESTs. Weakly similar to unnamed protein	6.44
25	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	6.42
25	440526	AI832243	Hs.211471	ESTs	6.42
	432727	AA305233	Hs.278712	eukaryotic translation initiation factor	6.41
	433009 435782	AA761668 N49433	Hs.285737	gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens	6.40
	415071	AK002197	Hs.284270	Homo sapiens cONA: FLJ20895 fis, clone A Homo sapiens cDNA FLJ11335 fis, clone Pt.	6.40 6.40
30	407162	N63855	Hs.142634	zinc finger protein	6.40
	446152	AI292036	Hs.150028	ESTs	6.40
	422828	AL133396	Hs. 121281	prion protein 2 (dublet)	6.40
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	6.40
25	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	6.40
35	429039	AI\$24793	Hs.301897	ESTs	6.40
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	6.40
	435159 429625	AA668879 AA455568	Hs.116649	ESTa	6.40
	430180	AA331406	Hs.193814 Hs.75456	ESTs A kinase (PRKA) anchor protein 10	6.40
40	408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	6.40 6.40
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	6.40
	449911	AJ262108	Hs.12653	ESTs	6.40
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	6.40
AE	440395	AA884412	Hs.216342	ESTS	6.37
45	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	6.37
	417771	AA804698	Hs.82547	retinoic acid receptor responder (lazaro	6.36
	417092 412227	H97508 AW902282	Hs.181165	eukaryotic translation elongation factor	6.36
	400845	AW302202		gb:QV3-NN1023-260400-169-g10 NN1023 Homo NA	6.36
50	403546	NA		NA NA	6.36 6.36
	412345	AW938386		gb:PM4-DT0057-201299-002-G10 DT0057 Homo	6.35
	422186	AW962364	Hs.129051	ESTs	6.34
	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	6.34
55	417687	AI828596	Hs.250691	ESTs	6.33
22	426223	AW977812	Hs.130391	EST ₅	6.32
	417588	Z44510 AW860548	11. 000cco	gb:HSC220091 normalized infant brain cDN	6.32
	432829 440495	AA887212	Hs.280658 Hs.14161	ESTs	6.31
	407771	AL138272	Hs.62713	hypothetical protein DKFZp434I1930 ESTs	6.31 6.31
60	417517	AF001176	Hs.82238	POP4 (processing of precursor , S. cerev	6.30
	431041	AA490967	Hs.197955	KIAA0704 protein	6.30
	445571	Al378000	Hs.158489	ESTs, Wealdy similar to 2184_HUMAN ZINC	6.30
	433309	AA807060	Hs.126558	ESTs	6.30
65	415659	W27214	Hs.78547	zinc finger protein (clone 647)	6.30
03	420271	A1954365	Hs.42892	ESTs	5.30
	426921 400950	AA037145 NA	Hs.172865	cleavage stimulation factor, 3' pre-RNA,	6.30
	429692	N48422	Hs:9977	NA EFT World similar to 024007 beauty of	6.30
	439813	AA846321	Hs.124501	ESTs, Wealdy similar to 834087 hypotheti ESTs	6.30
70	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxytic	6.30 6.30
	453596	AA441838	Hs.62905	hypothetical protein FLJ14834	6.30
	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 ffs, clone H	6.30
	435820	AA700580	Hs.189000	ESTs	6.30
75	452576	AB023177	Hs.29900	KIAA0960 protein	6.30
75	448924	AW450569	Hs.188399	ESTs	6.30
	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	6.30
	412591 426642	BE217736	Hs.292653	ESTs, Weakly similar to T26845 hypotheti	6.30
	419088	AW068223 AI538323	Hs.171581 Hs.52620	ubiquitin C-terminal hydrolase UCH37 integrin, beta 8	6.30
80	401424		14.36060	NA	6.30 6.30
-	412189	R60982	Hs.22581	ESTs	6.30
	435501	AW051819	Hs.129908	(GAA0591 protein	6.30
	408221	AA912183	Hs.47447	ESTs	6.28

	413943 416845	AW294416 H95279	Hs.144687	Homo saplens cDNA FLJ12981 fis, clone NT gb;yu20h02.s1 Soares fetal fiver spleen	6.28 6.27
	402732	NA ALZZZAZO	U. 404447	NA .	6.26
5	413224	AI732470	Hs.191157	ESTs, Wealdy similar to ALUT_HUMAN ALU S	6.24
,	415642 449284	U19878 8E502240	Hs.336224 Hs.38592	transmembrane protein with EGF-like and	6.24
	419548	AW978142	Hs.326248	hypothetical protein FLJ23342	6.24
	453880	AI803166	Hs.28462	Homo sapiens cDNA: FLJ22071 fis, clone H	6.23
	422675	BE018517	Hs.119140	ESTs, Weakly similar to 138022 hypotheti eukaryotic translation initiation factor	6.22 6.22
10	413384	NM_000401	Hs.75334	existoses (multiple) 2	
	445584	AF217518	Hs.8360	PTD012 protein	6.21 6.21
	451065	AW295132	Hs.222231	ESTs, Wealthy similar to granule cell mar	6.21
	420807	AA280627	Hs.57846	ESTs	6.20
	421155	H87879	Hs.102267	lysyl oxidase	6.20
15	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	6.20
	440209	H05049	Hs.22269	neurodn 3	6.20
	408170	AW204516	Hs.31835	ESTs	6.20
	433590	N98410	Hs.48364	Homo sapiens regulator of G-protein sign	6.20
	442008	AJ457814	Hs.270272	ESTs	6.20
20	420617	AK001652	Hs.99423	ATP-dependent RNA helicase	6.20
	402343			NA .	6.20
	432682	AJ376400	Hs.159588	ESTs	6.20
	452109	AI525873	Hs.61164	hypothetical protein FLJ14909	6.20
	429954	AI918130	Hs.21374	ESTs	6.20
25	417256	U94332	Hs.81791	tumor necrosis factor receptor superfami	6.20
	435525	AJ831297	Hs.123310	ESTs	6.20
	413604	R51767		gb:yg73g11_r1 Soares infant brain 1NIB H	6.20
	425305	AA363025	Hs.155572	Human clone 23801 mRNA sequence	6.20
20	443285	AJ301918	Hs.334264	ESTs	6.20
30	446565	D13757	Hs.311	phosphoribosyl pyrophosphate amidotransf	6.20
	451027	AW519204	Hs.40808	ESTs	6.20
	452243	AL355715	Hs.28555	programmed cell death 9	6.19
	429782	NM_005754	Hs.220689	Ras-GTP ase-activating protein SH3-domain	6.17
25	424060	X92108	Hs.138629	H.sapiens mRNA for subtelomeric repeat s	6,17
35	432494	AA551060		gb:nk74f02.s1 NCI_CGAP_Sch1 Homo sapiens	6.16
	448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT	6.14
	419638	N46504	Hs.91747	profilin 2	6.13
	445595	W25950	Hs.14512	DIPB protein	6.13
40	433036	AA574091	Hs.105964	ESTs	6.13
40	457155	AL110243	Hs.187991	DKFZP564A122 protein	6.13
	443715	AI583187	Hs.9700	cyclin E1	6.13
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	6.12
	453288	AA034319	Hs.29041	Homo sapiens cDNA FLJ14177 fts, clone NT	6.11
45	424897	D63216	Hs.153684	frizzled-related protein	6.11
45	429188	AB011171	Hs.198037	KIAA0599 protein	6.11
	434894	AW977850	Hs.23856	hypothetical protein MGC5297	6.10
	413339	AI818080	Hs.194290	ESTs	6.10
	453685	AL110309		gb:DKFZp564L0278_r1 564 (synonym: hfbr2)	6.10
50	421195	BE464560	Hs.133017	ESTs	6.10
20	453296	AA034413	Hs.62560	ESTs	6.10
	444985	AI677737	Hs.28329	hypothetical protein FLJ14005	6.10
	423492	AF020761	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homo	6.10
	419841	BE005848	Hs.7326	ESTa	6.10
55	429190	H18650	Hs.92602	ESTs	6.10
55	426116	AA858729	Hs.144694	ESTs	6.10
	451441	AA017601	Hs.84529	ESTs, Weakly similar to Z202_HUMAN ZINC	6.10
	401740 441953	MITTER	Us ganaces	NA Secretor of observation 10	6.10
		H11695	Hs.322901	disrupter of silencing 10	6.10
60	401464 405033	AF039241	Hs.9028	histone deacetylase 5	6.10
-	410743	AA089474	Hs.272153	NA EST-	6.10
	454758	AW845266	153.272133	ESTS	6.10
	417728	AW843266 AW138437	Hs.24790	gb:IL2-CT0031-160999-003-808 CT0031 Homo	6.10
	418553	T88964	ns.24/90	KIAA1573 protein	6.10
65	431617	AK000738	Hs.264636	gb:yd97a07.r1 Soares fetal liver spicen	6.09
<u> </u>		00044400	ms.20403b	hypothetical protein FLJ20731	6.08
	455608 450755	AA010984	Un 150464	gb:CM4-BN0Z20-080500-170-f03 BN0Z20 Homo	6.08
	455217		Hs.159464	ESTs	6.07
	437179	AW867534 AA393508	Hs.300642	gb:MR0-SN0037-160400-004-e05 SN0037 Homo	6.07
70	408622	AA056060	Hs.202577		6.06
. •	415308	F05251	116.2023//	Homo sapiens cDNA FLJ12166 fis, clone MA	6.06
	428417	AK001699	Hs.184227	gb:HSCO4H101 normalized infant brain cON	5.06
	426501	AW043782	Hs.293616	F-box only protein 21	6.05
	431077	A1669133	Hs.115660		6.03
75	403040	71003133	ns. 113000		6.03
	445704	AJ493742	Hs.165210	NA ESTe Maderalah similar in 120022 busan	6.02
	415637	R25517	113.103410		6.02
	427925	N51323	Hs.255935	gb:yg44f01.r1 Soares infant brain 1NIB H	6.02
	404702	NA NA	rn.∠00335	Homo sapiens, clone IMAGE:3448993, mRNA NA	6.02
		AF231338	Hs.222024		6.02 6.01
80	4331R3				
80	433183 437762				
80	433183 437762 443833	T78028 AI654108	Hs. 154679 Hs. 135125	synaptotagmin I	6.01 6.01

	420909	AJ640551	Hs.88878	Homo sapiens cDNA: FLJ23536 fs, clone L	6.00
	407612	U26403	Hs.37142	ephrh-A5	6.00
	450715 453853	AI266484 AL040600	Hs.31570 Hs.188083	ESTs, Weakly similar to KIAA1324 protein	6.00
5	444188	AI393165	Hs.699	ESTs	6.00
•	451813	NM_016117	Hs.27182	peptidylprolyl isomerase B (cyclophilin	6.00
	422505	AL120862	Hs.124165	phospholipase A2-activating protein ESTs	6.00
	420734	AW972872	Hs.293736	ESTs	6.00
	455082 .	BE148180		gb:RC0-HT0232-211099-011-e04 HT0232 Homo	6.00 6.00
10	444200	AA327113	Hs.149057	ESTs	6.00
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	6.00
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN 2	6.00
	428412	AA428240	Hs.126083	ESTs	6.00
16	407790	AI027274	Hs.288941	Homo sapiens cDNA FLJ 14866 fis, clone PL	6.00
15	428945	AW192803	Hs.98974	ESTs, Wealdy similar to S65824 reverse t	6.00
	431878	AA521207	Hs.270202	ESTs, Wealdy similar to ALU4_HUMAN ALU S	6.00
	425282	AW163518	Hs.155485	huntingtin interacting protein 2	6.00
	401093 411861	414/007076		NA	6.00
20	411800	AW867875 N39342	Hs.103042	gb:MR0-SN0040-050500-003-f11 SN0040 Homo	6.00
20	446925	AW974505	Hs. 176669	microtubule-associated protein 18	5.99
	401708	NA	rts. 170003	ESTS NA	5.98
	449894	AK001578	Hs.24129	CLL17 protein	5.98 5.97
	403278	NA		NA NA	5.96
25	455212	AW866330		gb:QV4-SN0024-080400-167-e01 SN0024 Homo	5.96
	410116	AW630671	Hs.58636	squamous cell carcinoma antigen recogniz	5.96
	441271	AA927290	Hs.130482	ESTs	5.95
	404072			NA	5.95
20	431596	T34708	Hs.272927	Sec23 (S. cerevisiae) homotog A	5.94
30	421622	AB037748	Hs.106204	KIAA1327 protein	5.93
	441300	R35063	Hs.181538	ESTs	5.92
	445517	AF208855	Hs.12830	hypothetical protein	5,91
	429559	AI985345	Hs.26425	ESTs	5.91
35	443767	BE562136	Hs.9736	proteasome (prosome, macropain) 26S subu	5.91
22	440510	H08427	Hs.309165	ESTs, Weakly similar to ISHUSS protein d	5.90
	414727	BE466904	11- 440000	gb:hz28f03.x1 NCI_CGAP_GC6 Homo sapiens	5.90
	451686 438032	AA059246	Hs.110293	ESTs	5.90
	450470	8E045624 Z75330	Hs.152992 Hs.286148	ESTs	5.90
40	430533	AA480895	Hs.201552	stromal antigen 1	5.90
	432662	AL049314	Hs.280700	ESTs, Weakly similar to T17288 hypotheti ESTs	5.90
	451742	T77609	Hs.117970	ankyrin 2, neuronal	5.90
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	5.90
	412537	AL031778	Hs.797	nuclear transcription factor Y, alpha	5.90 5.90
45	447233	AW246333	Hs.17901	Homo saplens, clone IMAGE:3937015, mRNA,	5.90 5.90
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	5.90
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	5.90
	433865	N29862	Hs.44104	ESTs	5.90
50	453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	5.90
50	448743	AB032962	Hs.21898	KIAA1138 protein	5.90
	447153	AA805202	Hs.315562	ESTs	5.90
	425793	AA363946	Hs.20969	ESTs	5.90
	404632 446364	ADOCCOA	11- 11010	NA .	5.90
55	452240	AB006624 AI591147	Hs.14912	KIAA0286 protein	5.90
55	410424	AA084984	Hs.61232	EST6	5.90
	404170	~~~~		gb:zn11a08.r1 Stratagene hNT neuron (937 NA	5.90
	458390	A1792585	Hs.133272	ESTs, Wealthy similar to ALUC_HUMAN !!!!	5.89
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	5.89 4.88
60	444406	AI147237	Hs.300697	immunoglobulin heavy constant gamma 3 (G	5.88 5.87
	413894	BE177983		gb:RC3-HT0600-230300-021-g10 HT0600 Homo	5.87
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	5.86
	446700	AW206257	Hs.156326	Human DNA sequence from clone RP11-145L2	5.86
65	443377	AJ792547	Hs.133292	ESTs	5.86
65	419162	AA234591	Hs.304123	ESTs	5.85
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	5.84
	428650	A1560456	Hs.107319	ESTs	5.84
	437410	AW023340	Hs.14880	ESTs	5.84
70	428303	AW974476	Hs.183601	regulator of G-protein signalling 16	5.84
, 0	401004	AMMERICA	11- 4-0	NA	5.83
	414504	AW069181	Hs.115175	sterile-alpha motif and leucine zipper c	5.83
	410979 424576	BE151480 BE154142	H- 00022	gb:RC0-HT0295-071199-011-e01 HT0295 Homo	5.82
	439352	BE614347	Hs.96833	ESTS	5.82
75	423057	AW961597	Hs.169615	hypothetical protein FLJ20989	5.81
	429250	H\$6585	Hs.130816 Hs.198308	ESTs. Moderately similar to 138022 hypot	5.80
	413048	M93221	Hs.75182	tryptophan rich basic protein	5.80
	451367	AA923729	Hs.26322	mannose receptor, C type 1 cell cycle related kinase	5.80
• •	418647	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo saniens	5.80
80	421589	AW954177	Hs.82919	cullin 2	5.80 5.80
	427969	NM_001963	Hs.2230	epidermal growth factor (beta-urogastron	5.80
	451406	A1694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	5.80
	436096	H55931	Hs.269582	ESTs	5.80

	443353	41013610	LL 133055	CCT-	
	457244	AI052659 AA581385	Hs.133255 Hs.162473	ESTs ESTs, Wealthy similar to 138022 hypotheti	5.80
	407746	AK001962	Hs.38114	hypothetical protein FLI11100	5.80 5.80
_	440688	AW404591	Hs.147440	ESTs, Weakly similar to Z192_HUMAN ZINC	5.80
5	445745	AB007924	Hs.13245	KIAA04S5 gene product	5.80
	405637	NA DADAGO	14 400544	NA COT-	5.80
	415293 440404	R49462 AI015881	Hs.106541 Hs.324527	ESTs mitochondrial ribosomal protein S5	5.80
	442227	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	5.80 5.80
10	423395	AA326613		gb:EST29922 Cerebellum II Homo sapiens c	5.80
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	5.80
	416000	R82342	Hs.79856	ESTs. Weakly similar to S65657 alpha-1C-	5.80
	422108 430818	AA297914 AI311928	Hs.111749	postmetotic segregation increased (S. ce gb:qo89h04.x1 NCI_CGAP_Kid5 Homo sepiens	5.80
15	444749	A1190672	Hs.65926	ESTs	5.80 5.80
	417515	L24203	Hs.82237	atavia-telangiectasia group D-associated	5.79
	456192	D84109	Hs.80248	RNA-binding protein gene with multiple s	5.78
	411253 417219	AW833897	ti- 220020	gb:QV0-TT0009-111199-055-b07 TT0009 Homo	5.78
20	409450	AW973473 AW628650	Hs.220938 Hs.61260	ESTs hypothetical protein FLJ13164	5.78 5.76
	412013	AA400753	Hs.43761	ESTs, Weakly similar to A46010 X-linked	5.76
	425566	AW162943	Hs.250618	UL16 binding protein 2	5.75
	417877	AI025829	Hs.86320	ESTA	5.75
25	437114 421238	AA836641 AB033101	Hs.163085	ESTs	5.75
23	428959	AF100779	Hs.102796 Hs.194680	Homo sapiens cDNA FLJ10708 fis, clone NT WNT1 inducible signating pathway protein	5.74 5.73
	415209	F00183	Hs.172004	650	5.73 5.73
	429922	Z97630	Hs.226117	H1 histone family, member 0	5.72
30	420022	AA256253	Hs.120817	ESTs	5.71
50	431485 424304	BE621320 NM 001395	Hs.257486	hypothetical protein FLJ20062	5.71
	434276	AF123659	Hs.144879 Hs.93505	dual specificity phosphatase 9 leucine zipper, putative tumor suppresso	5.71 5.71
	438085	R52518	Hs.7967	ESTs	5.70
25	444379	N99035	Hs.222657	ESTS	5.70
35	401348	NA		NA	5.70
	428878 422564	AA435884 AJ148006	Hs.48926 Hs.222120	ESTs ESTs	5.70
	452560	BE077084	Hs.336432	ESTs	5.70 5.70
40	408384	BE144344	Hs.7589	ESTs, Weakly similar to A46010 X-linked	5.70
40	409948	AA078643		gb:7P08801 Chromosome 7 Placental cDNA L	5.70
	421166	AA305407	Hs.102308	potassium inwardly-rectifying channel, s	5.70
	439231 439203	AW581935 AA448930	Hs.141480 Hs.8453	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	5.70
	442029	AW956698	Hs.14456	KIAA1587 protein neural precursor cell expressed, develop	5.70 5.70
45	451922	BE463995	Hs.211033	ESTs	5.70
	407808	AA663559	Hs.279789	histone deacetytase 3	5.70
	428161	M96954	Hs.182741	TIA1 cytotoxic granule-associated RNA-bi	5.70
	413430 428223	R22479 AA424313	Hs.167073 Hs.98402	Homo saplens cDNA FLJ13047 fis, clone NT ESTs	5.70 5.70
50	427972	AA864870	Hs.181304	putative gene product	5.70 5.70
	416283	NM_005429	Hs.79141	vascular endothelial growth factor C	5.70
	416319	AI815601	Hs.79197	CD83 antigen (activated 8 lymphocytes, I	5.70
	458044 432911	AW979114 AW807634	Hs.326135 Hs.279799	ESTs	5.70
55	411643	AI924519	Hs.192570	putative zinc finger protein NY-REN-34 a hypothetical protein FLJ22028	5.70 5.70
	408867	AA437199	Hs.656	cell division cycle 25C	5.70
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sap	5.70
	428822	W28418	Hs.30715	potassium voltage-gated channel, isk-rel	5.70
60	409570 457441	AW418720 8E467737	Hs.167583 Hs.146125	ESTs ESTs	5.70 5.70
	409101	NM_004297	Hs.50612	guarrine nucleotide binding protein (G pr	5.70
	420192	AA256281	Hs.105040	ESTs	5.69
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fs, clone HE	5.69
65	454511 419586	AW948146 AI088485	Hs.144759	gb:RC0-MT0013-280300-031-e02 MT0013 Homo	5.68
00	416777	AF146760	Hs.79844	ESTs, Wealthy similar to I38022 hypotheti DKFZP564M1416 protein	5.67 5.67
	435849	BE305242	Hs.16098	claudin 2	5.67
	457892	AA744389		gb:ny51e10.s1 NCI_CGAP_Pr18 Homo sepiens	5.66
70	450191	AW137243	Hs.222446		5.66
, 0	438653 422910	AW188099 AI269508	Hs.131813 Hs.121591		5.66
	453694	AW504918	Hs.258208		5.66 5.66
	445302	AK001537	Hs.12488	hypothetical protein FLJ 10675	5.66
75	446080	AJ221741	Hs.117777	ESTs	5.65
75	425474	Z48054	Hs.158084		5.55
	432542 446983	AW083920 AA157484	Hs.16098 Hs.97199	claudin 2 complement component C1q receptor	5.65
	420898	A8002379	Hs.100113	KIAA0381 protein	5.65 5.65
οΛ	401372			NA	5.64
80	428541	AJ862570	Hs.299214		5.63
	426249 459705	F05422 BE082764	Hs.168352		5.63
	451883	AL120634	Hs.270252 Hs.305923		5.63 5.62
					3.44



	426316	NM_002430	Hs.268515	meningioma (disrupted in balanced transl	5.62
	401183 426029	AW294138	U- 300333	NA CCT-	5.62
	443462	A1064690	Hs.255277 Hs.171176	ESTs ESTs	5.61
5	447102	BE167434	Hs.98471	ESTs, Wealdy similar to T18712 hypotheti	5.61 5.60
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	5.60
	444577	AJ207721	Hs.11393	RAD51 (S. cerevisiae) homolog C	5.60
	423605	AF047826	Hs.129887	cadherin 19, type 2	5.60
10	413447	AW969388	Hs.10450	Homo sapiens cDNA: FLJ22063 fis, clone H	5.60
10	442957 424296	AJ949952 AJ631874	Hs.49397 Hs.155140	ESTS	5.60
	430679	R44428	Hs.22801	casein kinase 2, alpha 1 polypeptide ESTs	5.60 5.60
	449358	AA001229	Hs.131436	ESTs	5.60
	418348	AI537167	Hs.96322	hypothetical protein FLJ23560	5.60
15	433133	AB027249	Hs.104741	PDZ-binding kinase: T-cell originated pr	5.60
	444059	R69743	Hs.116774	integrin, alpha 1	5.60
	438157 428233	AW137011 AJ358831	Hs.49576 Hs.20578	ESTs ESTs	5.60
	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fts, clone L	5.60 5.60
20	451652	AA018968	Hs.133538	ESTs	5.59
	422762	AL031320	Hs.119976	Human DNA sequence from clone RP1-20N2 o	5.59
	447591	AI675417	Hs.282855	ESTs	5.58
	417958	AA767382	Hs.193417	ESTs	5.57
25	438146 413595	Z36842 AW235215	Hs.57548 Hs.16145	ESTs ESTs	5.57
	422406	AF025441	Hs.116206	Opa-interacting protein 5	5.57 5.56
	420529	D25259	Hs.319844	ESTs, Moderately similar to 154374 gene	5.56
	439582	W79161	Hs.118327	Homo sapiens cDNA FLJ11522 fis, clone HE	5.56
20	408744	AW806177		gb:MR1-UM0108-130400-003-d04 UM0108 Homo	5.56
30	447230	AW972147	Hs.101395	hypothetical protein MGC11352	5.54
	428856 446813	AA435735 AA971436	Hs.183171 Hs.16218	hypothetical protein FLJ22002	5.54
	451424	AJ862026	Hs.302810	KIAA0903 protein Novel human gene mapping to chomosome 20	5.53 5.53
	410516	BE537917	Hs.90034	hypothetical protein FLJ21916	5.53
35	453994	BE180964	Hs.165590	ribosomal protein 613	5.53
	435583	AA767714	Hs.291627	ESTs	5.52
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	5.51
	408912 427966	AB011084 R97130	Hs.48924	KIAA0512 gene product; ALEX2	5.51
40	433611	AW327692	Hs.189699 Hs.3446	ESTs mitogen-activated protein kinase kinase	5.51 5.51
	401244		10.0740	NA	5.50
	410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo	5.50
	434006	AF113688		gb:Homo sapiens clone FLB4630	5.50
45	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	5.50
73	427507 423268	AF240467 BE386898	Hs.179152 Hs.131162	toli-like receptor 7	5.50
	405065	NA	ns.131162	ESTs, Weakly similar to ALU5_HUMAN ALU S NA	5.50
	444302	A1140115	Hs.225130	ESTs	5.50 5.50
50	418183	NM_001772	Hs.83731	CD33 antigen (gp67)	5.50
50	435586	AJ279137	Hs.151498	ESTs	5.50
	438279 427189	AA805166	Hs.154762	HIV-1 rev binding protein 2	5.50
	415263	HB2453 AA948033	Hs.5635 Hs.130853	ESTs ESTs	5.50
	441818	AI630451	Hs.7976	KIAA0332 protein	5.50 5.50
55	407834	AW084991	Hs.26100	ESTs	5.50
	404012	NA		NA	5.50
	449932	AI675444	Hs.263024	ESTs	5.50
	423760	AA775891	Hs.191980	ESTs	5.50
60	431576 423172	M76665 R15652	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	5.50
	422295	AF051151	Hs.114408	gb:HH503-F Adult heart, Clontech Homo sa toll-like receptor \$	\$.50 5.50
	429044	AJ261490	Hs.145527	ESTs	5.50
	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	5.50
65	414323	NM_014759	Hs.334688	KIAA0273 gene product	5.50
05	405511 444665	NA BE613126	110 47700	NA	5.49
	434434	AA633516	Hs.47783 Hs.157201	B aggressive lymphoma gene	5.49
	421997	R66740	Hs.110613	ESTs KIAA0220 protein	5.48 5.47
70	410276	AI554545	Hs.68301	ESTs	5.47
70	435887	AA954229	Hs.114052	ESTS	5.47
	453837	AL138387	Hs.256126	baculoviral IAP repeat-containing 7 (liv	5.47
	409517	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	5.47
	430387 401629	AW372884 NA	Hs.240770	nuclear cap binding protein subunit 2, 2	5.47
75	433071	BE150229	Hs.281564	NA retinal outer segment membrane protein 1	5.46 5.46
-	458247	R14439	Hs.209194	ESTs	5.46 5.46
	418049	AA211467	Hs.190488	Homo sapiens, Similar to nuclear localiz	5.45
	418247	R55174		gb:yg87h04.r1 Soares infant brain 1NIB H	5.45
80	453716	AA037675	Hs.152675	ESTs	5.44
50	431157 426873	AJ823969 AJ190540	Hs.132678	ESTS	5.44
	437092	AA744292	Hs.131092	ESTs gb:ny51d05.s1 NCI_CGAP_Pr18 Homo sapiens	5.43
	445782	AW407672	Hs.315367	Homo sapiens, Similar to hypothetical or	5.42 5.42
					V.72

	447393	Al377458	Hs.158831	EST	5.42
	425283	AA354338	Hs.131100	ESTs	5.42
	401208	NA		NA	5.42
-	430536	AJ809163	Hs.9908	nitrogen fixation cluster-like	5.42
5	405523			NA	5.42
	409012	AL117435	Hs.49725	DKFZP434I216 protein	5.41
	429803	W81489	Hs.223025	RAB31, member RAS oncogene family	5.41
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extraceflular mat	5.40
10	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	5.40
10	456027	BE327387	Hs.13913	KIAA1577 protein	5.40
	411897	AW875066	Hs.326876	Homo saplens SOX8 mRNA, complete cds	5.40
	449689	AF228421	Hs.23889	DKFZP564A032 protein	5.40
	432865	AJ753709	Hs.152484	ESTs, Wealthy similar to 138022 hypotheti	5.40
15	408248	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	5.40
15	418516	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, at	5.40
	423289	N77774		gb:yz83e01.r1 Soares_multiple_sclerosis_	5.40
	453365	AA035211	Hs.17404	ESTs	5.40
	406465	414477777	U- 47556	NA FOT-	5.40
20	441858	AW173339	Hs.135665	ESTs	5.40
20	432507	BE391093	Hs.324667	ESTs	5.40
	440570 445062	AI205712	Hs.125998	ESTs	5.40
	421639	Al339915	Hs.44324	ESTs	5.40
	410406	NM_012082 AI969703	Hs. 106309	Friend of GATA2	5.40
25	418939	AW630803	Hs.1466 Hs.89497	glycerol kinase	5.40
23	426010	AA136563	Hs.1975	Ismin B1	5.40
	400250	NA NA	113.1313	hypothetical protein FLJ21007 NA	5.40
	424650	AW576156	Hs.250824	Homo sapiens cONA: FLJ23435 ffs, clone H	5.40
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (tectin	5.40 5.39
30	433384	AI021992	Hs.124244	ESTs	5.38
-	428781	AF164799	Hs.193384	putatative 28 kDa protein	5.38
	438150	AA037534	Hs.79059	transforming growth factor, beta recepto	5.38
	400639			NA	5.38
	426485	NM_006207	Hs.170040	platelet-derived growth factor receptor-	5.37
35	424205	AA336825		gb:EST41732 Endometrial turnor Homo saple	5.36
	459596	H29554	Hs.113871	ESTs	5.36
	408234	AW993358	Hs.285814	sprouty (Drosophila) homotog 4	5.36
	414547	T47770	Hs.191463	ESTs	5.35
	419851	AA287987	Hs.13477	ESTs, Weakly similar to 1207289A reverse	5.35
40	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	5.34
	425764	AW996009	Hs.112572	Homo sapiens cDNA FLJ14130 fis, clone MA	5.34
	405352			NA	5.33
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	5.32
4.5	424284	BE541008	Hs.6193	hypothetical protein FLJ14590	5.32
45	427741	AW753185	Hs.180628	dynamin 1-like	5.31
	426021	AW770897	Hs.34392	ESTs, Weakly similar to I38022 hypotheti	5.31
	442186	AA984083	Hs.269746	ESTs, Wealty similar to T03306 PSD-95/SA	5.30
	437319	BE410958	Hs.56406	Homo sapiens cDNA FLJ13549 fis, clone PL	5.30
60	405287	NA		NA	5.30
50	427032	AF012023	Hs.173274	Integrin cytoplasmic domain-associated p	5.30
	415371	R15239		gb:yf89b02_r1 Soares infant brain 1NI8 H	5.30
	420024	AA252905	Hs.194477	E3 ubiquitin tigase SMURF2	5.30
	434408	AI031771	Hs.132586	ESTs	5.30
55	434739	AAB04487	Hs.144130	ESTs	5.30
22	421327	AAB37295	Hs. 188802	ESTs	5.30
	453058	AW612293	Hs.288684	Homo sepiens cONA FLJ11750 fis, clone HE	5.30
	448776 417845	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	5.30
	430264	AL117461 AA470519	Hs.82719	Homo sapiens mRNA; cDNA OKFZp586F1822 (f	5.30
60	411402		Hs.69855	gb:nc71f10.s1 NCI_CGAP_Pr1 Home saplens	5.30
<b></b>	419220	8E297855 AA811938	Hs.291759	NRAS-related gene ESTs	5.30
	407995	AI094748	Hs.100134	hypothetical protein FLJ12787	5.30
	459256	AW967468	Hs.99821		5.30
	452449	AW068658	Hs.20943	hypothetical protein FLJ14547 ESTs	5.30
65	430366	AI057368	Hs. 105575	ESTs	5.30
-	434360	AW015415	He 127780		5.30
	422560	F11469	Hs.118281	zinc finger protein 266	5.29
	441704	AI458766	Hs.201988		5.29
	443635	AI080230	Hs.134214		5.29
70	434342	AI791138	Hs.116768		5.29
-	423409	NM_006466			5.29
	449000	U69560	Hs.3826	kelch-like protein C3IP1	5.29
	452381	H23329	Hs.290880		5.29
	409068	AW236991	Hs.102495		5.29
75	434860	AA932386	Hs.292667		5.28
_	408096	BE250162	Hs.83765	dihydrofolate reductase	5.28
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	5.28
	435443	AJ248674	Hs.14295	ESTs	5.26
00	414269	AA298489	Hs.303171		5.26
80	408371	AF161545	Hs.279883		5.26
	401205	NA		NA	5.26
	450904	R07118	Hs.189924		5.26
	416351	H49704	Hs.173522	ESTs	5.26

	426524 412901	AA380611 AJ127359	Hs.163841	ESTs	5.25
	452487	AW207659	Hs.289088 Hs.6630	heat shock 90kD protein 1, alpha Homo sapiens cDNA FLJ13329 fis, clone OV	5.25 5.24
_	444825	AW167613	Hs.248	mitogen-activated protein kinase kinase	5.24
5	412953	Z45794	Hs.238809	ESTs	5.24
	404117	NA		NA	5.22
	427956	AL046175	Hs.108169	Homo sapiens mRNA; cDNA DKFZp586C1619 (I	5.22
	421787 437255	AA227068 R58970	Hs.108301 Hs.9887	nuclear receptor subfamily 2, group C, m ESTs	5.22
10	424697	AL136169	Hs.250708	CAAX box 1	5.22 5.20
-	449771	AI668702	Hs.54976	ESTs	5.20
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	5.20
	438885	AI886558	Hs.184987	ESTs	5.20
15	407182 452150	AA312551 W42490	Hs.230157 Hs.260844	ESTa ESTs	5.20
10	419680	AA249720	Hs.59335	ESTs	5.20 5.20
	438940	AF075045	Hs.271609	ESTs	5.20
	405362	NA		NA	5.20
20	449370	AK002114	Hs.23495	hypothetical protein FLJ11252	5.20
20	442353 409331	BE379594 M36634	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	5.20
	415397	H10818	Hs.53973	vasoactive intestinal peptide gb:ym04f10.r1 Soares infant brain 1NIB H	5.20 5.20
	406735	AA603092		gb:np37a01.s1 NCI_CGAP_Lu1 Homo sapiens	5.20
25	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, 81 (h	5.20
25	431480	AA837274	Hs.257005	hypothetical protein FLJ20837	5.20
	425523 425673	AB007948 R70318	Hs.158244 Hs.339730	KIAA0479 protein	5.20
	439267	AA287747	Hs.173012	ESTs ESTs, Weakly similar to A46010 X-Enked	5.20 5.20
	457030	Al301740	Hs.173381	dihydropyrimidinase-like 2	5.20
30	424638	AI472106	Hs.49303	Homo sepiens cDNA FLJ11663 fis, clone HE	5.20
	454434	AA083558	Hs.261286	ESTs	5.20
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	434803	AW974640	Hs.303413	ESTs, Weakly similar to 2109260A B cell ESTs	5.20 5.20
35	403199	NA		NA .	5.20
	435225	AJ021912	Hs.187983	ESTs	5.20
	451664	AA889081	Hs.153952	5 nucleotidase (CD73)	5.20
	440385 432328	AA884283 A1572739	Hs.192136 Hs.195471	ESTs	5.20
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	449841	AJ671502	Hs.199602	ESTS	5.19
	420303	AA258282	Hs.278436	KIAA1474 protein	5.19
45	429687 453345	A1675749 AA302862	Hs.211608 Hs.90063	nucleoporin 153kD neurocalcin delta	5.19
	447499	AW262580	Hs.147674	protocacherin beta 16	5.18 5.18
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	405114	NA		NA	5.18
50	431117 411995	AF003522 W49701	Hs.250500	delta (Orosophila)-like 1	5.18
50	401738	NA NA	Hs.29667	ESTs NA	5.17 5.17
	425250	AA353495	Hs.269762	ESTs, Weakly similar to A47582 B-cell gr	5.16
	454388	AA630905	Hs.333300	hypothetical protein FLJ14026	5.16
55	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	5.16
33	443646 436032	AI085198 AA150797	Hs.154226 Hs.109276	ESTs Intervie analtain	5.15
	456896	M97639	Hs.155585	latexin protein receptor tyrosine kinase-like orphan rec	5.15 5.15
	433672	BE281165	Hs.288038	TLS-essociated serine-arginine protein 1	5.15
60	432826	X75363	Hs.250770	ACO for serine protesse homologue	5.14
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	400205 430854	NA AW440369	Hs.47026	NA ESTs	5.14
	408771	AW732573	Hs.47584	potassium voltaga-gated channel, delayed	5.14 5.14
6	456804	AJ421645	Hs.139851	caveolin 2	5.14
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	421782	AB029290	Hs.108258	actin binding protein; macrophin (microf	5.05 5.05	
45	407976 400869	AI633875	Hs.77823	hypothetical protein FLJ21343 NA	5.04	
45	416153	R13894		gb:yf62a06.r1 Soares infant brain 1NIB H	5.04	
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CAT number:
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	TABLE 460			
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20	Pkey:	Con	que number con	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
	Ref:	Sec	pience source.	n chromosome 22" Dunham, et al. (1999) <u>Nature</u> 402:489-495.
		seq	neuce or municipal	CHURESUND 22 DURINGH, C. de. 1999 (1999) (1999)
	Strand:			nd from which exons were predicted.
25	Nt_position	i: inc	cates nucleoou	e positions of predicted exons.
25				An and the
	Pkey	Ref	Strand	NLposition
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30	400845	9188605	Phus	34428-34612
	408860	9757499	Minus	151830-152104,152649-152744
	400869	9838306	Ptus	29152-30102
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	400977	8072510	Plus	73950-74364
35	401004	7229982	Plus	62580-62772
	401093	8516137	Minus	22335-23166
	401183	7670214	Minus	39921-40601
	401205	9743388	Plus	167373-167433,167936-168031
	401208	7712287	Plus	163145-163281
40	401244	4827300	Minus	55359-56376
	401348	9930791	Minus	9365-9490
	401372	9944181	Plus	127056-127196
	401424	8176894	Ptus	24223-24428
	401581	9502454	Plus	9440-10165
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	402343	8099256	Plus	4677-6084
	402363	9454515	Plus	25693-25991
<i>E E</i>	402408	9796239	Minus	110326-110491
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	402709	8901246	Minus	56847-57055
	402732	9211639	Minus	147904-148107
	403040	3133144	Minus	91632-91788,97918-98115
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
60	403199	9958183	Minus	58895-59036,66618-66789
	403278	8072597	Plus	146823-146986
	403546	8078400	Plus	94703-94849
	403764	7717105	Minus	118692-118853
	403776	7770511	Minus	1414-1513,1624-1756
65	403859	7708954	Plus	113738-113858
	403973	8575876	Plus	93873-94384
	404012	8655948	Plus	551356-552233
	404029	7671252	Plus	108716-111112
	404072	9931705	Plus	49546-50498
70	404117		Plus	149723-149920
. •	404170		Plus	16835-169248
	404335		Minus	21030-21145,26504-26692
	404440		Phrs	80430-81581
	404632		Plus	45096-45229
75	404702		Plus	78043-78890
	404913			97717-97976
	404996			37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405033			142358-142546
				13855-14027
80	405065			97013-97560
ου	405114			89802-89999
	405287			97253-97742
	405352			105008-105142,105980-106091,140445-140556,142519-142641
	405362	2337862	Minus	Interior set interior interior interior interior interior.
				500

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5	405481 405511 405523 405543 405545 405637 405696 405770	3688109 9454623 9454643 9857582 1054740 6289229 4309923 2735037	Plus Plus Minus Plus Plus Minus	5718-5837,8719-8818 57731-57852 114550-114688,117265-117407,119490-119599,123237- 104333-104449 118677-118807,119091-119296,121626-121823 189852-189978 1865-2013,2124-2231 61057-62075	
10	406465	9795550	Plus	94502-94706,96776-96914,98795-98928,102423-102576	5,105087-105191,107023-107127,108852-108592
15	Table 47A	A lists about 370 ptor were switche Unique Exen D: Unigue Lide: Unigue	genes significan d and the ratio v ue Eos probese rplar Accession ene number ene gene title	FICANTLY DOWN-REGULATED IN STOMACH CANCER ofly down-regulated in stomach cancer compared to normal was equal to or less than 0.33. It identifier number number, Genbank accession number	COMPARED TO NORMAL STOMACH al stomach. These were selected as for Table 46A, except that the numerator and
20	Pkey 412859 423371	ExAccn NM_000705 AU076819	UnigeneID Hs.813 Hs.1650 Hs.158333	Unigene Title ATPase, H+/K+ exchanging, beta polypepti solute carrier family 26, member 3 protesse, serine, 7 (enterokinase)	R1 0.02 0.02 0.04
25	425607 429050 421996 441212 429093	U09860 X81333 AW583807 AW242447 NM_000253	Hs.194777	protesse, seame, r (entaconiase) meprin A, beta glucagon cytosofic beta-glucosidase microsomal triglyceride transfer protein	0.04 0.05 0.05 0.06
30	403697 402760	NA NA		NA NA	0.07 0.08

2 428285 AW340797 Hs.98434 0.08 0.08 Hs.87500 Hs.117050 419279 AA235900 ESTs 0.09 omithine carbamoyltransferase 422459 K02100 0.09 AF016833 mattase-glucoamylase (alpha-glucosidase) 422992 35 430867 M16404 Hs.248099 cholinergic receptor, muscarinic 2 453989 M63962 ATPase, H+fK+ exchanging, alpha polypept 0.10 443022 AL046485 Hs.207604 **ESTs** gb:RC1-8T0720-280300-011-f08 BT0720 Homo 0.10 413382 BE090689 450769 428070 AA057418 T63918 Hs.33654 FSTs 40 retinol-binding protein 2, cellular 0.10 Hs.182313 myocilin, trabecular meshwork inducible telomerase-associated protein 1 Hs.78454 Hs.232070 0.11 430073 U86136 latty-acid-Coenzyme A ligase, long-chain mal, T-cell differentiation protein 431716 D89053 0.12 416889 AW250318 Hs.80395 45 0.12 405650 NA AW583139 419219 401623 carboxypeptidase A2 (pancreatic) Hs.89717 0.12 0.13 KIAA0154 protein; ADP-ribosylation facto 400811 AF219139 Hs.87726 0.13 0.13 gb:MR0-HT0165-140200-009-d04 HT0165 Homo 455826 BE144228 50 414949 C15314 Hs.323349 gb:hSCG-3=stomach cancer gene-3 (oncogen gb:Human forkhead family (AFX1) mRNA, pa 0.13 S69741 407486 0.13 407494 U10072 401015 ŇA AU076646 Hs.171683 nuclear receptor subfamily 1, group H, m ESTs, Wealdy similar to T46608 zinc fing 0.14 426651 55 450926 443564 Hs 205591 A1744351 AI921685 Hs.199713 0 14 457955 457345 AI208986 Hs.143945 **ESTs** 0.14 0.14 Hs.192175 ESTs AI699933 RAB27A, member RAS oncogene family 417118 1138654 Hs.50477 0.14 0.15 60 BE162203 Hs.314758 ESTs 408518 444938 AW470690 Hs.148814 **ESTs** 0.15 403670 NA NA sucrase-isomaltase 432440 X63597 Hs.2996 0.15 0.15 Hs.259391 AW662740 **ESTs** 428492 65 443607 AJ452512 Hs.134069 0.15 FAT tumor suppressor (Drosophila) homolo Hs.166994 446914 BE044496 estrogen-related receptor gamma gb:PM1-HT0527-280200-005-a05 HT0527 Homo ESTs 424596 AB020639 Hs.151017 0.15 430350 BE169639 0.16 0.16 Hs.116195 431094 AW972276 70 NA AU076799 NA 419278 Hs.1247 apolipoprotein A-IV gb:MR0-HT0208-101299-202-e12 HT0208 Homo gb:Ur-H-8W0-aio-h-05-0-Ul.s1 NCI_CGAP_Su 0.16 455071 BE145826 454282 428848 AW296422 NM_000230 leptin (murine obesity homolog) 0.15 75 AW160725 R52804 Hs.312469 Hs.25956 451729 **ESTs** DKFZP564D206 protein 0.16 451103 Homo sapiens mRNA; cDNA DKFZp434M0223 (I 0.16 0.17 AL137479 BE048860 Hs.186655 Hs.120655 437157 0.17 gb:DKFZp434A1229_r1 434 (synonym: htes3) NA AL138411 NA 422731 0.17 0.17 80 402015 pregnancy specific beta-1-glycoprotein 3 gb:RC1-BN0056-230200-021-e11 BN0056 Homo 414758 H82022 Hs.282847 0.17 412793 AW997986 Hs.122082 0.17 AW292520 438152

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	401685	NA		NA	0.17
	441519	AA972740	Hs.127092	ESTs	0.17
	438327	H87407	Hs.172944	chorionic gonadotropin, beta potypeptide	0.17
-	402761	BE387621	Hs.108809	chaperonin containing TCP1, subunit 7 (e	0.17
5	424268	AA397653	Hs.307438	Human DNA sequence from clone 495010 on	0.18
	414507 413808	AW102637 J00287	Hs.13349 Hs.182183	Homo sapiens cDNA FLJ14647 fis, clone NT Homo sapiens mRNA for caldesmon, 3' UTR	0.18 0.18
	401132	NA	15.102100	NA	0.18
10	412374	X01388	Hs.73849	apolipoprotein C-III	0.18
10	423417	AP000365	Hs.128342	potassium large conductance calcium-acti	0.18
	447677	AJ419235	11- 121200	gb:t/21d02.x1 NCI_CGAP_Brn23 Homo sapien	0.18
	448828 424122	AI580296 AA335593	Hs.174782 Hs.116147	ESTs, Weakly similar to KIAA1437 protein ESTs	0.18 0.18
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	0.18
15	434597	AW974668		gb:EST386757 MAGE resequences, MAGM Homo	0.19
	428804	AK000713	Hs.193736	hypothetical protein FLJ20706	0.19
	410280	AA083558	Hs.261286	EST ₈	0.19
	409382 428062	AA071244 AA420683	Hs.98321	gb:zm73g03.r1 Stratagene neuroepithelium hypothetical protein FLJ14103	0.19 0.19
20	426069	H10807	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	0.19
	430135	NM_000035	Hs.234234	aldolase B, fructose-bisphosphate	0.19
	414802	AI793107	Hs.27018	Ris	0.19
	457432	NM_005136	Hs.268538	potassium voltage-gated channel, lsk-rel	0.19
25	446909 435447	AA004895 A1872932	Hs.30082	ESTs gb:wm72e03.x1 NCI_CGAP_Ut2 Homo sapiens	0.19 0.20
23	408611	NM_004367	Hs.46468	chemokine (C-C motif) receptor 6	0.20
	423577	AW810107	Hs.58633	Homo sapiens cDNA: FLJ22145 fis, clone H	0.20
	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN A	0.20
30	436741	AA860163	Hs.291319	ESTs	0.20
30	426635 418277	BE395109 AW135221	Hs.129327 Hs.130812	hypothetical protein MGC13057 ESTs	0.20 0.20
	448871	BE616709	Hs.159265	kruppel-related zinc finger protein hcKr	0.20
	459370	AA889982	Hs.271826	ESTs, Wealthy similar to 138022 hypotheti	0.21
25	427469	AA403084	Hs.269347	ESTs, Wealdy similar to 2109260A B cell	0.21
35	432887	AI926047	Hs.162859	ESTs	0.21
	421296 449216	NM_002666 AW295417	Hs.103253 Hs.224616	perilipin ESTs	0.21 0.21
	414835	AA156720	Hs.185342	ESTs	0.21
40	459233	AI939966		gb:MR0-CT0015-160799-002-b06 CT0015 Homo	0.21
40	439756	AL359651	Hs.283852	Homo sapiens mRNA full length insert cDN	0.21
	427167	AJ239507 AF154915	Hs.99196	hypothetical protein MGC11324	0.21
	400410 409828	AF 154915 AW501137	Hs.283958	homeo box D12 gb:UI-HF-BP0p-ail-e-12-0-UI.r1 NIH_MGC_5	0.21 0.22
	428470	AC002301	Hs.184507	Homo sapiens Chromosome 16 BAC clone CIT	0.22
45	455968	BE168828		gb:QV1-HT0517-020400-145-f04 HT0517 Homo	0.22
	404145	NA		NA .	0.22
	454011 430588	M31008 AI741461	Hs.37009	alkaline phosphatase, intestinal	0.22
	403652	NA	Hs.161904	ESTs NA	0.22 0.22
50	440410	AW204436	Hs.128715	ESTs	0.22
	453871	BE300380	Hs.69476	Homo sapiens cDNA FLJ12758 fis, clone NT	0.22
	458567	AI222075	Hs.147831	ESTs	0.22
	436004 417408	AA703332 F17211	Hs.196270 Hs.86092	folate transporter/carrier  Homo sapiens skeletal myosin light chain	0.22 0.22
55	448643	AI557531	115.00032	gb:pt2,1-06.D06.r tumor2 Homo sapiens cD	0.22
	404401	NA		NA	0.22
	428088	AA421130	Hs.112640	EST	0.22
	427074	AA527435	Hs.178589	hepatocellular carcinoma antigen gene 52	0.22
60	421972 429001	M18185 AF098951	Hs.1454 Hs.194720	gastric inhibitory polypeptide ATP-binding cassette, sub-family G (WHIT	0.22 0.22
•	441155	AW161008	Hs.7719	GABA(A) receptor-associated protein	0.22
	402750	NA		NA	0.22
	438587	AA811450	Hs.136984	ESTs	0.22
65	404848 427833	NA AA416615	U- 00242	NA CCT-	0.22
03	439907	AA853978	Hs.98242 Hs.124577	ESTs ESTs	0.23 0.23
	414373	AW162907	Hs.75969	proline-rich protein with nuclear target	0.23
	446817	AJ700684	Hs.134166	ESTs	0.23
70	437333	AA748898		gb:ny76h10.s1 NCI_CGAP_GCB1 Homo sapiens	0.23
70	404097	NA AW014174	Un 2010EE	NA rice forces protein	0.23
	446393 456328	T41368	Hs.301956	zinc finger protein gb:ph1d1_19/1TV Outward Alu-primed hncDN	0.23 0.23
	401042	NA		NA	0.23
25	458441	AW842283	Hs.79933	cyclin I	0.23
75	435547	AW117431	Hs.191906	ESTs	0.23
	429060	AW139155 AW954631	Hs.194995	hypothetical protein DKFZp43400320	0.23
	425158 448758	AW954631 AB018311	Hs.266940 Hs.21917	t-complex-associated-testis-expressed 1- KIAA0768 protein	0.23 0.23
	441240	AA923749	Hs.132442	ESTs	0.23
80	436562	H71937	Hs.322904	ESTs, Weakly similar to 138022 hypotheti	0.23
	424104	AA669515	Hs. 144950	ESTs	0.23
	447452 444515	BE618258 AW204908	Hs.102480 Hs.169979	Homo sapiens, clone IMAGE:3869590, mRNA, ESTs	0.23 0.24
	-40113	A11201300	16.103313	2018	0.24

	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	0.24
	406560 432408	NA N39127	Hs.332557	NA ESTs, Wealdy similar to A46010 X-linked	0.24 0.24
_	455699	BE068121	13.332331	gb:CM1-8T0368-061299-060-a02 BT0368 Homo	0.24
5	453979	M68895	Hs.76800	alcohol dehydrogenase 6 (class V)	0.24 0.24
	439657 407512	W93589 X15674		gb:zd95g05.s1 Soares_fetal_heart_NbHH19W gb:Human pTR5 mRNA for repetitive sequen	0.24
	440875	AW138036	Hs.201788	ESTs	0.24
• •	404753	NA		NA	0.24
10	411119	M60627	Hs.753	formyl peptide receptor 1	0.24 0.24
	418692 415327	AK000268 H22769	Hs.87383	hypothetical protein gb:ym54c02.r1 Soares infant brain 1NIB H	0.24
	429446	AI547111		gb:PN2.1_A01_G12.r mynorm Homo sapiens c	0.24
1.5	455391	BE156230		gb:QV0-HT0367-310100-102-c11 HT0367 Homo	0.25
15	422818	AA404290 AA678071	Hs.97848 Hs.194300	ESTs ESTs, Weakly similar to 138022 hypothe6	0.25 0.25
	435338 414203	BE262170	Hs.78629	ATPase, Na+fK+ transporting, beta 1 poly	0.25
	403941	NA		NA	0.25
20	414383	BE279406	20002	gb:601157981F1 NIH_MGC_21 Homo sapiens c	0.25 0.25
20	412008 424985	NM_001841 AI907236	Hs.73037 Hs.279935	cannabinoid receptor 2 (macrophage) Homo sapiens cDNA FLJ11780 fis, clone HE	0.25
	450736	AW970060	16.213333	gb:EST382140 MAGE resequences, MAGK Horno	0.25
	431185	H02767	Hs.28944	ESTs	0.25
25	455308	AW893949	11- 102000	gb:RC4-NN0027-060400-011-a09 NN0027 Homo ESTs, Moderately similar to KIAA0961 pro	0.25 0.25
23	435464 418525	BE548300 AW450369	Hs.192999 Hs.86937	ESTs	0.25
	402790		112.0000	NA	0.25
	411869	W20027	Hs.23439	ESTs CTA	0.25 0.25
30	400332 424884	S66407 AW299437	Hs.248032 Hs.225717	FLT4 ESTs	0.25
50	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [	0.25
	439780	AL109688		gb:Homo sapiens mRNA full length insert	0.25
	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	0.25 0.25
35	404900 441918	NA A1733373	Hs.128119	NA ESTs	0.25
55	441639	AJ133287	Hs.303953	ESTs	0.25
•	459396	AI907536	Hs.103869	ESTs	0.25
	452755	AW138937	Hs.213436	ESTs, Weakly similar to A34087 hypotheti Human DNA sequence from clone 1068E13 on	0.25 0.25
40	422183 415186	AA431698 AA160945	Hs.112794 Hs.14479	Homo sapiens cDNA FLJ14199 fis, clone NT	0.26
	429450	AA824451	Hs.94292	hypothetical protein FLJ23311	0.26
	455615	BE045344	Hs.274923	ESTs, Moderately similar to unnamed prot	0.26
	454633 424853	AW811380 BE549737	Hs.132967	gb:iL3-ST0143-290999-019-D05 ST0143 Homo Human EST clone 122887 mariner transposo	0.26 0.26
45	455802	BE141491	115.132307	gb:MR0-HT0080-011099-002-h06 HT0080 Homo	0.26
	414003	AA134472		gb:zo13c01.s1 Stratagene colon (937204)	0.26
	436363	AA843926	Hs.124434	ESTs neurofibromin 2 (bilateral acoustic neur	0.26 0.26
	456074 430569	BE409525 AF241254	Hs.902 Hs.178098	angiotensin I converting enzyme (peptidy	0.26
50	445635	A1769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.26
	405953	NA	44. 470004	NA Office	0.26 0.26
	411021 428443	F00055 BE618106	Hs.172004 Hs.184326	titin CDC10 (cell division cycle 10, S. cerevi	0.26
	434345	AF127772	710.101020	gb:Homo sapiens cell-line EBCASS clone E	0.26
55	455743	BE073754		gb:RC0-BT0561-210100-032-d07 BT0561 Homo	0.26
	451138 449528	W92287 H63337	Hs.40268 Hs.38178	ESTs hypothetical protein FLJ23468	0.26 0.26
	441040	AW449782	Hs.178803	ESTs	0.26
<b>C</b> 0	458830	AW501248	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	0.26
60	428861	AW352234	Hs.269365	ESTs, Wealdy similar to ALU8_HUMAN ALU S	0.26 0.27
	435469 427562	AW388237 R56424	Hs.191204 Hs.26534	ESTs ESTs	0.27
	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, s	0.2
65	423528	AB011137	Hs.300938	KIAA0565 gene product	0.2
65	406589	DC 220222	He 270626	NA FSTe	0.2 0.2
	450059 417296	BEZZ0223 L36196	Hs.279626 Hs.81884	ESTS sulfotransferase family, cytosolic, 2A,	0.2
	454007	AW015870	Hs.232081	ESTs	0.2
70	426062	N57014	Hs.75874	pregnancy-associated plasma protein A	0.2 0.2
70	441665 405037	Al301355 NA	Hs.151285	ESTs NA	0.2
	446820	AW295037	Hs.254986	ESTs	0.2
	448487	AJ523720	Hs.172567	ESTs	0.2
75	447567	AW474513		ESTs, Wealdy similar to I38931 Wiskoti-A	0.2 0.2
75	408540 407601	L13220 AC002300	Hs.639 Hs.37129	calbindin 3, (vitamin D-dependent calciu sodium channel, nonvoltage-gated 1, beta	0.2
	432501	BE546532	Hs.25682	Homo sapiens mRNA for KIAA1863 protein,	0.2
	401350	NA		NA	0.2
80	417569	R00271	Hs.144651	ESTs ESTs	0.2 0.2
90	443542 437105	AI927065 AA744554	Hs.145040 Hs.222127	ESTS	0.2
	432119	T80289	Hs.302041	Homo sapiens clone 24762 mRNA sequence	0.2
	419056	M89957	Hs.89575	CD79B antigen (immunoglobulin-associated	0.2

	427812	AA770424	Hs.98162	ESTS	0.28
	423557 445311	AB011176 AW027556	Hs.129801 Hs.156286	KIAA0604 gene product ESTs	0.28 0.28
	402758	NA	15.130200	NA	0.28
5	448240	AJ478345	Hs. 191034	ESTs	0.28
-	401333	NA		NA	0.28
	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	0.28
	454738	BE072139		gb:PM1-BT0533-291299-002-b05 BT0533 Homo	0.28
10	442896	R37725	Hs.261108	ESTs	0.28
10	447949	A1446820	Hs.165839	EST	0.28
	435625	H50654	Hs.113999	ESTs	0.28
	415817 438380	U88967 T06430	Hs.78867 Hs.6194	protein tyrosine phosphatase, receptor-t chondroifin sulfate proteoglycan BEHAB/b	0.28 0.28
	442967	AI025460	Hs.220977	ESTs	0.28
15	448062	AW295923	Hs.255472	KIAA1843 protein	0.28
	425860	L29339	Hs.1964	solute carrier family 5 (sodium/glucose	0.28
	451839	AI820516	Hs.16857	ESTs	0.28
	446000	AV656052	Hs.1504	hemopexin	0.28
20	443506	H10661	Hs.192124	ESTs, Weakly similar to 138022 hypotheti	0.28
20	418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	0.28
	445481 409337	AW561846 H71289	Hs.148836 Hs.220535	ESTs ESTs	0.28 0.28
	411414	AW897236	113.220000	gb:CM0-NN0057-150400-335-c06 NN0057 Homo	0.28
	427642	R40761	Hs.9834	ESTs	0.28
25	456392	W28766		gb:51d3 Human retina cDNA randomly prime	0.28
	409920	BE169746	Hs.12504	likely ortholog of mouse Arkadia	0.28
	410285	AA083609		gb:zm63d05.r1 Stratagene fibroblast (937	0.28
	442496	R55073	Hs.124130	ESTs	0.28
30	423770	AW976766 AK000214	Hs.132776	Homo sapiens cDNA FLJ10077 fis, clone HE	0.28
50	423467 458716	N99013	Hs.129014 Hs.16762	hypothetical protein FLJ20207 Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.29 0.29
	423235	AW410698	Hs.169917	neurabin II	0.29
	431087	H12723	Hs.290791	ESTs	0.29
	459106	AW589793	Hs.224713	ESTs	0.29
35	414870	N72264	Hs.300670	KIAA1204 protein	0.29
•	402243			NA	0.29
	432628	R02394	Hs.269436	ESTs, Moderately similar to PC4259 ferri	0.29
	404364	NA		NA NA	0.29
40	400480 456083	U46922	Hs.77252	NA Sports histidiae tried ease	0.29 0.29
40	446598	AW250546	HS.11232	fragile histidine triad gene gb:2821774.5prime NIH_MGC_7 Homo sapiens	0.29
	422201	NM_001505	Hs.113207	G protein-coupled receptor 30	0.29
	443919	AI091284	Hs.135224	ESTs, Weakly similar to A47582 B-cell gr	0.29
	453948	AI970797	Hs.64859	ESTs	0.29
45	403792	NA		NA	0.29
	418957	AI792615	Hs.188712	ESTs	0.29
	457960	AA771881	Hs.298149	ESTs	0.29
	404269 439309	AF090097	Hs.6524	NA Homo sapiens clone IMAGE 25997	0.29 0.29
50	458239	BE439877	Hs.283389	ESTs	0.23
٠,	414941	C14865	Hs.332341	ESTs	0.30
	404954			NA	0.30
	441609	AA946764	Hs.133460	ESTs	0.30
55	426895	AA416880	Hs.225738	ESTs	0.30
23	403182	NA		NA NA	0.30
	402319 429699	Al383469	Hs.159300	NA ESTs	0.30 0.30
	405669	NA	15.155500	NA	0.30
	459312	AF107457	Hs.37035	homeo box HB9	0.30
60	431853	AA521034	Hs.70834	ESTs	0.30
	449768	AI972746	Hs.102945	ESTs, Weakly similar to 178885 serine/th	0.30
	443609	AV650231	Hs.282941	ESTs, Highly similar to A Chain A, Human	0.30
	454293	H49739	Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	0.30
65	447569 400128	A1393202 NA	Hs.147554	hypothetical protein FLJ23392 NA	0.30 0.30
0,5	423208	AA323191	Hs.137064	cytopiasmic polyadenylation element bind	0.30
	434227	AF119893	Hs.63382	hypothelical protein PRO2714	0.30
	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	0.30
70	401165	NA		NA	0.30
70	415394	R19249	Hs.22654	sodium channel, voltage-gated, type I, a	0.30
	443110	AW352243	Hs.132665	ESTs	0.30
	426724	AA383623	Hs.293616	ESTs	0.30
	415035 409753	H42314 AA234847		gb:yo09e02.s1 Soares adult brain N2b5HB5 gb:zs37b10.r1 Soares_NhHMPu_S1 Homo sapi	0.30 0.31
75	459221	BE246522	Hs.306121	gb:2537610,F1 Soares_NRHMPU_51 Homo sapi leukocyte receptor cluster (LRC) encoded	0.31
. •	408895	AA058730	Hs.191464	ESTs	0.31
	405110	NA		NA .	0.31
	432430	AW079984	Hs.262480	ESTs, Weakly similar to PIHU86 salivary	0.31
90	426442	AA378656	Hs.106510	ESTs, Moderately similar to ALU2_HUMAN A	0.31
80	411765	H43346		gb:yp09a04.r1 Soares breast 3NbHBst Homo	0.31
	431854	AA383550	Hs. 271699	polymerase (DNA directed) iota	0.31
	457553 412301	AI861896 AW936328	Hs.304505	ESTs gb:QV4-DT0021-281299-070-f07 DT0021 Homo	0.31 0.31
	112301			Baran Long Language Control Long Language	0.51

	418626	AW299508	Hs.135230	ESTs	0.31
	416156	Z41922		gb:HSC038101 normalized infant brain cDN	0.31
	416275	H42823	Hs.155742	głyoxylate reductase/hydroxypyruvate red	0.31
_	419091	T85332	Hs.178294	ESTs	0.31
5	42011B	AW295297	Hs.182585	KIAA1276 protein	0.31
	451094	A1949825	Hs.260395	ESTs	0.31 0.31
	403214	NA wmmaaa	LL 224770	NA ESTs	0.31
	412717 428782	W00973 X12830	Hs.334728 Hs.193400	interleukin 6 receptor	0.31
10	449202	AW295154	Hs.255396	ESTs	0.31
10	433138	AB029496	Hs.59729	semaphorin sem2	0.31
	435602	AJ793222	Hs.166817	ESTs	0.31
	424844	D61524		gb:HUM413E07B Clontech human fetal brain	0.32
	435253	W91884		gb:zh47f08.s1 Soares_fetal_fiver_spleen_	0.32
15	455350	AW901809		gb:QV0-NN1020-170400-195-h02 NN1020 Homo	0.32
	416320	H47867	Hs.34024	ESTs	0.32
	406333			NA	0.32
	443652	AI080692	Hs.134229	ESTs, Weakly similar to I54401 hypertens	0.32
20	457103	AJ421187	Hs.189192	ESTs, Weakly similar to T COMPLEX TESTIS	0.32 0.32
20	423593	AA328144	11- 40343	gb:EST31752 Embryo, 12 week I Homo sapie	0.32
	453242	T98327 AA284166	Hs.18343 Hs.84113	ESTs cyclin-dependent kinase inhibitor 3 (CDK	0.32
	456281 403847	NA NA	115.04113	NA	0.32
	458711	AL036877	Hs.282878	ESTs	0.32
25	406242	NA	10.2020.0	NA .	0.32
	433493	AA594915	Hs.155087	ESTs	0.32
	458147	AW752597		gb:IL3-CT0214-161299-045-B06 CT0214 Homo	0.32
	437403	AI208149	Hs.121196	ESTS	0.32
••	407823	D44744	Hs.247447	ESTs	0.32
30	457300	AW297436	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone C	0.32
	436089	AA804957	Hs.119840	ESTs	0.32
	457463	AW877031	Hs.272321	hypothetical protein FLJ12571	0.32 0.32
	433370	AI084343	Hs.122310	ESTs	0.32
35	436298 419768	AW293496 T72104	Hs.180138 Hs.93194	ESTs apolipoprotein A-I	0.33
55	449428	AI651280	Hs.195685	ESTs	0.33
	406291	NA NA	113.133000	NA NA	0.33
	409699	BE154650		gb:PM3-HT0344-071299-003-c08 HT0344 Homo	0.33
	418162	T11958		gb:A802R Heart Horno sapiens cDNA clone A	0.33
40	408316	AW807771		gb:MR4-ST0098-090300-003-c05 ST0098 Homo	0.33
	404187	NA.		NA	0.33
	452992	AJ792376	Hs.31290	Homo sapiens clone 23832 mRNA sequence	0.33
	448355	AM93734	Hs.329374	ESTs	0.33
4.5	442423	BE326264	Hs.246842	ESTs	0.33
45	439474	AI824060	Hs.211501	ESTs	0.33 0.33
	457149	AA429575	Hs.297493	ESTs	0.33
	448623	BE613468	Hs.107515	ESTs, Wealdy similar to T00329 hypotheti gb:RC2-ST0301-120200-011-112 ST0301 Homo	0.33
	454790 419372	AW820852 W28781		gb:51h3 Human retina cDNA randomly prime	0.33
50	406293	NA NA		NA	0.33
50	422933	AF073931	Hs.122359	calcium channel, voltage-dependent, alph	0.33
	451818	AI819018	Hs.339668	ESTs	0.33
	441912	AA971484	Hs.159938	ESTs	0.33
	429013	AJ012590	Hs.194728	hexose-6-phosphate dehydrogenase (glucos	0.33
55	422304	AK002016	Hs.114727	Homo sapiens, clone MGC: 16327, mRNA, com	0.33
	457394	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	0.33
	406597			NA	0.33
	451636	AW173270	Hs.140444	ESTs	0.33 0.33
60	424226	N94153	Hs.19155	ESTs	0.33
UU	TABLE	47D-			
	Pkey:		ique Eos probeset ic	lentifier number	
	CAT nu		ne cluster number	reliance from the	
	Accessi		nbank accession nu	mbers	
65	. 40000	•			
	Pkey		er Accession	C	
	408316		AW807771 AW	179260 AW807851 AW179240 AW845961 AW807693 I	BE141176 AW807594 AW807772 AW845003 AW845963 AW179239
	409382				
70	409699			54785 AW458343 BE154816 BE154667	
70	409753				
	409828			501295 AW501212	
	410285			83790 AA112048	
	411414				
75	411765				
13	412301 412793				
	412793			90685 BE090697 BE090680 BE090691 BE090696 BE0	090698 BE090686
	414003			288 AW750262	
	414383				
80	415327		H22769 R3518	2 Z43545 F05783 N92089 H71928	
	416035	1567254_1	H42314 H4308	0 H45217 H15384	
	416156	1573980_1	Z41922 H2307	2 177322	
	418162		T11958 T1175	6 T11816 T20135 T19729 R45874	

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AA328144 AW962385 N30457
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                                           D61524 AA347654 AW961758
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316401_1
                                           AI547111 AW973749 AA558007
BE169639 AA476976
                                           AF127772 AF062358 AF060217 AA652270 F23288
AW974668 AA661959 AA649572 AA640401 AA640402
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                          389383 1
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BE072139 BE157977 BE157974 AW857974 AW817778
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BE145826 BE145815 BE145822 AW854707 BE145912
             454790
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                           1252281_1
                                            DETINOUS DETINOUS DETINOUS DE TINOST (UT DE TINOST (UT DE TINOST) A AW893949 AW893966 AW893966 AW8901809 AW8901795 AW8901795 AW8901792 AW8901744 AW8901753 AW8901807 AW8901798
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1789791_1
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              459233
 35
              TABLE 47C:
             Pkey:
Ref:
                                    Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
                                     sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Indicates DNA strand from which exons were predicted.
 40
              Strand:
              Nt_position:
                                     Indicates nucleotide positions of predicted exons.
                                                            Nt_position
110553-111119
              400480
                           8439796
                                             Minus
 45
              401015
                           8117441
                                             Plus
                                                             151364-151606
              401042
                           8117611
                                             Plus
              401132
                           8705350
                                                            85679-85795
                                             Minus
              401165
401333
                           9438376
9884881
                                                            168244-168423
13852-14861
                                             Plus
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              401350
                           9931226
                                                             14471-14623
                                                             163249-163623
              401623
                           8575907
                                             Plus
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Plus
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147744-147861
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402790
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4835258
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Minus
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76723-77027,79317-79484
               403182
                                              Plus
               403214
                                              Minus
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88377-88537
               403652
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               403670
                                              Minus
  65
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                            7230192
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                                              Minus
                            7708844
7454203
                                              Plus
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                                              Plus
Plus
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                            9863643
4481839
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32986-33202
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                                                             71066-71326
14770-14931
                                              Plus
   75
               404753
                                              Plus
                404848
                             8248647
                                                              23955-24034,25143-25264
                                              Minus
                             7331453
               404900
                                              Plus
                                                              22032-22219
                                                              131720-132042
127374-127578
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                             7387327
                                              Plus
                             7543748
8096888
               405037
                                              Minus
   80
                                                              118940-119100
               405110
                                              Minus
               405650
                             4926905
                                              Minus
                                                              71743-72291
                             4508140
                                                              14130-14270
               405669
                                              Plus
                             7960374
                                                              65101-65574
                                              Minus
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. . . .

	405242	7417725	Minus	36736-36951
	406291	5686274	Ptus	9562-9867
	406293	5686274	Minus	17646-17953
_	406333	9213235	Plus	64689-64798
5	406560	7711569	Minus	35162-35292
	406589	8224211	Plus	38806-38989
	406597	8248613	Minus	132738-132985,134266-134425,135034-135192,135471-135608,137345-137478,138768-138912

TABLE 48A: ABOUT 426 GENES UPREGULATED IN MELANOMA RELATIVE TO NORMAL BODY TISSUES
Table 48A lists about 426 genes upregulated in melanoma relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Placy:

Unique Eos probeset identifier number
ExAcon:

Exemplar Accession number, Genbank accession number
UniquenelD:

Uniquene gene title

Uniquene gene title

Rt:

Mean of metanoma Als divided by the mean of normal fissue Als, where the minimum value for the numerator and denominator was set to 1.0 10

15

Unique Eos probeset identifier number
Exemplar Accession number, Genbank accession number
Unigene number
Unigene gene title
Mean of melanoma Als divided by the mean of normal tissue Als, where the minimum value for the numerator and denominator was set to 1.0

20	Pkey	.ExAcon	UnigenetD	Unigane Title	R1
	426555	NM 000372	Hs.2053	tyrosinase (oculocutaneous albinism IA)	376.61
	428655	H05769	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp	324.36
	430377 453344	NM 001922 BE349075	Hs.301865 Hs.44571	dopachrome tautomerase (dopachrome delta ESTs	231.30 180.67
25	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	107.36
23	417166	AA431323	Hs.42146	ESTs	97.76
	425234	AW152225	Hs.165909	ESTs, Weakly similar to 138022 hypotheti	96.76
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	94.52
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	90.88
30	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transi	87.91
-	443983	H04482	Hs.163724	ESTs	85.55
	428513	BE220806	Hs.184697	Homo sapiens clone 23785 mRNA sequence	85.03
	419956	AL137939	Hs.40096	cadherin 19, type 2	84.27
	423605	AF047826	Hs. 129887	cadherin 19, type 2	80.88
35	430540	AW245422	1.0.145557	Homo sapiens cDNA: FLJ22105 fis, clone H	80.64
	416975	NM 004131	Hs.1051	granzyme 8 (granzyme 2, cytotoxic T-lymp	79.09
	421633	AF121860	Hs.106260	sorting nexin 10	71.52
	442064	AI422867	Hs.88594	ESTs	69.88
_	418310	AA814100	Hs.86693	ESTs	67.94
40	423799	AW026300	Hs.132906	19A24 protein	67.64
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	63.24
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	63.18
	432882	NM 013257	Hs.279696	serum/glucocorticoid regulated kinase-li	62.33
	454088	AW062425		gb:CMO-CT0042-090899-018-f01 CT0042 Homo	61.62
45	430838	N46664	Hs.169395	hypothetical protein FLJ12015	60.52
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	59.73
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	59.33
	450800	BE395161	Hs.1390	proteasome (prosome, macropain) subunit,	59.00
50	441224	AU076964	Hs.7753	catumenin	58.27
50	408418	AW963897	Hs.44743	KIAA 1435 protein	56.79
	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	56.45
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	56.29
	420674	NM 000055	Hs.1327	butyrylchofinesterase	56.15
55	407856	AA045281	Hs.266175	phosphoprotein associated with GEMs	55.82
55	420552	AK000492	Hs.98806	hypothetical protein	55.39
	442355 429747	AA456539 M87507	Hs.8262	lysosomal-associated membrane protein 2	54.97 53.95
	410174	AA306007	Hs.2490 Hs.59461	caspase 1, apoptosis-related cysteine pr	52.85 52.00
	437396	BE140395	Hs.21621	DKFZP434C245 protein	52.00 51.97
60	409557	BE182896	Hs.3686	hypothetical protein OKFZp762O076 ESTs	51.64
oo	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	51.42
	414403	AW969551	Hs.76064	ribosomal protein L27a	50.58
	452958	AA883929	Hs.40527	ESTs	50.21
	458997	AW937420	113.7002	ESTs	49.97
65	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	49.85
	435905	AW997484	Hs.5003	KIAA0456 protein	48.76
	424800	AL035588	Hs.153203	MycD family inhibitor	48.33
	426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	47.91
	408548	AA055449	Hs.63187	ESTs, Weakly similar to ALUC_HUMAN !!!!	47.45
70	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	46.52
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	45.79
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	45.52
	430066	AI929659	Hs.237825		45.45
	417427	M90391	Hs.82127	interleukin 16 (lymphocyte chemoattracta	44.58
75	450447	AF212223	Hs.25010	hypothetical protein P15-2	43.36
	446019	A1362520		histone deacetylase 3	43.03
	430015	AW768399		ESTs	42.45
	446880	AJ811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	42.36
00	409327	L41162	Hs.53563	collagen, type IX, alpha 3	42.30
80	425390	AI092634	Hs.156114		41.42
	411088	BE247593	Hs.145053		41.21
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	40.94
	441590	A1623207	Hs.190537	ESTs	40.66
				500	

	457465 430280	AW301344 AA361258	Hs.122908 Hs.237868	DNA replication factor interleukin 7 receptor	39.91 38.91
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	38.70
5	421282	AA286914	Hs.40782	ESTs	38.55 38.00
J	448275 453912	BE514434 AL121031	Hs.20830	kinesin-fike 2 SWI/SNF related, matrix associated, acti	37.94
	414844	AA296874	Hs.77494	deoxyguanosine kinase	37.88
	421305	BE397354	Hs.324830	diptheria toxin resistance protein requi	37.70 37.64
10	439352 409078	BE614347 AW327515	Hs.169615	hypothetical protein FLJ20989 ESTs	37.30
10	449845	AW971183	Hs.6019	DnaJ (Hsp40) hornolog, subtamily C, membe	37.27
	444184	T87841	Hs.282990	Human DNA sequence from clone RP1-28H20	37.21
	445819 451418	A1767472 BE387790	Hs.146290 Hs.26369	ESTs, Weakly similar to putative p150 (H hypothetical protein FLJ20287	37.21 37.00
15	433226	AW503733	Hs.9414	KIAA1488 protein	36.88
••	445784	AI253155	Hs.146065	ESTs	35.36
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	33.09 32.05
	407756 447937	AA116021 AL109716	Hs.38260 Hs.20034	ubiquitin specific protease 18 Homo sapiens mRNA full length insert cDN	31.00
20	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	30.76
	429083	Y09397	Hs.227817	BCL2-related protein A1	30.73 28.45
	444570 446839	H58373 BE091926	Hs.332938 Hs.16244	hypothetical protein MGC5370 mitotic spindle coiled-coil related prot	27.62
	433576	BE080715	Hs.161091	ESTs .	27.42
25	422173	BE385828	Hs.250619	phorbalin-like protein MDS019 (CEM15)	27.36
	408962 442757	BE386436 AI739528	Hs.44317 Hs.28345	SRY (sex determining region Y)-box 10 ESTs	26.66 25.94
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	25.39
20	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	24.55
30	438461	AW075485	Hs.286049	phosphoserine aminotransferase KIAA0129 gene product	22.48 22.15
	427581 435256	NM 014788 AF193766	Hs.179703 Hs.13872	cytokine-like protein C17	20.61
	409988	N27687	Hs.334334	transcription factor AP-2 alpha (activat	19.79
25	444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibito	19.73 19.27
35	417404 458098	NM 007350 BE550224	Hs.82101	pleckstrin homology-like domain, family metallothionein 1E (functional)	18.09
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	16.95
	446054	AB014537	Hs.13604	KIAA0637 gene product	15.67 15.54
40	432606 414696	NM 002104 AF002020	Hs.3066 Hs.76918	granzyme K (serine protease, granzyme 3; Niemann-Pick disease, type C1	15.06
70	457211	AW972565	Hs.32399	ESTs, Weakty similar to S51797 vasodilat	14.89
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity la, re	14.84
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to minichromosome maintenance deficient (S.	14.61 14.12
45	424308 421334	AW975531 BE297729	Hs.154443	gb:601175625F1 NIH_MGC_17 Homo sapiens c	13.94
	422423	AF283777	Hs.116481	CD72 antigen	13.77
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	13.33 12.76
	416406 427536	D86961 BE277141	Hs.79299 Hs.115803	fipoma HMGIC fusion partner-like 2 gb:601178666F1 NIH_MGC_20 Homo sapiens c	12.76
50	423198	M81933	Hs.1634	cell division cycle 25A	12.66
	430770	AA765694	Hs.123296	ESTs	12.58 12.09
	407833 430822	AW955632 AJ005371	Hs.66666 Hs.248017	ESTs, Weakly similar to S19560 profine-r glyceraldehyde-3-phosphate dehydrogenase	11.46
	424259	AK001776	Hs.143954		10.58
55	446950	AA305800	Hs.5672	hypothetical protein AF140225	10.04 9.98
	420956 448356	AA351584 AL120837	Hs.100543 Hs.20993	Homo sapiens clone 24505 mRNA sequence high-glucose-regulated protein 8	9.88
	428799	AJ478619	Hs.104677	ESTS	9.56
60	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp5660134 (fr	9.03 9.01
UU	447769 408393	AW873704 AW015318	Hs.320831 Hs.23165	Homo sapiens cDNA FLJ14597 fis, clone NT ESTs	8.99
	407966	AA295052	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	8.99
	450534	AI570189	Hs.25132	KIAA0470 gene product	B.91
65	410101 417129	Al338045 Al381800	Hs.203559 Hs.300684		8.90 8.86
03	453507	AF083217	Hs.33085	WD repeat domain 3	8.68
	442739	NM 007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	8.45
	456249		Hs.82508 Hs.15557	HRIHFB2206 protein 3 polymerase (DNA directed), eta	8.38 8.35
70	437786 448410		Hs.21126		8.20
	442711	AF151073	Hs.8645	hypothetical protein	8.14
	408405		Hs.44672		7.96 7.88
	420208 415929		Hs.95972 Hs.49344		7.79
75	449217		Hs.23262	ribonuclease, RNase A family, k6	7.66
	451239	H24302	Hs.23127	ESTs	7.50 7.40
	442426 447233		Hs.33293 Hs.17901		7.40 7.39
~ ~	439574		119,11301	ESTs .	7,13
80	431360	NM 000422			7.12
	412438 452882		Hs.11074 Hs.19627		6.96 6.87
	436581		Hs. 18021		6.64
				61	^

	431317 443264	AA502682 BE221477		gb:ng23d01.s1 NCI_CGAP_Ov2 Homo sapiens ESTs, Moderately similar to A47582 B-cel
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H
	408367	AK001178		homolog of rat orphan transporter v7-3
,	413283	R78669		hypothetical protein similar to swine ac
	453878	AW964440		DC32
	424148	BE242274 NM 004519	Hs. 1741 Hs. 40866	integrin, beta 7 potassium voltage-gated channel, KQT-lik
	407876 409512	AW979187	Hs.293591	metanoma differentiation associated prot
	427951	AI826125	Hs.43546	ESTs
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD
	416640	BE262478	Hs.79404	neuron-specific protein
	446830	BE179030		Human DNA sequence from clone RPS-1174N9
	452629	W02772	Hs.180178	Homo sapiens, clone IMAGE:3947276, mRNA,
,	427390	AI432163	Hs.268231	Homo sapiens cDNA: FLJ23111 fis, clone L
	427853	AJ569798	Hs.98260	ESTs
	434398	AA121098	Hs.3838 Hs.24724	serum-inducible kinase (SNK) MFH-amplified sequences with leucine-ric
	450256 428524	AA285887 AA429772	113.24724	ESTs
)	431797	BE169641	Hs.270134	hypothetical protein FLJ20280
	418403	086978	Hs.84790	KIAA0225 protein
	411524	AW850303		gb:IL3-CT0219-191199-030-F09 CT0219 Homo
	426158	NM 001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v
	443086	AW977125		sine oculis homeobox (Drosophila) homolo
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L
	406843	AW196933	Hs.119598	ribosomal protein L3
	430594	AK000790	Hs.246885 Hs.19192	hypothetical protein FLJ20783 cyclin-dependent kinase 2
	447674 410491	BE270640 AA465131	HS.19192 Hs.64001	Homo sapiens clone 25218 mRNA sequence
)	420338	AA825595	Hs.88269	Homo sepiens, clone MGC:17339, mRNA, com
	409264	NM 014937	Hs.52463	KIAA0966 protein
	414734	AA151712	Hs.82572	ESTs
	426759	A1590401	Hs.21213	ESTs
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec
•	428612	AA770001	11- 900001	ESTs
	413550	W03011	Hs.306881	MSTP043 protein
	447349	A1375546		gb:tc23d04.x1 Soares_total_fetus_Nb2HF8_ Target Exon
	403328 452840	A1097393	Hs.43481	hypothetical protein DKFZp564K192
)	439310	AF086120	Hs.102793	ESTs
•	451281	A1768965	Hs.292708	ESTs
	431183	NM 006855	Hs.250696	KOEL (Lys-Asp-Ghr-Leu) endoplasmic retic
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,
	435963	AF271212	Hs.322901	disrupter of silencing 10
5	418699	BE539639	Hs.173030	ESTs, Weakly similar to ALUS_HUMAN ALU S
	414770	BE257224		Homo sapiens, clone IMAGE:3873720, mRNA
	419628	H67546	Hs.49768	ESTs
	420258	AA477514	Hs.96247 Hs.310735	transfin-associated factor X ESTs, Moderately similar to ALU7_HUMAN A
0	446341 420267	AL040763 N37030	Hs.310735 Hs.173337	ESTs Moderately sometar to ALO/_Homely A
_	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi
	432888	T86823		gb:yd81a08.s1 Soares fetal liver spleen
	453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6
_	418340	NM 013286	Hs.84162	chromosome 3p21.1 gene sequence
5	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy
	447484	AA464839	Hs.292566	
	452036	NM 003966	Hs.27621	sema domain, seven thrombospondin repeat gb:Human glyceraldehyde-3-phosphate dehy
	406903	K03121		go:numan gryceraidenyde-3-prospnate deny dihydropyrimidinase-like 3
0	405451 434203	BE262677	Hs.283558	
-	450088	AW292933	Hs.254110	
	421535	AB002359	Hs.105478	phosphoribosylformylglycinamidine syntha
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S
_	451259	NM 006052	Hs.26146	Down syndrome critical region gene 3
5	452548	AL050321	Hs.301532	
	432195	AJ243669	Hs.8127	KIAA0144 gene product
	445101	175202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (1
	425913	AA365799 AW504365	He 24142	SEC22, vesicle trafficking protein (S. c Wiskott-Aldrich syndrome protein interac
0	423494 442092	AW504365 AW578669	Hs.24143	hypothetical protein FLJ12439
_	424954	NM 000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)
	427719	Al393122	Hs.134726	
	415310	R16313		gb:yf93h09.r1 Soares infant brain 1NIB H
_	416058	L08895	Hs.78995	MADS box transcription enhancer factor 2
5	427828	AI024471	Hs.98232	ESTs
	410079	U94362	Hs.58589	glycogenin 2
	420265	AA756209	Hs.88087	ESTs
	426181	AA371422	Hs.33437	
80	431639		Hs.26617	
,0	410275		Hs.61796	calpastatin
	422150 429238		Hs.19828	
	429230		Hs.47166	
		2202.011		

	425050	BE391854	Hs.7970	gb:601285394F1 NIH_MGC_44 Homo sapiens c	3.82
	425050 442271	AF000652	Hs.8180	syndecan binding protein (syntenin)	3.81
	410235	AA082977		gb:zn07h10.r1 Stratagene hNT neuron (937	3.79
•	408535	BE294925	Hs.46680	CGI-12 protein	3.78 3.76
5	424624 411400	AB032947 AA311919	Hs.151301 Hs.69851	Ca2+dependent activator protein for secr nucleotar protein family A, member 1 (H/	3.74
	458215	AA928160	15.03631	gb:on86/10.s1 Soares_NFL_T_GBC_S1 Homo s	3.73
	452874	AK001061	Hs.30925	hypothetical protein FLJ 10199	3.72
10	442643	U82756		PRP4/STK/WD splicing factor	3.70
10	447471	AF039843	Hs.18676 Hs.108646	sprouty (Drosophila) homolog 2 Homo sapiens cDNA FLJ14934 fis, clone PL	3.70 3.67
	447644 422616	AW861622 BE300330	Hs.118725	selenophosphate synthetase 2	3.64
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	3.64
	418180	BE618087	Hs.83724	hypothetical protein MGC5466	3.62
15	423032	AJ684746	Hs.119274	RAS p21 protein activator (GTPase activa	3.62 3.62
	425569 412156	AA359597 H29487	Hs.301701 Hs.17110	Homo sapiens cDNA FLJ12073 fis, done HE Homo sapiens mRNA; cDNA DKFZp434C2016 (f	3.61
	417426	NM 002291	Hs.82124	taminin, beta 1	3.61
	407188	AA457592		gb:aa92f11.s1 Stratagene fetal retina 93	3.61
20	426600	NM 003378	Hs.171014	VGF nerve growth factor inducible	3.61 3.60
	440760 448481	AK001145 W15284	Hs.284216 Hs.74832	hypothetical protein FLJ10283 ESTs	3.59
	414111	BE047679	Hs.152982	hypothetical protein FLJ13117	3.59
	437862	AW978107	Hs.5884	Homo sapiens mRNA; cDNA DKFZp586C0224 (f	3.59
25	409703	NM 006187	Hs.56009	Z-5-oligoadenylate synthetase 3 (100 k	3.59
	406981	S71129	Hs.293189	acetylcholinesterase (YT blood group) ESTs	3.59 3.58
	431586 415173	AW971100 AW501735	Hs.180059	ESTS	3.57
	430512	AF182294	Hs.241578	U6 snRNA-essociated Sm-like protein LSm8	3.57
30	446126	AW085909		pleckstrin homology domain interacting p	3.57
	409305	AA070078		gb:zm60f05.r1 Stratagene fibroblast (937	3.57 3.56
	433867	AK000596 AI299050	Hs.3618 Hs.143835	hippocatcin-like 1 gb:gn14d12.x1 NCI_CGAP_Lu5 Homo sapiens	3.56
	459721 441412	AI393657	Hs.159750	ESTs	3.55
35	416114	AI695549	Hs.183868	glucuronidase, beta	3.55
	454870	AW836081		gb:PMO-LT0019-090300-002-e11 LT0019 Homo	3.54
	443105	X96753	Hs.9004	chondroitin sulfate proteoglycan 4 (meta	3.53 3.51
	444680 413949	AI186671 AA316077	Hs.22670 Hs.75639	ESTs Human TB1 gene mRNA, 3' end	3.51
40	437033	AW248364	Hs.5409	RNA polymerase I subunit	3.50
. •	412141	AI183838	Hs.48938	hypothetical protein FLJ21802	3.49
	437158	AW090198		KIAA1150 protein	3.48 3.47
	432642	BE297635	Hs.3069 Hs.132447	heat shock 70kD protein 98 (mortalin-2) ESTs	3.47
45	440634 445652	AA921767 AL117473	Hs.13036	DKFZP727A071 protein	3.46
	429500	X78565	Hs.289114		3.43
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	3.43
	426141	C05886	Hs.293972		3.40 3.40
50	424321 449209	W74048 BE616830	Hs.1765 Hs.294145	lymphocyte-specific protein tyrosine kin ESTs	3.39
50	408304	AW810279	113.201114	gb:MR4-ST0125-151299-029-a09 ST0125 Homo	3.37
	416561	D87328	Hs.79375	holocarboxylase synthetase (biotin-[prop	3.35
	422947	AA305782	Hs.122552		3.34 3.34
55	453005 409430	AW055308 R21945	Hs.31803 Hs.346735		3.32
73	417386	AL037228	Hs.82043		3.32
	440999	AI951562	Hs.126370		3.31
	407516	X64974	11- 01014	gb:H.sapiens mRNA HTPCRH02 for offactory	3.31 3.31
60	450065 416902	AL050107 AA375634	Hs.24341 Hs.288974	transcriptional co-activator with PDZ-bi hypothetical protein FLJ12528	3.28
00	432878	BE386490	Hs.27966		3.28
	443296	AI765288	Hs.313347		3.27
	429954	AJ918130	Hs.21374		3.25 3.25
65	428044 425317	AA093322 AW205118	Hs.30140 Hs.21054		3.25
05	418064	BE387287	Hs.83384		3.25
	432917	NM 014125	Hs.24151		3.24
	447871	BE297946	Hs.23905		3.24
70	414829	AA321568 AW968934	Hs.77436 Hs.17310		3.24 3.23
70	426996 416188		Hs.79070		3.22
	429530		Hs.99362		3.21
	445174	AV652850	Hs.17200	4 titin	3.19
75	459227			ESTs	3.19 3.15
75	439039		Hs.48713 Hs.88556		3.15
	418803 420005				3.15
	422511			38 collagen, type XVII, alpha 1	3.14
00	452480	AI903526		gb:RC-BT031-090199-063 BT031 Homo sapien	3.14
80	445701				3.14 3.14
	410678 458664		Hs.29373	gb:go18h07.x1 NCI_CGAP_Lu5 Homo sapiens	3.13
	436315		Hs.27935		3.13

				A LATE (DOLDOW)	3 1 2
	430441 435080	BE398091 AI831760	Hs.155111	desmoplakin (DPI, DPII) hypothetical protein FLJ14428	3.12 3.12
	425606	U52112	Hs.158331	renin-binding protein	3.11
-	432978	AF126743	Hs.279884	DNAJ domain-containing	3.11
5	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	3.10 3.10
	446627 427647	AI973016 W19744	Hs.15725 Hs.180059	hypothetical protein S88148 Horno sapiens cDNA FLJ20653 fis, clone KA	3.09
	417211	T97617	Hs.269092	ESTs	3.08
10	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.08
10	448752	AA593857	Hs.300842 Hs.268906	KIAA1608 protein	3.07 3.07
	416355 425345	H49875 AU077297	Hs.155894	ESTs protein tyrosine phosphatase, non-recept	3.07
	410321	Y12860	Hs.62245	solute carrier family 25 (mitochondrial	3.07
15	411395	AA889673	Hs.7542	KIAA1802 protein	3.07
15	416065 432343	BE267931 NM 002960	Hs.78996 Hs.2961	proliferating cell nuclear antigen \$100 calcium-binding protein A3	3.06 3.06
	457991	BE539951	Hs.306996	Homo sapiens, clone IMAGE:3447073, mRNA,	3.05
	433201	AB040896	Hs.21104	KIAA1463 protein	3.03
20	416178	A1808527	Hs.192822	serologically defined breast cancer anti	3.02 3.01
20	411975 448719	AI916058 AA033627	Hs.144583 Hs.21858	ESTs trinucleotide repeat containing 3	3.00
	419870	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.00
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	2.94
25	415668 453256	AW957684 AI565587	Hs.306814 Hs.32556	hypothetical protein FLJ21889 KIAA0379 protein	2.93 · 2.81
23	435256	A1469355	Hs.127310	ESTs	2.75
	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	2.60
	408209	NM 004454	Hs.43697	ets variant gene 5 (ets-related molecule	2.59
30	440457 415314	BE387593 N88802	Hs.21321 Hs.5422	Homo sapiens clone FLB9213 PRO2474 mRNA, gfycoprotein M6B	2.55 2.51
30	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	2.50
	424085	NM 002914	Hs.139226	replication factor C (activator 1) 2 (40	2.48
	410600	AW575742	Un 4000C7	ESTs, Moderately similar to S65657 alpha	2.48 2.43
35	439180 444809	AI393742 BE207568	Hs.199067 Hs.208219	v-erb-b2 avian erythroblastic leukemia v oculospanin	2.39
-	453837	AL138387	Hs.256126	baculoviral IAP repeat-containing 7 (liv	2.39
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	2.37
	411358 427550	R47479 BE242818	Hs.94761 Hs.311609	KIAA1691 protein nuclear RNA helicase, DECD variant of DE	2.35 2.34
40	426312	AF026939	Hs.181874	interferon-induced protein with tetratri	2.29
	448569	BE382657	Hs.21486	signal transducer and activator of trans	2.27
	418661	NM 001949	Hs.1189	E2F transcription factor 3	2.24 2.21
	459373 417437	BE408266 U52682	Hs.301406 Hs.82132	hypothetical protein PP3501 interferon regulatory factor 4	2.21
45	436700	AI693690	Hs.301406	hypothetical protein PP3501	2.18
	450690	AA296696	Hs.333418	FXYD domain-containing ion transport reg	2.15
	432800 421773	BE391046 W69233	Hs.278962 Hs.112457	AIM-1 protein ESTs	2.15 2.09
	409415	AA579258	Hs.6083	Homo sapiens cDNA: FLJ21028 fis, clone C	2.03
50	433364	AI075407	Hs.296083	ESTs, Moderately similar to I54374 gene	2.02
	412609	Z48804	Hs.74124	ocular albinism 1 (Nettleship-Falls)	2.01 2.01
	443950 451537	NM 001425 R56631	Hs.9999 Hs.26550	epithelial membrane protein 3 retinoid X receptor, gamma	2.00
	427080	AW068287	Hs.301175		1.96
55	413190	AA151802	Hs.40368	adaptor-related protein complex 1, sigma	1.94
	412926 453779	A1879076 N35187	Hs.75061 Hs.43388	macrophage myristoytated alanine-rich C 28kD interferon responsive protein	1.91 1.86
	453107	NM 016113	Hs.279746		1.86
<b>60</b>	430637	BE160081	Hs.256290		1.86
60	408561 413171	AI308037 AA318325	Hs.84120 Hs.75219	hypothetical protein MGC13016 tyrosinase-related protein 1	1.84 1.83
	406016	MUIOZ	NS.73213	Target Exon	1.82
	446644	NM 003272		transmembrane 7 superfamily member 1 (up	1.81
65	431836	AF178532	Hs.271411		1.77 1.77
03	439496 447604	BE615501 AW089933	Hs.32343 Hs.301342	Homo sapiens, Similar to RIKEN cDNA 1110 hypothetical protein MGC4342	1.76
	438866	U44385	Hs.325495		1.74
	440672	AF083811	Hs.7345	MAD1 (mitotic arrest deficient, yeast, h	1.70
70	416091	AF295370	Hs.283082		1.69 1.67
, 0	446291 422532	BE397753 AL008726	Hs.14623 Hs.11812	interferon, gamma-inducible protein 30 protective protein for beta-galactosidas	1.67
	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	1.67
	412580	AA113262	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	1.67
75	448258 414945	8E386983 8E076358	Hs.343214 Hs.77667		1.66 1.66
. 5	425262	D87119	Hs.15541		1.65
	439237	AW408158	Hs.31889	3 ESTs, Weakly similar to A47582 B-cell gr	1.64
	427923	AW274357	Hs.30140		1.63 1.62
80	424825 441859	AF207069 AW194364	Hs.15335 Hs.94814		1.60
	445982	BE410233	Hs.13501	pescadillo (zebrafish) homolog 1, contai	1.58
	412939	AW411491	Hs.75069		1.58
	417237	H86385	Hs.81737	palmitoyl-protein thioesterase 2	1.56



	412856	BE386745	Hs.74631	basigin (OK blood group)	1.56
	447200	BE543146	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.54
	409614	BE297412	Hs.55189	hypothetical protein	1.53
-	450663	H43540	Hs.25292	ribonuclease HI, large subunit	1.53
5	423397	NM 001838	Hs.1652	chemokine (C-C motif) receptor 7	1.49 1.48
	425535	AB007937	Hs.158287	KIAA0468 gene product	1.46
	409340	BE174629	Hs.321130 Hs.16134	hypothetical protein MGC2771 serine/threonine kinase 10	1.46
	446755 454429	AW451473 BE273437	Hs.301406	hypothetical protein PP3501	1.46
10	425722	AI659076	Hs.97031	hypothetical protein MGC13047	1.45
	414509	AW161311	Hs.76294	CD63 antigen (melanoma 1 antigen)	1.44
	452203	X57522		transporter 1, ATP-binding cassette, sub	1.43
	436378	AJ227874	Hs.99244	ESTs	1.42
	424218	AF031824	Hs.143212	cystatin F (leukocystatin)	1.42
15	436456	AW292677	Hs.248122	G protein-coupled receptor 24	1.42
	439740	AL365512	Hs.6657	hypothetical protein bK1048E9.5	1.42
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.42
	427634	AL399745	Hs.18449	hypothetical protein MGC10820	1.40 1.40
20	403409	45404050	11. 40450	NM_005929:Homo sapiens antigen p97 (mela	1.34
20	434262	AF121858	Hs.12169	sorting nexts 8	1.32
	413566	AW604451 AW250549	Hs.285814 Hs.180577	sprouty (Drosophila) homolog 4 granulin	1.32
	427730 411742	AW247593	Hs.71819	eukaryotic translation initiation factor	1.31
	450395	BE048545	Hs.161757	ESTS	1.30
25	413291	NM 006278	Hs.75268	sialyttransferase 4C (beta-galactosidase	1.26
20	442609	AL020996	Hs.8518	selenoprotein N	1.24
	416929	N20535		melastatin 1	1.21
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.21
	454478	AW805749		superoxide dismutase 2, mitochondrial	1.20
30	437723	AI672731	Hs.13256	ESTs	1.18
	416350	AF188625	Hs.189507	phospholipase A2, group IID	1.08
	TABLE 4		aus Fan amba	ant identifies number	
35	Pkey: CAT num		ne cluster numb	set identifier number	
33	Accessio		bank accessio		
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	Pkey	CAT Numbe	r Accession		
	430540	713_2	RC017171	BC012195 NM_007126 AF100752 AL137377 Z707	8 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418
40		-	RM045810	ALLI20387 RG770238 RG686740 RG913323 B1759	980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AWZ45847
			AI7701711	BF196861 BE856897 AA463876 A1375927 AA64881	0 AA948193 AA490916 AI459893 AI458188 AI240408 AI191843 AI131029 AW768399
			Al365196	AW337984 AW026150 BE466591 BE674599 AI8184	38 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567
			BE732715	BM043200 BE900263 BE900706 BE731097 BE390	023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610
15			BE561530	BE560537 BE903782 BE732947 BIZZ7Z04 BG761	05 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420
45			8E298109	AWZ454ZZ AI4Z3847 AI914618 H8U334 BESU IUU9	AL531791 Al435581 BF793112 AL577303 AA373265 BE745965 BF743630 BEB79296 AW517572 AA773468 BG259694 BE391163 BG621529 Al421728 BG767231 BM462953
			AI359493	BMU18538 AI683260 AWU/2430 F 2020 I AW IS 1403	5 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512
			WED732 U	WEEGO DICOERORO AIONSONE H19721 W17051 W77	68 BI262010 AAB44319 W74143 W72214 N85194 BE734033 BG164099 AA931069
			F13645 R	41394 AK025758 RG180977 RF349455 AA812018 A	A740241 A1027722 A1150356 AA886395 AW977627 BE220225 AA884082 AW518114
50			A1243844	AAR09493 AA481029 AA825718 AI347866 AI43167	0 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103
			AW00818	8 R07703 AA989120 AA745235 AW028983 AA7891	02 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809
			BE002760	BG746251 BE962912 BM454584 AL134894 BF104	082 H80591
	454088	1007145_1	AW06242	5 AW062411	
	458997	11847_4	BM45304	1 AA760783 BE218582 AI340046 AW166131 BF515	854 AI630296 AA461307 AI090881 AW023059 AA155797 AA115486 AL597396
55			AW88900	4 AW937420 AA137082 AA013374 BG619478 BG4	11839
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			BE73271	5 RM043200 RE900263 RE900706 BE731097 BE39	0023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610
			BE56153	0 RE560537 RE903782 BE732947 BI227204 BG761	305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420
			RE20810	9 AW245422 AI423847 AI914618 H80534 RE30100	I AL 531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296
65			AIRCOAGR	DM018508 AIGROPEN AW072450 F20201 AW1514	5 AW517572 AA773468 BG259694 RE391163 BG621529 Al421728 BG767231 BM402953
			BG34052	4 W52648 AA113434 BE785431 BI041981 BG8323	35 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512
			W527331	WASSON DICOSRORO AIONSONS H19721 W17NS1 W77	958 R1762010 AAR44319 W74143 W7Z714 N85194 BE734033 BG164099 AA931009
			F13645 F	R41394 AK025758 BG180977 BE349455 AA812018	AA740241 Al027722 Al150356 AA886395 AW977627 BE220225 AA884082 AW518114
70			A1243844	AA809493 AA481029 AA825/18 AI34/866 AI4316	70 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103
70			AW00818	88 R07703 AA989120 AA746235 AW028983 AA789 10 BG746251 BE962912 BM454584 AL134894 BF10	102 AU185751 AW971465 AA489681 AW971893 AW612086 BED77936 BI860809
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	458098	23945_1	AA83251	19 AF086393 AV733386 BE465409 N29245 W07677	121 A1694996 BE327781 BE327407 BE833829 AA989054 AA459718 BE833855 BE550224 AA482971 BE503548 H18151 AA461301 W79223 W74510 A1090689 AL600773 AL600781
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80		267495_1	AA83251 N46003 BG75835 BG53285	19 AF086393 AV733386 BE465409 N29245 W07677 R28075 R34182 BE071550 AW885857 A1276145 A1	AA482971 BE503548 H18151 AA461301 W79223 W74510 A1090689 AL600773 AL600761 276696 H97808 N20540 A1468553



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	446830	41421_1	BC020595 BI488 AW370623 AA39 BI489433	1430 BG 168023 BE 179030 AW294203 BF849776 AA459064 A!917452 AW403072 W27419 BF914568 BF798468 AW370558 T35055 39232 AA214221 AW802987 BF902228 AW370622 BF819597 AW370567 BF914313 AW954040 BF060706 AA194237 T25074 C01285
	428524	1382184_1	AI208080 AA44	2862 AAA29772
5	411524	1089114_1		50589 AW850318 AW850303
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23	442643	2736_1	DOGG FRO DO	207474 AFD4E3E0 ABA 004607 D1766186 DE357010 RG500792 RIR62776 AL 121371 BG574833 AA703250 AA179511 AW032000
			44000450 4504	AAAA ALOCOO KA AMOO OAAA AMOO OAAA AAAAAA AAAAA AAAAAA AAAAAAA AAAAAA
			AA035630 AI2	89987 A1184802 A1681331 AW592416 A1138377 A1139266 AA961714 A1800163 AA418751 AW451928 AA668676 A1273444 A494387 76555 BF196021 AA700055 AA609305 AA772596 A1635758 A1635749 H95459 AW610290 BE464994 AA527138 BF374802 A1800175
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50			D1 10 11005 DC	
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35	446126	610_2	A 4 227722 4 A	240240 DIO2047 DIO2068 ALC2680 AIGQ3827 AAG51731 AI7DIDI3 HMD6H789 AW3395UD AA293UZI BIRDY IUD AI430003 AYYJO IZUJ
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40	409305	109927_1	AA071475 AA	112236 AA070648 AA071243 AA081725 AA085187 AA070078 854404 AW578594 AW578581 BF507971 AW196760 AA779923 AA707233 AI555913 AA948295 AW089222 AW291883
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50	459227	639802_1		1971179 A1934948
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55	410600	497855_1	BF347859 A	K30 AW37/76 D0074 M99616 AA 191322 AW499617 AL601010 AW575742 AA729043 BE463447 AA086179 BE549623 A1335824 AW408712 BM149172 M_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 BI8233519
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			00000000	4000040 A1CO0444 A174077E A1000170 DC0C7C75 A1/27/27 A11158R60 RE300655 AW1/0/// AA560900 AL5/1009 AL5/0000 AL5/09/09
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			OF DTACOS D	CDN45CD ALCTA4CD D1414CCD2 A12CC14 A1C2RR73 A1475625 AA9A871D AARS4054 AA45/D3/ AAU31644 AA332421 AVY/39439
			AW361447 E	15788505 AIGR7897 AAR30989 AAR57356 AAR53084 BM009154 AA135727 HU5927 HZ3433 K4ZZ44 N/3337 AW300003 AW300001
65			AACTOTAT A	1 CCC 474 A A 125770 DC 774050 DC 014200 HRR457 AA627746 RISS0716 BI753586
	416929		BC017849 B	C005892 N42983 BF691239 N42991 N29240 N40292 N33322 N33330 N20535 NW798102 AW805749 AW805872 BF985060 AW794380 BF380449 AW794466 AW794538
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	TABLE	48C:		
70	Pkey:		Inique number cor	responding to an Eos probeset
	Ref:	S	equence source.	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
	C1 1			n chromosome 22" Dunham, et al. (1999) <u>Nature</u> 402:489-495.
	Strand: Ni_pos			nd from which exons were predicted. e positions of predicted exons.
75	·41_pos	unger, li	re-sense HUMGUIU	A bondering at the security angular
	Pkey	Ref	Strand	Nt_position
	403328		Minus	120428-120703
	405451		Minus	145949-146227 41341-41940
80	406016 403409		Plus Plus	6860-7054,12573-12771

#### WO 03/025138

Table 49A fists about 1127 genes upregulated in primary melanoma and/or melanoma metastases relative to normal body fissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hut03 Genectip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (A), a normalized value reflecting the retative level of mRNA expression.

Pkey:

Unique Eos probeset identifier number

ExAcon:

Explain Accession number, Genbank accession number

Unigenel D:

Unique Tite:

Unique Tite:

Unique gene title

St:

90th percentile of primary melanoma and melanoma metastasis Als divided by the 90th percentile of normal tissue Als

90th percentile of primary melanoma and melanoma metastasis Als divided by the 90th percentile of heart, liver, tung, and kidney Als

10

	Pkey	ExAcon	11-1	14.1			
	452020		UnigenelD	Unigene Title	RI	R2	R3
15	452838	U65011	Hs.30743	preferentially expressed antigen in meta	14.05	11.83	14.05
13	426555	NM_000372	Hs.2053	tyrosinase (ocutocutaneous albinism IA)	13,15	13.27	13,15
	430377	NM_001922	Hs.301865	dopachrome tautomerase (dopachrome delta	11,77	7.43	11.77
	420208	BE276055	Hs.95972	silver (mouse homotog) like	10.53	19.95	10.27
	431360	NM_000427	Hs.251680	loricrin	9.78	7.09	0.89
	430822	AJ005371	Hs.248017	glyceratdehyde-3-phosphate dehydrogenase	9.40	7.20	
20	422158	AA586894	Hs.112408	\$100 calcium-binding protein A7 (psories			8.84
	419628	H67546	Hs.49768	ESTs	8.03	10.27	12.84
	438549	BE386801	Hs.21858		7.56	8.92	6.49
				trinucleotide repeat containing 3	7.52	5.47	15.47
	430686	NM_001942	Hs.2633	desmoglein 1	6.06	4.13	3.31
25	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	5.86	9.22	0.77
25	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	5.84	3.46	5.84
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	5.82	3.94	5.82
	414812	X72755	Hs.77367	monokine induced by gamma interferon	5.81	3.33	6.79
	453344	BE349075	Hs.44571	ESTs			
	425088	AA663372	Hs. 169395		5.78	3.07	5.98
30	402075	74000012	110.102030	hypothetical protein FU12015	5.60		· 5.60
	416975	NM_004131	11- 4054	ENSP00000251056*:Plasma membrane calcium	5.12	4.22	5.12
			Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	5.09	3.33	4.14
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	5.06	5.78	5.06
	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	5.04	6.77	9.42
20	430838	N46664	Hs.169395	hypothetical protein FLJ12015	5.03	3.06	5.03
35	417542	J04129	Hs.82269	progestagen-associated endometrial prote	4.93	8.13	
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti			5.41
	408962	BE386436	Hs.44317		4.78	2.93	4.78
	410361	BE391804		SRY (sex determining region Y)-box 10	4.75	3.28	5.30
			Hs.62661	guarrylate binding protein 1, interferon-	4.70	3.11	4.70
40	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.68	2.27	4.68
40	407756	AA116021	Hs.38260	ubiquitin specific protease 18	4.65	3.21	3.31
	417166	AA431323	Hs.42146	ESTs	4.56	5.23	4.56
	421773	W69233	Hs.112457	ESTs	4.52	11,11	0.96
	442711	AF151073	Hs.8645	hypothetical protein	4.37		
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat		3.70	4.30
45	428513	BE220806			4.37	3.08	6.75
	447937		Hs.184697	Homo sapiens clone 23785 mRNA sequence	4.32	2.61	4.32
		AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	4.31	3.13	4.31
	451099	RS2795	Hs.25954	interleukin 13 receptor, alpha 2	4.28	2.89	2.17
	433658	L03678	Hs.156110	immunoglobulin kappa constant	4.18	2.68	5.92
	420301	AA767526	Hs.22030	paired box gene 5 (8-cell lineage specif	4.16	2.57	4.16
50	433447	U29195	Hs.3281	neuronal pentraxin ()	4.15	2.26	
	446341	AL040763	Hs.310735	ESTs, Moderately similar to ALU7_HUMAN A			6.46
	408380	AF123050	Hs.44532	dubiculia	4.10	4.04	4.54
	421379				4.02	2.46	5.33
		Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	4.02	3.48	3.19
55	421633	AF121860	Hs.106260	sorting nextin 10	4.01	2.61	3.36
"	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	3.96	2.68	3.96
	417355	D13168	Hs.82002	endothelin receptor type B	3.95	2.46	3.66
	420267	N37030	Hs.173337	ESTs	3.88	3.87	3.88
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi			
	427528	AU077143	Hs.179565		3.61	3.04	7.94
60	405451		1.5.17.5005	minichromosome maintenance deficient (S.	3.79	2.23	3.79
••	44907B	AK001256	Hs.22975	dihydropyrimidinase-like 3	3.78	3.74	4.06
				KIAA1576 protein	3.76	2.83	3.76
	423799	AW026300	Hs.132906	19A24 protein	3.75	2.36	3.75
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	3.73	2.59	6.97
	444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibito	3.72	2.15	3.92
65	427666	AI791495	Hs.180142	calmodulin-like skin protein (CLSP)	3.69	4.17	1.18
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t		2.08	
	422423	AF283777	Hs.116481	CD22 antique	3.64		3.64
	419956	AL137939	Hs.40096	CD72 antigen	3.64	2.94	3.64
				cadherin 19, type 2	3.56	2.22	4.68
70	420338	AA825595	Hs.88269	Homo sapiens, clone MGC: 17339, mRNA, com	3.55	2.96	4.70
70	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.54	1.96	3.54
	458079	A1796870	Hs.54277	DNA segment on chromosome X (unique) 992	3.53	2.18	3.27
	444381	BE387335	Hs.283713	ESTs. Weakly similar to S64054 hypotheti	3.48	2.83	11.00
	449722	BE280074	Hs.23960	cyclin 81	3.48	2.10	
_	438380	T06430	Hs.6194	•			4.64
75	452744	AI267652	Hs.246107	chondroitin sulfate proteoglycan BEHAB/b	3.47	3.90	4.98
	447210	AF035269		Homo sapiens mRNA; cDNA DKFZp434E082 (Ir	3.45	2.38	3.45
			Hs.17752	phosphatidylserine-specific phospholipas	3.44	3.83	2.09
	428804	AK000713	Hs. 193736	hypothetical protein FLJ20706	3.43	2.39	3.43
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	3.41	4.33	5.41
00	423605	AF047826	Hs.129887	cadherin 19, type 2	3.40	1.97	4.06
80	421508	NM_004833	Hs.105115	absent in melanoma 2	3.38	2.77	5.46
	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	3.36		
	430770	AA765694	Hs.123296	ESTs		2.41	3.36
	445784	AI253155			3.36	2.08	3.83
	773107	WEST 133	Hs.146065	ESTs ·	3.32	2.02	3.80

	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.32	1.87	3.76
	448966	AW372914	Hs.86149	phosphoinosital 3-phosphate-binding prot	3.31 3.28	2.10 2.04	3.31 3.28
	441224 428242	AU076964 H55709	Hs.7753 Hs.2250	catumenin teukemia inhibitory factor (cholinergic	3.26 3.26	243	3.56
5	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	3.24	2.94	2.85
	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	3.23	1.84	3.87
	415668	AW957684	Hs.306814	hypothetical protein FLJ21889	3.22	3.10	3.13
	442757	A1739528	Hs.28345	ESTs	3.22 3.18	3.41 2.50	1.45 3.18
10	426317 432874	AA312350 W94322	Hs.169294 Hs.279651	transcription factor 7 (T-cell specific, melanoma inhibitory activity	3.18	5.31	4.55
••	412561	NM_002286	Hs.74011	lymphocyte-activation gene 3	3.17	3.09	4.28
	443983	H04482	Hs.163724	ÉSTs	3.16	2.21	3.16
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	3.14	1.74	3.25
15	422353 422424	T55979 A1185431	Hs.115474 Hs.296638	replication factor C (activator 1) 3 (38 prostate differentiation factor	3.14 3.10	2.07 3.20	3.33 2.15
13	435256	AF193766	Hs.13872	cytokine-like protein C17	3.10	2.23	3.10
	401747			Homo sapiens keratin 17 (KRT17)	3.10	2.10	3.02
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	3.08	3.08	4.00
20	419870	AW403911	Hs.266175	phosphoprotein associated with GEMs Pirin	3.07 3.06	3.16 2.92	3.07 4.20
20	432878 401454	BE386490	Hs.279663	NM_014226*:Homo sapiens renal turnor anti	3.05	1.96	3.05
	410079	U94362	Hs.58589	glycogenin 2	3.01	2.26	3.27
	426501	AW043782	Hs.293616	ESTs	3.01	2.00	3.68
25	418310	AA814100	Hs.86693	ESTs	3.00	2.35	6.76
23	422283 422309	AW411307 U79745	Hs.114311 Hs.114924	CDC45 (cell division cycle 45, S.cerevis solute carrier family 16 (monocarboxylic	2.96 2.96	2.31 2.49	3.78 4.74
	408418	AW963897	Hs.44743	KIAA1435 protein	2.94	1.80	2.94
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	2.93	1.74	2.93
20	416640	BE262478	Hs.79404	neuron-specific protein	2.93	2.78	3.09
30	443264 410491	BE221477	Hs.132137	ESTs, Moderately similar to A47582 B-cel	2.92 2.91	2.35 2.83	4.27 3.84
	405545	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence Target Exon	2.90	2.44	2.90
	451537	R56631	Hs.26550	retinoid X receptor, gamma	2.90	4.09	3.40
25	439926	AW014875	Hs.137007	ESTs .	2.90	2.43	2.90
35	406673	M34996	Hs.198253	major histocompatibility complex, class	2.89	3.22 3.90	1.44 2.89
	418007 440065	M13509 W03476	Hs.83169 Hs.266331	matrix metalloproteinase 1 (interstitial hypothetical protein MGC4595	2.89 2.89	3.90 4.40	3.05
	442739	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	2.88	2.36	4.54
40	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum com	2.86	3.23	1.95
40	407856	AA045281	Hs.266175	phosphoprotein associated with GEMs	2.84	1.84	2.84
	430540 424153	AW245422 AA451737	Hs.141496	Homo sapiens cDNA: FLJ22105 fis, clone H MAGE-like 2	2.84 2.84	1.80 2.26	2.92 2.84
	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	2.81	2.91	0.83
	431317	AA502682		gb:ng23d01.s1 NCI_CGAP_Ov2 Homo sapiens	2.81	2.17	2.96
45	424800	AL035588	Hs.153203	MyoD family inhibitor	2.80	2.06	4,10
	448111 431183	AA053486 NM_006855	Hs.20315 Hs.250696	interferon-induced protein with tetratri	2.79 2.78	1.85 2.34	2.42 6.53
	448719	AA033627	Hs.21858	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic trinucleotide repeat containing 3	2.78	3.75	4.01
	427951	AI826125	Hs.43546	ESTs	2.78	1.99	2.70
50	453912	AL121031		SWVSNF related, matrix associated, acti	2.77	2.28	2.77
	426711 409430	AA383471 R21945	Hs.343800 Hs.346735	conserved gene amplified in osteosarcoma splicing factor, arginine/serine-rich 5	2.75 2.74	1.98 3.18	2.75 3.60
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	2.72	2.24	2.72
	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	2.72	2.31	3.59
55	420552	AK000492	Hs.98806	hypothetical protein	2.72	1.85	2.72
	409103 439963	AF251237 AW247529	Hs.112208 Hs.6793	XAGE-1 protein platelet-activating factor acetythydrola	2.72 2.71	2.18 2.20	2.72 4.48
	413171	AA318325	Hs.75219	tyrosinase-related protein 1	2.71	5.74	2.62
<b>60</b>	436700	AI693690	Hs.301406	hypothetical protein PP3501	2.71	3.37	3.32
60	419098	AA234041	Hs.87271	ESTs .	2.70	3.53	1.35
	436608 418067	AA628980 AJ127958	Hs.192371 Hs.83393	down syndrome critical region protein DS cystatin E/M	2.69 2.68	2.48 3.04	2.69 0.56
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.67	2.36	3.16
	437723	AJ672731	Hs.13256	ESTs	2.66	2.16	2.66
65	411252	AB018549	Hs.69328	MD-2 protein	2.66	1.81	2.66
	424321 453837	W74048 AL138387	Hs.1765 Hs.256126	lymphocyte-specific protein tyrosine kin bacutoviral IAP repeat-containing 7 (liv	2.66 2.65	2.43 3.71	3.92 2.80
	434826	AF155661	Hs. 22265	pyruvate dehydrogenase phosphatase	2.64	1.85	4.72
-	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	2.64	2.07	2.64
70	444371	BE540274	Hs.239	forkhead box M1	2.64	2.82	4.46
	435291	BE568452	Hs.344037	protein regulator of cytokinesis 1	2.63	1.81 2.38	2.95 10.12
	439310 420218	AF086120 AW958037	Hs.102793	ESTs ribosomal protein L4	2.62 2.62	2.80	2.62
	438746	AI885815	Hs.184727	Human melanoma-associated antigen p97 (m	2.60	3.27	2.12
75	432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	2.60	2.67	3.03
	408367	AK001178	Hs.44424	homolog of rat orphan transporter v7-3	2.59	3.22	2.59
	408527 444809	AL135018 BE207568	Hs.33074 Hs.208219	Homo sapiens, clone IMAGE:3606519, mRNA, oculospanin	2.58 2.58	1.69 2.77	2.05 2.88
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	2.58	1.83	2.58
80	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	2.55	3.70	3.28
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	2.55	2.14	1.62
	410174 447735	AA306007 AA775268	Hs.59461 Hs.6127	DKFZP434C245 protein Homo sapiens cDNA: FLJ23020 fis, clone L	2.55 2.54	2.07 2.17	2.55 4.01
				coprome co cocooce no, como C			

	422173	BE385828	Hs.250619	phorbolin-like protein MDS019 (CEM15)	2.53	1.68	3.16
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.53	2.74	3.93
	437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	2.52	1.62	3.17
	448140	AF146761	Hs.20450			2.67	1.88
5				BCM-like membrane protein precursor	2.51		
,	442426	Al373062	Hs.332938	hypothetical protein MGC5370	2.51	2.68	4.57
	417427	M90391	Hs.82127	interleukin 16 (lymphocyte chemoattracta	2.51	1.74	2.68
	427581	NM_014788	Hs.179703	KIAAD129 gene product	2.51	1.67	2.24
	432800	BE391046	Hs.278962	AIM-1 protein	2.51	5.55	2.42
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	2.50	1.95	241
10	410326	AI368909	Hs.47650	ESTs	2.50	2.85	2.63
	452833	BE559681	Hs.30736	KIAA0124 protein	2.50	3.14	3.07
	410016	AA297977	Hs.57907	small inducible cytokine subfamily A (Cy	2.49	3.38	291
	429083						
		Y09397	Hs.227817	BCL2-related protein A1	2.48	1.85	2.70
16	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	2.48	2.33	2.99
15	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	2.47	1.88	4.14
	412970	AB026436	Hs.177534	dual specificity phosphatase 10	2.45	2.00	0.98
	401780			NM_005557*:Homo sapiens keratin 16 (foca	244	2.30	1.39
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	2.44	1.57	0.88
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	2.42	1.91	2.56
20	417880	8E241595	Hs.82848	selectin L (lymphocyte adhesion molecule	2.42	2.31	4.27
20							
	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	2.41	2.73	241
	415752	BE314524	Hs.78776	putative transmembrane protein	2.41	2.07	3.41
	409703	NM_006187	Hs.56009	2'-5'-ofigoadenylate synthetase 3 (100 k	2.41	2.34	3.26
0.5	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	2.40	1.65	2.40
25	453857	AL080235	Hs.35861	DKFZP586E1621 protein	2.40	2.18	8.13
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	2.40	2.88	2.46
	403328			Target Exon	2.39	2.00	1.95
	427540	R12014	Hs.20976	ESTs	2.39	1.73	3.24
	449523	NM_000579					
30			Hs.54443	chemokine (C-C motif) receptor 5	2.39	1.96	. 2.39
50	433848	AF095719	Hs.93764	carboxypeplidase A4	2.38	2.45	2.65
	438501	Z44110	Hs.86149	phospholnositol 3-phosphate-binding prot	2.38	1.85	2.38
	430056	A1929659	Hs.237825	signal recognition particle 72kD	2.38	1.60	2.79
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.37	1.99	6.23
	450447	AF212223	Hs.25010	hypothetical protein P15-2	2.37	1.72	3.24
35	458997	AW937420		ESTs	2.37	1.57	3.27
	451446	AI826288	Hs.171637				
	408838			hypothetical protein MGC2628	2.35	1.90	2.39
		A1669535	Hs.40369	ESTs	2.35	1.59	2.71
	448275	BE514434	Hs.20830	kinesin-fike 2	2.35	2.19	2.35
40	424148	BE242274	Hs.1741	integrin, beta 7	2.35	1.89	3.07
40	410700	AA352335	Hs.65641	hypothetical prolein FLJ20073	2.35	1.65	2.35
	409105	AW467539	Hs.255877	ESTs	2.35	2.50	2.35
	452882	AW972990	Hs.196270	folate transporter/carrier	2.34	2.12	2.90
	425606	U52112	Hs.158331	renin-binding protein	2.34	2.69	1.69
	433576	BE080715	Hs.161091	ESTs	2.34	3.74	2.34
45							
43	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac	2.34	2.08	4.48
	431620	AA126109	Hs.264981	2-5-oligoadenylate synthetase 2 (69-71	2.33	2.43	2.66
	436614	AW104388	Hs.149091	ESTs	2.33	3.37	2.33
	425289	AW139342	Hs.155530	Interferon, gamma-inducible protein 16	2.33	1.67	4.28
	426827	AW067805	Hs.172665	methylenetetrahydrotolate dehydrogenase	2.33	1.58	0.40
50	430015	AW768399		ESTs	2.33	1.76	2.33
	421282	AA286914	Hs.40782	ESTs	2.32	1.65	2.49
	447737	AK000643	Hs.19404	DKFZPS64L0862 protein	2.32	2.16	1.48
	432540	AI821517			2.32		
			Hs.105866	ESTs		1.58	2.35
55	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	2.32	2.46	9.99
"	414829	AA321568	Hs.77436	pleckstrin	2.32	1.91	2.32
	425390	AJ092634	Hs.156114	protein tyrosine phosphatase, non-recept	2.31	1.63	2.31
	448569	8E382657	Hs.21486	signal transducer and activator of trans	2.31	2.79	2.41
	428819	AL135623	Hs.193914	KIAA0575 gene product	2.30	1.60	2.95
	409512	AW979187	Hs.293591	metanoma differentiation associated prot	2.30	1.95	3.66
60	425231	AA527161		ESTs	2.28	1.96	2.36
	416091	AF295370	Hs.283082	defensin, beta 3	2.28	2.76	2.18
	418478	U38945	Hs.1174	cyclin-dependent kinase Inhibitor 2A (me	2.27	2.88	2.46
	427719	AI393122	Hs.134726	ESTs	2.27	1.88	2.29
	431830	Y16645					
65			Hs.271387	small inducible cytotine subfamily A (Cy	2.27	2.16	4.09
05	457465	AW301344	Hs.122908	ONA replication factor	2.26	2.23	2.26
	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	2.26	2.13	3.16
	442485	BE092285	Hs.29724	hypothetical protein FLJ13187	2.26	1.75	2.84
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.26	3.38	2.56
	449317	AW293413	Hs.132906	19A24 protein	2.26	2.04	2.73
70	429922	297630	Hs.226117	H1 histone family, member 0	2.26	1.59	2.38
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	2.25	1.86	3.07
	425388	AA329384	Hs.156110	immunoglobulin kappa constant	2.25		2.25
			113. 1301 10			1.91	
	417282	AA195203		RAB5C, member RAS oncogene family	2.25	2.23	3.20
75	406687	M31126		matrix metalloproteinase 11 (stromelysin	2.24	2.69	2.78
75	437862	AW978107	Hs.5884	Homo sapiens mRNA; cDNA DKFZp586C0224 (f	2.23	2.20	2.51
	408015	AW136771	Hs.244349	epidermal differentiation complex protei	2.23	4.59	2.47
	442503	AF147078	Hs.150853	p53-responsive gene 5	2.23	3.62	0.85
	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	2.22	1.60	1.69
	424825	AF207069	Hs.153357	procollagen-lysine, 2-oxoglutarate 5-dio	2.22	5.53	2.46
80	417693	AW959741	Hs.40368	adaptor-related protein complex 1, sigma		2.40	
					2.21		4.37
	422947	AA306782	Hs.122552	G-2 and S-phase expressed 1	2.21	2.06	2.32
	445875	AF070524	Hs.13410	Homo sapiens clone 24453 mRNA sequence	2.20	2.69	2.91
	417366	BE185289	Hs.1076	small proline-rich protein 1B (comifin)	2.20	2.26	3.79

	450065	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	2.20	1.96	2.44
	423397	NM_001838	Hs.1652	chemokine (C-C motif) receptor 7	2.20	3.28	2.99
	427051	BE178110	Hs.173374	Homo sapiens cDNA FU10500 fis, clone NT	2.20	1.98	3.40
-	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.20	1.44	2.31
5	409354	N68188	Hs. 159472	Homo sapiens cDNA: FLJ22224 fis, clone H	2.18	244	2.70
	418941 424723	AA452970	Hs.239527 Hs.152337	E1B-55kDa-associated protein 5	2.18	1.75	2.70
	430132	BE409813 AA204686	Hs.234149	protein arginine N-methyltransferase 3(h hypothetical protein FLJ20647	2.18 2.18	1.55 1.43	2.44 2.37
	452194	AJ694413	113.254143	Ubiquitin-like protein FAT 10777 - diubiq	2.17	3.07	1.76
10	417933	X02308	Hs.82962	Drymidylate synthetase	217	1.86	4.15
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TTT3 co	2.17	2.38	2.91
	425317	AW205118	Hs.210546	interleukin 21 receptor	2.17	2.02	2.22
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	2.16	1.87	2.49
1.5	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	2.16	1.55	2.26
15	452958	AA883929	Hs.40527	ESTs	2.15	1.56	2.84
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	2.15	1.76	2.97
	426153 430580	AF057169	Hs.182771 Hs.300697	vitelliform macular dystrophy (Best dise	215	1.85	2.74
	451952	AA806105 AL120173	Hs.301663	immunoglobulin heavy constant gamma 3 (G ESTs	2.14 2.13	1.88 2.08	4.99 2.13
20	450534	AI570189	Hs.25132	KIAA0470 gene product	2.12	1.67	3.41
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	2.12	1.75	2.27
	432734	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	2.12	2.14	2.49
	413190	AA151802	Hs.40368	adaptor-related protein complex 1, sigma	2.12	2.46	2.67
25	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	2.12	2.16	2.82
25	429624	AA458648	Hs.99476	ESTs, Weakly similar to 13131848 alpha1	2.11	2.01	0.68
	447178	AW594641	Hs. 192417	ESTs	2.10	2.52	2.10
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	2.10	1.52	4.01
	452110 436797	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	2.10	1.53	2.10
30	453256	AA731491 AI565587	Hs.334477 Hs.32556	hypothetical protein MGC14879 KIAA0379 protein	2.10 2.09	1.55 2.13	· 2.41 2.89
50	405547	7300000	113.32330	NM_018833*:Homo sapiens transporter 2, A	2.09	261	2.09
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	2.09	1.76	4.10
	412609	248804	Hs.74124	ocular albinism 1 (Nettleship-Falls)	2.09	3.91	2.38
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	2.09	1.62	1.28
35	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.08	1.86	2.08
	447377	X77343	Hs.334334	transcription factor AP-2 alpha	2.08	2.83	2.08
	423198	M81933	Hs.1634	cell division cycle 25A	2.08	1.66	2.23
	433068	NM_006456	Hs.288215	sialytransferase	2.08	1.94	2.60
40	409038 452392	T97490 L20815	Hs.50002 Hs.507	smatl inducible cytokine subtamily A (Cy comeodesmosin	2.07 2.07	1.91 3.96	3.62 0.97
-10	403532	20013	115.507	NM_024638:Homo sapiens hypothetical prot	2.07	1.88	2.68
	439859	AW292872	Hs.124554	ESTs	2.07	1.72	2.22
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	2.07	2.26	4.22
	442643	U82756		PRP4/STK/WD splicing factor	2.07	1.74	1.90
45	426312	AF026939	Hs.181874	interferon-induced protein with tetratri	2.06	2.08	1.43
	409988	N27687	Hs.334334	transcription factor AP-2 alpha (activat	2.06	2.12	2.06
	408548	AA055449	Hs.63187	ESTs, Weakly similar to ALUC_HUMAN !!!!	2.06	1.65	2.91
	442271	AF000652	Hs.8180	syndecan binding protein (syntenin)	2.06	1.97	2.42
50	414142 420931	AW368397 AF044197	Hs.334485	hemicentin (fibulin 6)	2.05	2.44	2.05
50	450325	AI935962	Hs.100431 Hs.91973	small inducible cytokine B subfamily (Cy ESTs	2.05 2.05	2.37 1.67	2.05 1.82
	424090	X99699	Hs.139262	XIAP associated factor-1	2.05	1.56	1.99
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	2.04	1.52	2.07
	413794	AF234532	Hs.61638	myosin X	2.04	2.02	2.11
55	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	2.04	4.57	1.64
	425580	L11144	Hs.1907	galanin	2.04	1.67	2.26
	420052	AA418850	Hs.44410	ESTs	2.03	1.90	2.21
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	2.03	1.53	2.31
60	416406 426759	D86961 Al590401	Hs.79299 Hs.21213	lipoma HMGIC fusion partner-like 2 ESTs	2.02 2.02	1.73 1.86	2.02 5.47
00	432435	BE218886	Hs.282070	ESTs	2.02	1.39	1.67
	444184	T87841	Hs.282990	Human DNA sequence from clone RP1-28H20	2.02	1.57	2.02
	421574	AJ000152	Hs.105924	defensin, beta 2	2.02	2.22	2.15
	411358	R47479	Hs.94761	KIAA1691 protein	2.01	2.55	1.75
65	408209	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	2.01	2.58	2.39
	409262	AK000631	Hs.52256	hypothetical protein FLI20624	2.01	1.50	2.01
	400750			Target Exon	2.01	1.73	2.09
	439496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN cDNA 1110	2.01	2.42	0.78
70	420460 446839	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.01	1.65	1.72
	427647	BE091926 W19744	Hs.16244 Hs.180059	mitotic spindle colled-coil related prot Homo sapiens cDNA FLJ20653 fis, clone KA	2.01 2.00	1.61 2.11	1.03 2.33
	436200	R51386	Hs.124881	ESTs	2.00	1.89	2.24
	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	1.99	1.50	1.99
~-	420005	AW271106	Hs.133294	ESTs	1.99	2.03	2.59
75	417848	AA206581	Hs.116586	ESTs, Weakly similar to JC5314 CDC28/cdc	1.99	1.42	2.17
	435545	AA587415	Hs.28107	ESTs	1.99	1.89	1.99
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	1.99	2.23	3.44
	444342	NM_014398		similar to lysosome-associated membrane	1.99	2.05	0.32
80	453905	NM_002314		LIM domain kinase 1	1.98	2.48	2.79
50	453884 459373	AA355925 BE408266	Hs.36232	KIAA0186 gene product	1.98	1.93	1.98
	422809	AK001379	Hs.301406 Hs.121028	hypothetical protein PP3501 hypothetical protein FU10549	1.98 1.98	2.22 1.68	1.91 1.98
	452840	AI097393	Hs.43481	hypothetical protein DKFZp564K192	1.98	1.67	2.18
	,40.0						~.10

	409178	BE393948	Hs.50915	kattikrein S	1.98	3.76	1.37
	420991		Hs.287379	Homo sapiens mRNA for FLJ00111 protein,	1.98	1.90 1.88	2.63 1.23
	414020		Hs.75703	small inducible cytokine A4 (homologous chondroitin suffate proteoglycan 4 (meta	1.97 1.97	1.95	5.55
5	443105 413450	X96753 Z99716	Hs.9004 Hs.75372	N-acelytgalactosaminidase, alpha-	1.97	1.77	1.97
-	431574	AW572659	Hs.261373	hypothetical protein dJ434O14.3	1.97	1.73	3.89
	408561	AJ308037	Hs.84120	hypothetical protein MGC13016	1.97 1.97	2.89 1.95	2.08 2.65
	421866 405506	M24470	Hs.1435	guanosine monophosphate reductase Target Exon	1.96	1.72	2.27
10	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	1.96	1.74	2.35
	437379	AL359575	Hs.23765	Homo sapiens mRNA; cDNA DKFZp547M123 (fr	1.95	2.09	277
	448356	AL120B37	Hs.20993	high-glucose-regulated protein 8	1.95 1.95	1.66 2.38	2.58 1.95
	453931	AL121278	Hs.25144	ESTs minichromosome maintenance deficient (S.	1.95	1.63	2.82
15	424308 429547	AW975531 AW009166	Hs.154443 Hs.99376	FGENESH predicted novel secreted protein	1.94	2.02	1.35
13	442064	Al422867	Hs.88594	ESTs	1.94	1.49	2.21
	400533			ENSP00000209376°:PRED65 protein (Fragmen	1.94	1.69 1.71	1.94 2.40
	448752	AA593867	Hs.300842	KIAA1608 protein CGI-12 protein	1.94 1.94	1.69	2.93
20	408636 439569	BE294925 AW602166	Hs.46680 Hs.222399	CEGP1 protein	1.93	1.62	3.21
20	405779	ANOUZIOU	14.22255	NM_005367:Homo sapiens metanoma antigen,	1.93	1.83	1.99
	444570	H58373	Hs.332938	hypothetical protein MGC5370	1.93	1.97	1.93 1.61
	446950	AA305800	Hs.5672	hypothetical protein AF140225	1.93 1.93	1.56 2.12	2.63
25	409185 409098	AW961601 AA132672	Hs.252406 Hs.7984	hypothetical protein FLJ12296 similar to pleckstrin homology, Sec7 and coiled/coi	1.92	212	2.51
23	413916	N49813	Hs.75615	apolipoprotein C-II	1.92	1.98	0.22
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	1.92	1.65	6.39
	402994			NM_002463*:Homo sapiens myxovirus (influ	1.92 1.92	2.45 2.69	1.89 · 2.30
30	425722 421958	AI659076 AA357185	Hs.97031 Hs.109918	hypothetical protein MGC13047 ras homolog gene family, member H	1.92	2.10	2.93
50	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	1.91	1.57	1.91
	415402	AA164687	Hs.177576	mannosyl (alpha-1,3-)-glycoprotein beta-	1.91	1.44	1.68
	430280	AA361258	Hs.237868	interleukin 7 receptor	1.90	1.52 2.16	1.14 1.21
35	426251	M24283	Hs.168383	intercellular adhesion molecula 1 (CD54) Homo sapiens, Similar to RIKEN cDNA 2700	1.90 1.90	1.84	2.07
33	440773 427923	AA352702 AW274357	Hs.37747 Hs.301406	hypothetical protein PP3501	1.90	4.26	1.70
	426470	AA528794	Hs.128644	ESTs	1.90	2.69	2.04
	409557	BE182896	Hs.3686	ESTs	1.90	2.01	1.90
40	429714	BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	1.90 1.89	2.49 1.89	2.52 1.49
40	428125 427634	AA393071 AI399745	Hs.182579 Hs.18449	leucine aminopeptidase hypothetical protein MGC10820	1.89	3.59	1.71
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	1.89	1.67	1.45
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	1.89	2.55	1.39
4.5	448243	AW369771		integrin, beta 8	1.89	1.96 1.70	1.89 1.10
45	416114	A1695549	Hs.183868	glucuronidase, beta	1.89 1.88	1.86	2.04
	425935 440672	Z98200 AF083811	Hs.163724 Hs.7345	HSPC019 protein MAD1 (mitotic arrest deficient, yeast, h	1.88	4.16	1.78
	430171	AF086289	Hs.234766	skin-specific protein	1.87	2.70	0.75
60	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	1.87	2.25	1.87 1.46
50	454294	AB000734	Hs.50640	JAK binding protein	1.87 1.87	1.98 2.73	1.71
	417370 409417	T28651 AA156247	Hs.82030 Hs.104879	tryptophanyl-tRNA synthetase serine (or cysteine) proteinase inhibito	1.87	1.79	2.72
	401781	741100211	1101101010	Target Exon	1.87	1.68	1.16
	440590	A1863446	Hs.266308	mosaic serine protease	1.86	1.79	1.13 4.39
55	428450	NM_014791		KIAA0175 gene product ribonucteotide reductase M2 polypeptide	1.86 1.86	1.72 1.81	1.86
	433675 429323	AW977653 NM_001649	Hs.75319 Hs.2391	apical protein, Xenopus laevis-like	1.86	1.57	1.86
	433001	AF217513	Hs.279905	done HQ0310 PRO0310p1	1.85	1,71	5.82
	453107		Hs.279746	vanilloid receptor-like protein 1	1.85	2.75	1.84 2.79
60	430441	BE398091	U- 0000C	desmoplakin (DPI, DPII)	1.85 1.85	1.80 1.80	1.86
	417512 423673		Hs.82226 Hs.1695	glycoprotein (transmembrane) nmb matrix metalloproteinase 12 (macrophage	1.85	1.94	1.85
	431958		Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.85	1.72	2.52
	414737		Hs.125087	ESTs	1.84	1.90	1.84
65	439979		Hs.6823	hypothetical protein FLJ10430	1.84 1.84	1.57 1.41	1.84 0.12
	428311		1 Hs.183671 Hs.48938	tryptophan 2,3-dioxygenase hypothetical protein FLJ21802	1.84	1.70	3.15
	412141 428515		Hs.285229	plexin C1	1.84	1.66	1.84
	427914		Hs.20575	ESTs	1.84	2.32	217
70	439352		Hs.169615	hypothetical protein FLJ20989	1.84	1.55	1.84 1.75
	413276		Hs.833	interferon-stimulated protein, 15 kDa hypothetical protein FLJ14428	1.83 1.83	3.20 1.62	1.47
	435080 407966		Hs.155111 Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	1.83	1.58	2.11
	42153		Hs.105478	phosphoribosylformylglycinamidine syntha	1.83	1.73	2.18
75	433029	NM_01432	2 Hs.279926	opsin 3 (encephalopsin)	1.83	1.96	1.83
	42615			v-erb-b2 avian erythroblastic leukernia v	1.83 1.82	1.61 2.44	2.46 1.82
	426890 41102		Hs.41294 Hs.67846	ESTs leukocyte immunoglobulin-like receptor.	1.82	2.24	2.01
	44185			ESTs, Weakly similar to FIG1 MOUSE FIG-1	1.82	2.72	2.16
80	43743			hypothetical protein DKFZp762H1311	1.82	1.50	1.82
	44835		Hs.108923	RAB38, member RAS oncogene family	1.82	2.52 1.43	1.76 0.68
	42067- 43921		i5 Hs.1327 Hs.41322	_ butyrylchofinesterase ESTs	1.82 1.82	1.88	2.43
	40321	, 11JJ00J	FI3.41322	-010			

	432810	AA863400		ESTs	1.82	1.43	1.82
	417404	NM_007350	Hs.82101	pleckstrin hornology-like domain, family	1.82	1.98	1.82
	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	1.82	1.63	1.82
5	436456 418918	AW292677 X07871	Hs.248122 Hs.89476	G protein-coupled receptor 24 CD2 antigen (p50), sheep red blood cell	1.82 1.82	2.80 2.28	2.18 2.00
•	424755	AB033094	Hs.152925	KIAA1268 protein	1.82	1.85	1.62
	436315	BE390513	Hs.27935	hypothetical protein MGC4837	1.82	1.74	5.18
	420783 417105	A1659838	Hs.99923 Hs.81226	lectin, galactoside-binding, soluble, 7	1.81 1.81	1.87 1.88	0.80 2.03
10	423961	X60992 D13666	Hs.136348	CD6 antigen periostin (OSF-2os)	1.81	1.73	2.45
	446019	Al362520		histone deacetylase 3	1.81	1.39	2.24
	412580	AA113262	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	1.81	3.05	1.58
	409415	AA579258	Hs.6083	Homo sapiens cDNA: FLJ21028 fis, clone C	1.80	2.00	1.78
15	453684 446921	AK001922 AB012113	Hs.34578 Hs.16530	alpha2,3-sialyttransferase small inducible cytokine subfamily A (Cy	1.80 1.80	1.98 1.56	1.22 1.71
••	453779	N35187	Hs.43388	28kD interferon responsive protein	1.80	2.42	2.04
	434706	AI656291	Hs.116394	ESTs	1.80	1.58	1.80
	416065	8E267931	Hs.78996	profiferating cell nuclear antigen	1.80	1.79	2.51
20	453331 429412	A1240665 NM_006235	Hs.2407	ESTs POU domain, class 2, associating factor	1.79 1.79	1.43 1.46	2.33 4.46
	428784	Y12851	Hs.193470	purinergic receptor P2X, figand-gated io	1.79	2.30	1.79
	453507	AF083217	Hs.33085	WD repeat domain 3	1.79	1.49	1.51
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	1.79	1.57	2.00
25	439237 406672	AW408158 M26041	Hs.318893 Hs.198253	ESTs, Weakly similar to A47582 B-cell gr major histocompatibility complex, class	1.79 1.79	2.26 1.76	2.22 1.78
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	1.79	1.43	3.32
	452698	NM_001295	Hs.301921	chemokine (C-C motif) receptor 1	1.78	1.66	1.29
	424954 436378	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	1.78	1.73	2.35
30	421778	AJ227874 AA428000	Hs.99244 Hs.283072	ESTs actin related protein 2/3 complex, subun	1.78 1.78	1.84 1.66	. 1.78 3.67
	421948	L42583	Hs.334309	keratin 6A	1.78	1.74	3.00
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	1.77	2.27	2.13
	437317 427318	AA748613	Hs.311977	ESTs, Highly similar to SWVSNF related,	1.77 1.77	1.98	2.32
35	418403	AF186081 D86978	Hs.175783 Hs.84790	zinc transporter KIAA0225 protein	1.76	1.61 1.49	0.92 2.24
	421433	AI829192	Hs.22380	ESTs	1.76	1.49	2.52
	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	1.76	1.74	1.76
	428655	H05769 BE277141	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp	1.76	1.43 2.12	1.76 1.76
40	427536 433364	AI075407	Hs.115803 Hs.296083	gb:601178556F1 NIH_MGC_20 Homo saplens c ESTs, Moderately similar to I54374 gene	1.76 1.76	1.86	1.48
	401994			Target Exon	1.75	1.44	1.75
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ty	1.75	1.69	1.79
	408633 429978	AW963372 AA249027	Hs.46677	PRO2000 protein	1.75 1.75	1.46 1.60	1.68 1.92
45	450690	AA296696	Hs.333418	ribosomal protein S6 FXYD domain-containing ion transport reg	1.75	2.13	2.03
	456967	AW004056	Hs.168357	T-box 2	1.74	1.95	1.42
	417866	AW057903	Hs.82772	collagen, type XI, alpha 1	1.74	2.64	2.01
	428746 432642	AW503820 BE297635	Hs.192861 Hs.3069	Spi-B transcription factor (Spi-1/PU.1 r	1.74 1.74	2.82 1.51	2.31 1.62
50	429505	AW820035	Hs.278679	heat shock 70kD protein 9B (mortalin-2) a disintegrin and metalloproteinase doma	1.73	1.54	3.15
	412851	AJ826502	Hs.97269	ESTs	1.73	1.67	1.05
	453953	AW408337	Hs.36972	CD7 antigen (p41)	1.73	2.22	2.28
	430413 419485	AW842182 AA489023	Hs.241392 Hs.99807	small inducible cytokine A5 (RANTES)	1.73 1.73	2.05 1.71	1.47 1.73
55	447217	BE465754	Hs.17778	ESTs, Weakly similar to unnamed protein neuropilin 2	1.73	1.62	4.70
	437673	AW665665	Hs.153034	ESTs	1.72	1.55	2.10
	437879	BE262082	Hs.5894	hypothetical protein FLJ10305	1.72	2.50	1.80
	448410 413313	AK000227 NM_002047	Hs.21126 Hs.283108	hypothetical protein FLJ20220 glycyl-tRNA synthetase	1.72 1.72	1.48 2.19	3.98 1.62
60	452203	X57522	15.200100	transporter 1, ATP-binding cassette, sub	1.72	2.68	1.68
	443950	NM_001425	Hs.9999	epithelial membrane protein 3	1,71	2.17	2.24
	403969	********	11- 486404	ENSP0000034663:Zinc finger protein 131	1.71	1.31	1.71
	450832 453005	AW970602 AW055308	Hs. 105421 Hs. 31803	ESTs ESTs, Wealdy similar to N-WASP [H.sapien	1,71 1.71	1.33 1.67	2.38 1.95
65	439783	AI125760	Hs.24835	hypothetical protein FLJ14594	1.71	2.10	2.20
	418678	NM_001327		cancer/lestis antigen (NY-ESO-1)	1.71	3.86	1.76
	432259	BE269103	Hs.274201	60S acidic ribosomal protein PO	1.71	1.85	1,94
	420340	NM_000734		CD3Z antigen, zeta polypeptide (TIT3 com	1,71	2.12	1.98
70	428289 424006	M26301 AF054815	Hs.2253 Hs.137548	complement component 2 CD84 antigen (leukocyte antigen)	1,71 1,70	2.46 1.70	0.76 2.78
. •	440039	Z46188	Hs.6874	. KIAA0472 protein	1.70	2.24	1.60
	406646	M33600	Hs.308026	major histocompatibility complex, class	1.70	2.27	1.33
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	1.70	2.77	2.07
75	420286 430255	A1796395 AK000703	Hs.111377 Hs.323822	ESTs Homo sepiens mRNA for KIAA1551 protein,	1.70 1.69	1.50 1.44	3.21 1.69
	445247	AW274290	Hs.153997	ESTs	1.69	2.57	1.65
	436965	Z11894	Hs.156110	gb:H.sapiens rearranged mRNA for immunog	1.69	1.52	3.13
	410257	BE244044	Hs.61469	hypothetical protein	1.69	1.99	1.97
80	424663 427792	NM_002351 M63928		SH2 domain protein 1A, Duncan's disease	1.69 1.69	1.76 1.98	1.69 2.48
30	458098	BE550224	Hs.180841	tumor necrosis factor receptor superfami metallothionein 1E (functional)	1.68	1.83	1.68
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	1.68	1.57	4.09
	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	1.68	1.64	0.68



	421563	NM_006433	Hs.105806	granulysin	1.68	2.24	1.55
	448775	AB025237	Hs.388	nudix (nucleoside diphosphate linked moi	1.68	1.98	2.05 1.68
	451418 440457	BE387790	Hs.26369 Hs.21321	hypothetical protein FLJ20287  Homo saplens clone FLB9213 PRO2474 mRNA,	1,68 1,68	1.35 1.88	1.63
5	438866	8E387593 U44385	Hs.325495	tissue inhibitor of metafloproteinase 2	1.67	2.54	1.90
•	401760			Target Exon	1.67	1.93	1.61
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	1.67	1.85	4.25
	445644	NM_003272	Hs.15791	transmembrane 7 superfamily member 1 (up	1.67	1.94 1.65	1.48 0.90
10	415701 450293	NM_003878 N36754	Hs.78619 Hs.171118	gamma-glutarnyl hydrolase (conjugase, fol hypothetical protein FLJ00026	1.67 1.67	1.54	1.95
- 0	412856	BE386745	Hs.74531	basigin (OK blood group)	1.67	2.71	1.47
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	1.66	1.82	1.19
	424399	AI905687		AJ905687:IL-BT095-190199-019 BT095 Homo	1.66	3.65	0.44
15	432355 427239	AA534416 BE270447	Hs.162185	ESTs, Wealtly similar to S42799 garp prec ubiquitin carrier protein	1.66 1.66	1.98 2.94	1.45 1.92
13	425262	D87119	Hs.155418	GS3955 protein	1.66	2.36	1.66
	413869	NM_00087B	Hs.75596	interleukin 2 receptor, beta	1.66	1.86	1.90
	406698	X03068	Hs.73931	major histocompatibility complex, class	1.65	2.05	1.31
20	446217 400222	A1651594	Hs.99709	ESTs NM_002082*:Homo sapiens G protein-couple	1,65 1,65	1.98 1.74	1.77 1.81
20	432468	AW402155	Hs.3003	CD3E antigen, epsilon polypeptide (TiT3	1.65	2.50	1.77
	417237	H86385	Hs.81737	palmitoyl-protein thioesterase 2	1.65	2.89	1.57
	433012	NM_004045	Hs.279910	ATX1 (antioxidant protein 1, yeast) homo	1.64	2.76	1.26
25	446291 433867	BE397753 AK000696	Hs.14623 Hs.3618	interferon, gamma-inducible protein 30 hippocatcin-like 1	1.64 1.64	1.96 1.47	1.24 1.00
23	433671	AW138797	Hs.132906	19A24 protein	1.64	2.17	1.96
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	1.64	2.18	1.43
	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	1.64	1.47	1.64
30	409264 431836	NM_014937 AF178532	Hs.52463 Hs.271411	KIAA0966 protein beta-site APP-cleaving enzyme 2	1.64 1,64	1.46 2.58	. 4.89 1.79
20	414586	AA306160	Hs. 16488	lymphocyte cytosolic protein 1 (L-plasti	1.63	1.72	1.88
	418117	AJ922013	Hs.83498	linker for activation of T cells	1.63	1.98	1.99
	448304	BE622768 AB007937	Hs.290356	mesoderm development candidate 1	1,63 1,63	1.67 2.56	1.86 1.97
35	425535 453258	AW293134	Hs.158287 Hs.32597	KIAAD458 gene product ring finger protein (C3H2C3 type) 6	1.63	1.46	2.43
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	1.63	1.34	1.94
	447321	AW271217	Hs.281434	Homo sapiens cONA FLJ14028 fis, clone HE	1.63	1.96	1.77
	422192 450701	AA305159 H39960	Hs.113019 Hs.288467	fts485 hypothetical protein XP_098151 (leucine-	1.62 1.62	1.45 2.23	1.62 1.53
40	419381	AB023420	Hs.90093	heat shock 70kD protein 4	1.62	1.57	2.38
	424779	AL046851	Hs.153053	CD37 antigen	1.62	1.92	2.10
	413283	R78669	Hs.23756	hypothetical prolein similar to swine ac	1.62	1.41	1.12
	414907 414159	X90725 AW511414	Hs.77597 Hs.257352	polo (Drosophia)-like kinase apolipoprotein L, 6	1.62 1.62	2.03 1.89	2.13 1.32
45	410055	AJ250839	Hs.58241	gene for serine/threonine protein kinase	1.52	1.81	1.27
	428179	A1127772	Hs.279696	serum/glucocorticoid regulated kinase-li	1.62	1.50	2.13
	436251 451708	BE515065 Al306536	Hs.296585 Hs.60975	nucleolar protein (KKE/D repeat) ESTs	1,61 1,61	1.71 2.31	2.02 1.70
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	1.61	1.53	2.50
50	410600	AW575742		ESTs, Moderately similar to S65657 alpha	1.61	1.83	1.69
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	1.61 1.61	1.56 1.58	1.61 1.85
	440201 414368	AL359588 W70171	Hs.7041 Hs.75939	hypothetical protein DKFZp762B226 uridine monophosphate kinase	1.61	1.59	2.75
	454429	BE273437	Hs.301406	hypothetical protein PP3501	1.61	3.54	1.52
55	422257	NM_001716		Burkitt lymphoma receptor 1, GTP-binding	1.61	2.15	1.54
	426437 408826	BE076537 AF216077	Hs.169895 Hs.48376	ubiquitin-conjugating enzyme E2L 6 Homo sapiens clone HB-2 mRNA sequence	1.60 1.60	2.01 2.00	1.36 1.60
	414761	AU077228	Hs.77256	enhancer of zeste (Orosophila) homolog 2	1.60	1.38	2.23
۲0	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	1.60	1.78	2.59
60	411263 417324	BE297802 AW265494	Hs.69360	kinesin-like 6 (mitotic centromere-assoc ESTs	1.60 1.60	1.78 2.48	2.07 1.91
	430325	AF004562	Hs.239356	syntaxin binding protein 1	1.60	1.74	2.53
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	1.60	1.46	2.46
65	434449	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	1.60	1.81	3.00
U)	443378 417437	AW392550 U52682	Hs.9280 Hs.82132	proteasome (prosome, macropain) subunit, interferon regulatory factor 4	1.59 1.59	1.88 1.90	1.68 2.26
	437949	U78519	Hs.41654	ESTs, Weakly similar to A46010 X-linked	1.59	2.14	1.59
	401797			Targel Exon	1.59	1.82	1.78
70	449720 424971	AA311152 AA479005	Hs.288708 Hs.154036	hypothetical protein FLJ21562 tumor suppressing subtransferable candid	1.59 1.59	1.45 1.82	4.69 1.68
70	415474	NM_014252		solute carrier family 25 (mitochondrial	1.58	1.51	0.30
	430017	AA263172	Hs.35	protein tyrosine phosphatase, non-recept	1.58	1.72	2.46
	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	1.58	1.85	1.94
75	434094 428844	AA305599 AW972635	Hs.238205 Hs.301904	hypothetical protein PRO2013 hypothetical protein FLJ12671	1.58 1.58	1.25 1.72	2.09 1.80
	440942	AW246547	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	1.58	2.60	1.58
	419596	BE379320	Hs.91448	MKP-1 like protein tyrosine phosphalase	1.58	1.84	1.22
	401151	AICTTON	Un 100027	Target Exon	1.58 1.58	2.43 1.40	1.60
80	441590 418677	A/623207 S83308	Hs.190537 Hs.87224	ESTs SRY (sex determining region Y)-box 5	1.56 1.58	1.68	1.58 1.58
-	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	1.58	2.28	1.60
	418739	AA310964	Hs.88012	SHP2 interacting transmembrane adaptor	1.58	214	2.10
	418216	AA662240	Hs.283099	AF15q14 protein	1.57	1.46	1.57

	427700 436485	AA262294 X59135	Hs.180383 Hs.156110	dual specificity phosphatase 6 immunoglobulin kappa constant	1.57 1.57	1.42 1.49	0.88 2.69
	404872			ENSP00000243173*:DJ1109J22.1 (novel home	1.57	1.46	1.36
5	408212	AA297567	Hs.43728	hypothetical protein	1.57	1.55	2.73
5	414699 444006	AI815523 BE395085	Hs.76930 Hs.10086	synuclein, atpha (non A4 component of am type I transmembrane protein Fn14	1.57 1.57	1.36 1.70	1.57 1.13
	432946	U60899	Hs.279854	mannosidase, alpha, class 2B, member 1	1.57	1.75	1.57
	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	1.57	2.26	2.10
10	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	1.57	2.09	1.57
U	402876 439627	BE621702	Hs.29076	NM_022161*:Homo sapiens fivin inhibitor- hypothetical protein FLJ21841	1.56 1.56	2.28 2.97	1.45 1.54
	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyttransferase 1	1.56	1.75	1.88
	450663	H43540	Hs.25292	ribonuclease HI, large subunit	1.56	2.76	1.67
15	425818 422765	AB021225	Hs.159581	matrix metalloproteinase 17 (membrane-in bacutoviral IAP repeat-containing 5 (sur	1.56 1.56	2.36 1.78	1.83 2.06
13	456508	AW409701 AA502764	Hs.1578 Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	1.56	1.32	2.70
	453613	F06838	1.5.1.25.152	ESTs	1.56	1.76	1.B4
	428379	X06026	Hs.2259	CO3G antigen, gamma polypeptide (TiT3 co	1.56	1.43	1.56 3.15
20	429500 444652	X78565 BE513613	Hs.289114 Hs.11538	hexabrachion (tenascin C, cytotactin) actin related protein 2/3 complex, subun	1.56 1.56	1.47 2.01	1.56
-0	420842	AI083668	Hs.50601	hypothetical protein MGC10986	1.55	2.24	1.90
	447513	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A	1.55	1.24	3.07
	408901 437669	AK001330 Al358105	Hs.48855 Hs.123164	hypothetical protein FLJ10468 ESTs, Wealdy similar to match to ESTs AA	1.55 1.55	1.79 1.83	2.17 1.96
25	439437	AI207788	Hs.343628	sialytransferase 48 (beta-galactosidase	1.55	1.63	2.20
	418835	AL023694	Hs.88977	hypothetical protein dJ511E16.2	1.55	1.73	1.50
	448533	AA311426	Hs.21635	tubulin, gamma 1	1.54 1.54	2.02 2.52	1,67 1.52
	447763 430223	BE619911 NM_002514	Hs.115803 Hs.235935	hypothetical protein nephroblastoma overexpressed gene	1.54	1.54	3.03
30	448258	BE386983	Hs.343214	hypothetical protein FLJ20396	1.54	1.97	1.53
	440165	AW014718	Hs.7753	calumenin	1.54	1.53	2.55
	433376 445982	AJ249361 BE410233	Hs.74122 Hs.13501	caspase 4, apoptosis-related cysteine pr pescadillo (zebrafish) homolog 1, contai	1.54 1.54	1.34 2.21	1.69 1.54
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.54	2.50	1.94
35	416926	H03109	Hs.263395	HT018 protein	1.54	1.41	2.01
	431630 442159	NM_002204 AW163390	Hs.265829 Hs.278554	integrin, atpha 3 (antigen CD49C, atpha heterochromatin-like protein 1	1.54 1.54	1.89 1.93	1.23 1.79
	420421	AF281133	Hs.343589	exosome component Rrp41	1.53	2.47	1.61
40	406973	M34996	Hs.198253	major histocompatibility complex, class	1.53	1.62	1.19
40	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	1.53 1.53	1.74 2.49	1.37 1.59
	423420 429359	AI571364 W00482	Hs.128382 Hs.2399	Homo sapiens mRNA; cDNA DKFZp76111224 (f matrix metalloproteinase 14 (membrane-in	1.53	2.72	1.54
	429837	NM_003896	Hs.225939	sialyltransferase 9 (CMP-NeuAc:lactosylc	1.53	1.64	2.40
45	412939	AW411491	Hs.75069	eukaryotic translation elongation factor	1.52	1.98	0.98
43	410678 431186	BE540516 NM_012249	Hs.293732 Hs.250697	hypothetical protein MGC3195 ras-like protein	1.52 1.52	1.39 1.91	2.17 1.82
	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.52	1.57	1.82
	422532	AL008726	Hs.118126	protective protein for beta-galactosidas	1.51	2.08	1.19
50	413063 417308	AL035737 H60720	Hs.75184 Hs.81892	chitinase 3-like 1 (cartilage glycoprote KIAA0101 gene product	1.51 1.51	1.50 1.42	0.67 7.41
50	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, ty	1.51	2.75	1.51
	405204			NM_002086*:Homo sapiens growth factor re	1.51	1.44	1.53
	424481 422516	R19453 BE258862	Hs.1787 Hs.117950	proteolipid protein 1 (Petizaeus-Merzbac multifunctional polypeptide similar to S	1.51 1.50	1.92 1.61	2.32 1.47
55	418827	BE327311	Hs.47166	НТ021	1.50	1.35	3.53
	427550	BE242818	Hs.311609	nuclear RNA helicase, DECD variant of DE	1.50	1.55	2.09
	432992 442432	BE270472 BE093589	Hs.279900 Hs.38178	HSPC015 protein hypothetical protein FLJ23468	1.50 1.50	1.82 1.34	0.82 4.87
	413566	AW604451	Hs.285814	sprouty (Drosophila) homolog 4	1.50	3.05	1.51
60	422615	8E300330	Hs.118725	selenophosphale synthetase 2	1,50	1.36	0.46
	431222 421861	X56777 \$78798	Hs.273790 Hs.108966	zona pellucida glycoprotein 3A (sperm re	1.50 1.49	2.05 1.52	1.78 2.62
	422684	BE561617	Hs.119192	phosphatidylinositol-4-phosphate 5-kinas H2A histone family, member Z	1.49	1.53	2.02
	452363	AI582743	Hs.94953	Homo sapiens, Similar to complement comp	1.49	2.02	1.41
65	411825 409425	AK000334 U40462	Un 54450	hypothetical protein FLJ20327	1,49 1,49	2.55 1.77	1.38 1.49
	431070	AW408164	Hs.54452 Hs.249184	zinc finger protein, subfamily 1A, 1 (he transcription factor 19 (SC1)	1,49	1.79	1.75
	427080	AW068287	Hs.301175	ras-related C3 botulinum toxin substrate	1.49	1.57	2.14
70	440676	NM_004987		LIM and senescent cell antigen-like doma	1.49	1.42	1.46
70	411296 442894	BE207307 W02112	Hs.10114 Hs.8836	growth suppressor 1 parvin, beta	1.49 1.49	1,74 2,25	1.50 1.51
	416361	AW204907	Hs.6872	ESTs, Weakly similar to CA13_HUMAN COLLA	1.49	2.06	1.89
	424162	AA336229	Hs.93135	ESTs, Weakly similar to ALU2_HUMAN ALU S	1.49	1.59	1.65
75	447131			retinoic acid receptor responder (tazaro	1,49 1,49	2.00 2.12	1.22 1.41
, ,	427759 422846		Hs.2200 Hs.1583	perforin 1 (pore forming protein) neutrophil cytosolic factor 1 (47kD, chr	1.49	1.61	1.67
	417007	AF224741	Hs.80768	chloride channel 7	1.48	1.94	1.71
	421924		Hs.109606	coronin, actin-binding protein, 1A	1.48	1.68	1.67
80	422241 410741		Hs.170121 Hs.324473	protein tyrosine phosphatase, receptor t mitogen-activated protein kinase 1	1.48 1.48	1.43 1.37	2.25 3.17
	447471	AF039843	Hs. 18676	sprouty (Drosophila) homolog 2	1.48	1.35	1.45
	427247		Hs.174103	integrin, alpha L (antigen CD11A (p180),	1.47	1.58	1.48
	442945	AI024849	Hs.131853	ESTs	1.47	1.73	1.38

	447200	BE543146	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.47	1.89	1.60
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	1.47	2.03	1.47
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.47	1.86	1.93
5	416350	AF188625	Hs.189507	phospholipase A2, group IID	1.47	2.92	1.49
J	458207 447940	T28472	Hs.7655	U2 small nuclear ribonucleoprotein auxil	1.47	1.61 1.93	1.73
	446106	D86982 AA377165	Hs.20060 Hs.44833	KIAA0229 protein ESTs	1.47 1.47	1.56	1.72 1.63
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.47	1.78	1.84
	432615	AA557191	Hs.55028	ESTs, Wealty similar to 154374 gene NF2	1.47	2.04	1.47
10	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	1.47	1.76	1.83
	402294			Target Exon	1.47	1.27	1.46
	430147	R60704	Hs.234434	hairy/enhancer-of-split related with YRP	1.46	2.00	1.59
	414324 400270	Y14768	Hs.890	lymphotoxin beta (TNF superfamily, membe	1.45 1.46	1.58 1.42	2.15 2.32
15	414805	D14694	Hs.77329	NM_000026":Homo sapiens adenylosuccinata phosphatidytserine synthase 1	1.46	2.07	1.40
	419625	U91616	Hs.182885	nuclear factor of kappa light polypeptid	1.45	1.78	1.53
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	1.45	1.31	0.90
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	1.45	213	1.46
20	453350	AI917771	Hs.61790	hypothetical protein FLJ23338	1.45	200	1.39
20	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	1.45	1.37	3.17
	411619	AI418509	Hs.71040	hypothetical protein FLJ20425	1.45	1.39	3.01
	424218 450395	AF031824 BE048545	Hs.143212 Hs.161757	cystatin F (leukocystatin) ESTs	1.45 1.45	1.82 2.40	1.44 1.33
	438555	AJ222089	Hs.143878	Horno sapiens mRNA for FLJ00024 protein,	1.45	1.91	1.65
25	422497	D29642	Hs.1528	KIAA0053 gene product	1,45	1.94	1.49
	400991			Target Exon	1.45	2.10	1.42
	431779	AW971178	Hs.268571	apolipoprotein C-I	1.45	1.53	0.42
	424618	L29472	Hs.1802	major histocompatibility complex, class	1.44	1.96	1.86
30	423032	AJ684746	Hs.119274	RAS p21 protein activator (GTPase activa	1.44	1.34	3.36
30	424232 438291	AB015982 BE514605	Hs.143460 Hs.289092	protein kinase C, nu	1.44 1.44	1.28 1.63	2.94 1.45
	445745	AB007924	Hs.13245	Homo sapiens cDNA: FLJ22380 fis, clone H KIAA0455 gene product	1.44	1.17	1.43
	449209	BE616830	Hs.294145	ESTs	1.44	1.35	2.48
	410129	BE244074	Hs.58831	regulator of Fas-induced apoptosis	1.44	2.10	1.79
35	401284			Target Exon	1.44	1.71	1.44
	422675	BE018517	Hs.119140	eukaryotic translation initiation factor	1.44	1.68	1.45
	433020	A1375726	Hs.279918	hypothetical protein	1.44	1.37	2.02
	420042	AW015140	Hs.161723	ESTs	1.44	2.02	1.29
40	453878 427268	AW964440 X78520	Hs.19025 Hs.174139	DC32	1.44 1.44	1.69 1.45	1.44 1.96
10	417386	AL037228	Hs.82043	chloride channel 3 D123 gene product	1,43	1.32	2.81
	409197	N54706	Hs.303025	chromosome 11 open reading frame 24	1.43	1.80	1.17
	411009	W37572	Hs.285864	ESTs	1.43	1.57	1.72
45	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	1.43	1.36	1.49
45	416084	L16991	Hs.79006	deoxythymidylate kinase (thymidylate kin	1.43	2.15	1.57
	407826	AA128423	Hs.40300	calpain 3, (p94)	1.43	1.61	1.69
	439070 444090	AJ733278 S69115	Hs.7621 Hs.10306	ESTs	1.43 1.43	2.10 2.09	1.40 1.24
	420162	BE378432	Hs.95577	natural killer cell group 7 sequence cyclin-dependent kinase 4	1.43	2.13	1.54
50	442591	AW292797	1.0.00011	hypothetical protein MGC10772	1.43	2.11	1.61
	451668	Z43948	Hs.326444	cartilage acidic protein 1	1.43	1.49	1.16
	423639	AB037826	Hs.130411	KIAA1405 protein	1.42	2.08	1.51
	426234	BE314534	Hs.168159	apoptosis regulator	1.42	1.57	1.31
55	424263 430294	M77640	Hs.1757	L1 cell adhesion molecule (hydrocephalus	1.42	1.88	1.63
55	447126	AI538226 AW150632	Hs.32976 Hs.170307	guanine nucleotide binding protein 4 Ral guanine nucleotide exchange factor R	1.42 1.42	1.46 1.36	3.18 1.38
	432241	AI937060	Hs.6298	KIAA1151 protein	1.42	1.58	1.98
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (plate)	1,41	2.09	1.29
	434262	AF121858	Hs.12169	sorting nexin 8	1.41	3.07	1,41
60	432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKFZp434K1815 (f	1.41	1.82	1.43
	402474	100000		NM_004079:Homo sapiens cathepsin S (CTSS	1.41	1.32	1.24
	419897 417621	X90826 AV654694	Hs.93649	upstream transcription factor 2, c-los i	1.41 1.41	1.69	1.80
	424441	X14850	Hs.82316 Hs.147097	Interferon-induced, hepatitis C-associat H2A histone family, member X	1.41	1.22 1.74	1,74 2,15
65	406663	U24683	10.147037	Immunoglobulin heavy constant mu	1.41	1.51	2.03
	409614	BE297412	Hs.55189	hypothetical protein	1,41	1.54	2.20
	443885	H91806	Hs. 15284	ESTs	1.41	1.19	1.41
	412276	BE262621	Hs.73798	macrophage migration inhibitory factor (	1.40	1.88	1.24
70	425179	AJ224442	Hs.155020	putative methyltransferase	1.40	1.84	1.47
70	418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.40	1.27	2.79
	432403 417389	AA550815 BE260964	Hs.124840 Hs.82045	ESTs middine (neurite growth-promoting factor	1.40 1.40	1.83 1.65	1.44 2.51
	422596	AF063611	Hs.118633	2-5-oligoadenylate synthetase-like	1.40	2.57	1.44
_	435292	N20514	Hs.172965	ESTs	1.40	1.91	1.43
75	419424	BE041820	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	1.39	1.57	1.37
	425068	AL048716	Hs.154387	KIAA0103 gene product	1.39	1.27	3.18
	426020	AL110195	Hs.166017	microphthalmia-associated transcription	1.39	2.26	1.40
	427740	BE242604	Hs.180616	CD36 antigen (collagen type I receptor,	1.39	1.76	0.99
80	403022	AA0120+2	11- 70040	C21000178*:gi[7341207 gb]AAF61215.1 AF22	1.39	1.74	1.36
50	416111 410103	AA033813 AW903666	Hs.79018	chromatin assembly factor 1, subunit A ( gb:CM4-NN1032-280300-122-b02 NN1032 Homo	1.39 1.39	1.72 1.46	1.39 1.34
	439180	AL393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.39	1.35	1.79
	414057	AI815559	Hs.75730	signal recognition particle receptor (d	1.39	1.49	1.17

	416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membr	1.39	1.52	1.44
	423984	AF163825	Hs.136713	pre-B lymphocyte gene 3	1.39	3.02	1.52
	448484	BE613340	Hs.334725	Homo sapiens, Similar to RIKEN cDNA 9430	1.38	1.81	1.39
_	436856	A1469355	Hs.127310	EST ₈	1.38	1.35	0.99
5	437179	AA393508		serologically defined colon cancer antig	1.38	1.26	4,14
	437912	BE278594	Hs.5912	F-box only protein 7	1.38	2.03	1.40
	448564	AIB79317	Hs.334691	splicing factor 3a, subunit 1, 120kD	1.38	1.52	1.38
	439981	AI348408	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	1.38	1.48	1.38
10	432812	A1935412	Hs.50162	ESTs	1.38	1.43	2.18
10	406826	AW516005	Hs.84298	CD74 entigen (invariant polypeptide of m	1.38	1.87	1.28
	445962	AI351421	Hs.279709	muscle specific ring finger protein 1	1.38	1.46	2.23
	408787	NM_014784	Hs.47822	Rho guanine exchange factor (GEF) 11	1.38	1.98	1.50
	428044	AA093322	Hs.301404	RNA binding motif protein 3	1.38	1.29	2.04
16	412926	AI879076	Hs.75061	macrophage myristoylated atanine-rich C	1.38	1.52	2.62
15	418255	AW135405	Hs.37251	ESTs	1.38	1.44	1.75
	419745	AF042001	Hs.93005	stug (chicken homotog), zinc finger prot	1.37	1.51	1.37
	448977	X91809	Hs.22698	regulator of G-protein signalling 19	1.37	1.98	1.45
	422609	Z46023	Hs.118721	sialidase 1 (lysosomal sialidase)	1.37	1.75	1.31
20	435458	F11872	Hs.4892	Homo sapiens clone 24841 mRNA sequence	1.37	1.38	2.80
20	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	1.37	1.61	1.62
	429849	U33053	Hs.2499	protein kinase C-like 1	1.37	1.71	1.45
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	1.37	1.62	1.82
	452923	BE276018	Hs.288940	five-span transmembrane protein M83	1.37	1.86	1.37
25	453941 446755	U39817 AW451473	Hs.36820 Hs.16134	Bloom syndrome	1.37 1.37	1.59	1.37
LJ	439755	AW748482	Hs.77873	serine/threonine kinase 10		1.82	1.48
	447630	AI660149	Hs.44865	87 homotog 3 hymphoid enhancer-binding factor 1	1.36 1.36	2.10 1.79	1.35
	413821	AA844126	Hs.55964	ESTs, Weakly similar to C4HU complement	1.36	1.91	1.67 1.39
	445823	A1478563	Hs.145519	FKSG87 protein	1.36	1.29	0.33
30	456760	AW961251	Hs.127828	guanine nucleotide binding protein (G pr	1.36	1.33	2.01
-	402542	A11301401	143.121020	Target Exon	1.36	1.66	1.46
	451050	AW937420		ESTs	1.36	2.00	1.36
	444501	AW247624	Hs.11342	niniurin 1	1.36	1.59	1.14
	413291	NM_006278	Hs.75268	siałytransferase 4C (beta-galactosidase	1.36	2.55	1.42
35	438129	AA778647	1.0 0200	gb:af87d03.s1 Soares_testis_NHT Homo sap	1.36	1.46	1.32
	428398	A1249368	Hs.98558	ESTs	1.36	1.25	4.95
	439704	AW020018	Hs.293267	ESTs	1.36	1.84	1.48
	428782	X12830	Hs.193400	Interleukin 6 receptor	1.36	1.27	0.58
	437316	A1683454	Hs.46801	GCN5 (general control of amino-acid synt	1.35	2.10	1.29
40	439246	AJ498072		membrane-associated tyrosine- and threon	1.35	1.81	1.63
	403409			NM_005929:Homo sapiens antigen p97 (meta	1.35	1.64	1.35
	446342	BE298665	Hs. 14845	Homo sapiens mRNA; cDNA DKF2p564D016 (fr	1.35	1.37	2.33
	437740	AA810265	Hs.122915	ESTs	1.35	1.91	1.35
4.5	423973	AF038461	Hs.136574	arachidonate 12-lipoxygenase, 12R type	1.35	1.53	1.10
45	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	1.35	1.89	1.57
	457760	AA668123	Hs.134170	ESTs	1.35	2.03	1.43
	439769	AA448828	Hs.30596	Homo sapiens mRNA full length insert cDN	1.35	2.06	1.41
	406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of m	1.35	1.77	1.27
50	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	1.35	1.52	0.51
20	421777	BE562088	Hs.108196	HSPC037 protein	1.34	1.65	1.61
	400328	X87344		transporter 2, ATP-binding cassette, sub	1.34	1.77	1.02
	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	1.34	1,77	1.15
	428977	AK001404	Hs.194698	cyclin B2	1.34	1.53	1.82
55	418283 425848	S79895	Hs.83942	cathepsin K (pycnodysostosis)	1.34	1,33	3.45
"	431211	BE242709 M86849	Hs.159637 Hs.323733	vatyl-tRNA synthetase 2	1.34	2.11	1.32
	422758	AF152329	Hs.284180	gap junction protein, beta 2, 26kD (conn	1.34 1.34	1.27 1.61	1.97
	421579	NM_002975	Hs.105927	protocadherin gamma subfamily C, 3 stem cell growth factor; lymphocyte secr	1.34	1.75	1.75 1.81
	416374	NM_001154	Hs.300711	annexin AS	1.34	1.68	1.55
60	451092	AI207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein,	1.34	1.87	0.81
	424778	AA251048	Hs.153042	lymphocyte antigen 9	1.34	1.94	1.42
	421703	AI936513	Hs.1416	Fc tragment of IgE, low affinity II, rec	1.33	2.19	1.48
	416700	AW498958	Hs.343475	cathepsin D (lysosomal aspartyl protease	1.33	1.96	1.18
	425923	NM_005026	Hs.162808	phospholnositide-3-kinase, catalytic, de	1.33	1.70	1.60
65	418803	U50079	Hs.88556	histone deacetylase 1	1.33	1.28	2.65
	427730	AW250549	Hs.180577	granufin	1.33	2.09	1.35
	441174	BE312775	Hs.294005	Homo sapiens, clone IMAGE:3050476, mRNA,	1.33	2.05	1.33
	412738	N34731	Hs.74562	siah binding protein 1; FBP interacting	1.33	1.85	1.35
70	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	1.33	1.31	2.06
70	422599	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	1.33	1.77	1.43
	422997	BE018212	Hs.122908	DNA replication factor	1.33	1.91	1.39
	415323	8E269352	Hs.949	neutrophil cylosofic factor 2 (65kD, chr	1.33	1.16	0.60
	409119	AA531133	Hs.4253	hypothetical protein MGC2574	1.33	1.52	1.34
75	419652	AL157485	Hs.91973	hypothetical protein	1.32	2.07	1.29
75	415697	AI365603	Hs.198271	DKFZP566I1024 protein	1.32	2.00	1.33
	434359	AF129536	Hs.284226	F-box only protein 6	1.32	2.07	1.39
	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	1.32	1.25	1,91
	444029	AW160993	Hs.326292	hypothetical gene DKFZp434A1114	1.32	1.63	1.44
80	456974	M12529	Hs.169401	apolipoprotein E	1.32	1,47	0.85
OU	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	1.32	251	1.23
	448610	NM_006157 NM_001621	Hs.21602 Hs.170087	nel (chicken)-like 1	1.31	3.12	1.31
	426490 427584	8E410293	Hs.179718	aryl hydrocarbon receptor v-myb avian myeloblastosis viral oncogen	1.31	1.21	1.65
	421304	02-10233	119.173710	- myo avian mjeropiastosis vita oncogen	1,31	1.68	1.47

	417059	AL037672	Hs.81071	extracellular matrix protein 1 squatene epoxidase	1.31 1.31	1.30 1.45	2.14 1.43
	407777 408536	AA161071 AW381532	Hs.71465 Hs.135188	ESTs	1.31	1.38	0.90
	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-recept	1.31	1.81	1.49
5	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	1.31	1.63	1.31
•	409154	U72882	Hs.50842	interferon-induced protein 35	1.31	1.69	1.29
	425003	AF119046	Hs.154149	apunnic/apyrimidinic endonuclease(APEX	1,31	1.74	1.39
	441406	Z45957	Hs.7837	phosphoprotein regulated by mitogenic pa	1.31	1.43	0.94 1.34
10	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.30 1.30	2.53 1.38	1.38
10	417361	NM_000275	Hs.82027	ocutocutaneous atbinism II (pink-eye dil Rho GDP dissociation inhibitor (GDI) atp	1.30	2.11	1.36
	425676 427289	AW410656 AI097346	Hs.159161	phosphoserine aminotransferase	1.30	2.27	1.48
	427747	AW411425	Hs.180655	serine/threonine kinase 12	1.30	1.68	1.79
	422296	AA360231	Hs.114416	Homo sapiens, Similar to transducin (bet	1.30	1.50	1.30
15	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	1.30	1.42	2.13
	423062	NM_003655	Hs.5637	ESTs	1.30	1.58	1.30 1.35
	439740	AL365512	Hs.6657	hypothetical protein bK1048E9.5	1.30 1.30	1,77 1.57	1.51
	409340	BE174629	Hs.321130	hypothetical protein MGC2771 polymerase (RNA) II (DNA directed) polyp	1.30	1.67	1.44
20	416920 430451	AA176455 AA836472	Hs.80475 Hs.297939	cathepsin B	1.30	1.49	1.16
20	457400	AF032906	Hs.252549	cathepsin Z	1.30	1.40	1.21
	403506	75 5525-5		C3001912:gi]6677647[ref]NP_033602.1] zin	1.29	1.88	1.26
	424867	AI024860	Hs.153591	Not56 (D. melanogaster)-like protein	1.29	2.64	1.31
25	408815	AW957974	Hs.25485	hypothetical protein FLJ22341	1.29 1.29	1.79 1.59	1.36 1.80
25	416322	BE019494	Hs.79217	pyrroline-5-carboxylate reductase 1 ESTs, Weakly similar to PNL1_HUMAN PEANU	1.29	2.01	1.43
	440795 421846	AA262133 AA017707	Hs.99741 Hs.1432	protein kinase C substrate 80K-H	1.29	1.70	1.34
	425966	NM_001761	Hs.1973	cyclin F	1.29	1.63	1.50
	446766	AF083208	Hs.16178	apoptosis antagonizing transcription fac	1.29	1.71	. 1.40
30	406827	AA971409		gb:op92c04.s1 NCI_CGAP_Lu5 Homo sapiens	1.29	2.04	1.35
	418613	AA744529	Hs.86575	mitogen-activated protein kinase kinase	1.29	1.41	1.94 1,29
	443086	AW977125	450440	sine ocufis homeobox (Orosophila) homolo	1.29 1.29	1.24 1.99	1.36
	439146	AW138909	Hs.156110 Hs.3838	immunoglobulin kappa constant serum-inducible kinase (SNK)	1.29	1.18	1.32
35	434398 418322	AA121098 AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (COK	1.29	1.31	2.19
33	400261	70204100	16.04110	Eos Control	1.29	1.59	1.36
	413781	J05272	Hs.850	IMP (inosine monophosphate) dehydrogenas	1.29	1.67	1.53
	412315	AW936678		gb:PM2-DT0023-080300-004-a04 DT0023 Homo	1.28	1.26	1.07
40	420372	AW960049	Hs.293660	Homo sapiens, clone IMAGE:3535476, mRNA,	1.28	1.85 1.45	1.40 1,14
40	425449	X52056	Hs.157441	spteen focus forming virus (SFFV) provir superoxide dismutase 2, mitochondrial	1.28 1.28	2.29	1.07
	454478 410275	AW805749 U85658	Hs.61796	transcription factor AP-2 gamma (activat	1.28	1.20	0.93
	406016	003030	143.01130	Target Exon	1.28	1.47	1.31
	449609	BE246434	Hs.289026	guanine πucleotide binding protein (G pr	1.28	1.26	3.02
45	426059	BE292842	Hs.166120	interferon regulatory factor 7	1.28	1.76	1.23
	412773	H15785	Hs.74573	similar to vaccinia virus Hindlil K4L OR	1.28	1.60 1.51	1.30 1.22
	452700	AI859390	Hs.288940	five-span transmembrane protein M83	1.28 1.28	2.02	1.08
	408543 408822	N78098 AW500715	Hs.44289 Hs.57079	ESTs Homo sapiens cDNA FLJ13267 fis, clone OV	1,27	1.28	3.51
50	425069	AA687465	Hs.298184	potassium voltage-gated channel, shaker-	1.27	1.66	1.39
50	444681	AJ243937	Hs.288316	chromosome 6 open reading frame 9	1.27	1.47	1.55
	430794	NM_000166	Hs.333303	gap junction protein, beta 2, 26kD (conn	1.27	1.81	0.89
	430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgiz	1.27	1,35 1,67	1.68 1.31
55	440502	AJ824113	Hs.78281	regulator of G-protein signalling 12	1.27 1.27	1.30	1.30
33	441598 431921	A1733219 N46466	Hs.58262 Hs.58879	ESTs ESTs	1.27	2.00	1.16
	459345		113.000.0	gb:UI-HF-BN0-ald-h-11-0-UI.r1 NIH_MGC_50	1.26	1.44	1.33
	452436		Hs.31447	ESTs, Moderately similar to A46010 X-lin	1.26	1.20	1.45
	426334		Hs.169358	hypothetical protein	1.26	1.22	1.89 1.51
60	414044		Hs.75721	profilin 1 ENSP00000223174*:KJAA0783 PROTEIN.	1.26 1.26	1.48 1.19	2.25
	405268		9 Hs.79389	Protein kinase C-binding protein NELL2	1.26	1.19	4.03
	416602 439529		Hs.293984	hypothetical protein MGC13102	1.26	1.83	1.19
	421254		Hs. 102950	coat protein gamma-cop	1.26	1.61	1.23
65	417785		Hs.82568	cytochrome P450, subfamily XXVIIA (stero	1.26	1.84	0.68
	419395		Hs.90280	5-aminoimidazole-4-carboxamide ribonucle	1.26	1.66	1.34
	418968			cholesteryl ester transfer protein, plas	1.26 1.26	1.42 1.29	1,19 1,28
	441553			ESTs secreted phosphoprotein 1 (osteopontin,	1.25	1.22	0.65
70	445619 424624		Hs.313 Hs.151301	Ca2+dependent activator protein for secr	1.25	1.17	2.95
70	450087			MUM2 protein	1.25	1.78	1.28
	42960		Hs.210778	hypothetical protein FLJ10989	1.25	1.18	1.25
	42938	AF023268		secretory carrier membrane protein 3	1.25	2.22	1.25
26	44025			Homo sepiens, clone IMAGE:3687782, mRNA,	1.25	1.90 1.32	1.39 1.53
75	41675			hypothetical protein FLJ10116	1.24 1.24	1.96	1.32
	43546			G protein beta subunit-like hypothetical protein FLJ11354	1.24	1.61	1.32
	45062 40021		, 113.33319	NM_007002:Homo sapiens cell membrane gly	1.24	1.68	1.32
	43501		Hs.110024	NM_020142:Homo sapiens NADH:ubiquinone o	1.24	1.76	1.25
80	41473	3 BE514535	Hs.77171	minichromosome maintenance deficient (S.	1.24	1.82	1.42
	40685			major histocompatibility complex, class	1.24	1.68	1.19
	44849			ESTs	1.24 1.24	1.73 1.70	1.29 1.38
	44008	7 W28969	Hs.7718	hypothetical protein FLJ22678	1.64		
				536			

	411355	M76477	Hs.289082	GM2 ganglioside activator protein	1.24	1.61	1.16
	426502	Y07759	Hs.170157	myosin VA (heavy polypeptide 12, myoxin)	1.24	2.65	1.24
	452056	AW955065	Hs.101150	Homo sapiens, clone IMAGE:4054156, mRNA,	1.24	1.49	1.50
5	427390 429954	A1432163 A1918130	Hs.268231 Hs.21374	Homo sapiens cDNA: FLJ23111 fis, done L ESTs	1.24 1.23	1.17 1.19	2.10 4.77
•	421178	BE267994	Hs.102419	zinc finger protein	1.23	1.62	1.28
	442609	AL020996	Hs.8518	setenoprotein N	1.23	2.30	1.24
	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	1.23	1.18	0.90
10	410127	AA354313	Hs.58685	CD5 antigen (p56-62)	1.23	1.68	1.23
10	452244	N33530	Hs.176674	ESTs	1.23	2.93	1.23
	406718 436939	AA505525 AA853680	Hs.169476 Hs.5345	glyceraldehyde-3-phosphate dehydrogenase arginyl aminopeptidase (aminopeptidase B	1.23 1.23	1.56 1.68	1.29 1.23
	414457	AW514320	Hs.76159	ATPase, H transporting, tysosomal (vacuo	1.23	1.58	1.20
	416929	N20535		melastatin 1	1.23	1.92	1,20
15	401106			Target Exon	1.23	1.82	1.29
	408981	AW500797	Hs.49427	Gem-interacting protein	1.23	1.40	1.59
	413317	U53225	Hs.75283	sorting nexts 1	1.23	1.43	1.44
	422481 425455	AL050163 AL137522	Hs.117339 Hs.157777	DNAX-activation protein 10 casein kinase 1, gamma 1	1.23 1.23	1.71 1.95	1.24 1.29
20	451524	AK001466	Hs.26516	hypothetical protein FLJ 10604	1.23	2.07	1.27
	414399	L47345	Hs.155202	transcription elongation factor B (SIII)	1.22	1.87	1.19
	422034	AC006486	Hs.333069	Els2 repressor factor	1.22	1.55	1.21
	434224	AA380731	Hs.84	interleukin 2 receptor, gamma (severe co	1.22	1.55	1.51
25	429574	BE268321	Hs.208912	hypothetical protein MGC861	1.22	1.49	1.48
23	411742 449027	AW247593 AJ271216	Hs.71819 Hs.22880	eukaryotic translation initiation factor	1.22 1.22	1.64 1.63	1.40 1.30
	418004	U37519	Hs.87539	dipeplidylpeplidase III aldehyde dehydrogenase 3 family, member	1.22	1.03	0.71
	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N1923	1.22	2.20	1.26
••	422739	H20106	Hs.119591	adaptor-related protein complex 2, sigma	1.21	1.55	. 1.21
30	424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	1.21	1.13	3.29
	404186	********	11- 201210	NM_019602:Homo sapiens butyrophilin-like	1.21	1.59	1.21
	447604 427979	AW089933 BE379776	Hs.301342 Hs.181309	hypothetical protein MGC4342 proteasome (prosome, macropain) subunit,	1.21 1.21	1.25 1.14	2.00 1.25
	414509	AW161311	Hs.76294	CD63 antigen (metanoma 1 antigen)	1.21	1.39	1.25
35	428468	AA171388	Hs.184482	DKFZP586D0624 protein	1.21	1.66	1.22
	419700	AF084935	Hs.92357	galactokinase 1	1.21	1.63	0.74
	430948	AI347578	Hs.124015	hypothetical protein MGC2605	1.21	1.48	1.21
	448143	AF039704	Hs.20478	ceroid-lipofuscinosis, neuronal 2, late	1.20	1.75	1.23
40	448499 442173	BE613280 N76101	Hs.77550 Hs.8127	hypothetical protein MGC1780 KIAA0144 gene product	1.20 1.20	1.54 1.54	1.29 1.31
10	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	1.20	1.18	1.11
	448230	BE395949	Hs.94814	hypothetical protein MGC2865	1.20	1.83	1.19
	403817			NM_015271:Homo sapiens tripartite motif-	1.20	1.22	1.61
45	411678	AI907114	Hs.71465	squatene epoxidase	1.20	1.15	2.01
45	452423	AA991724	Hs.180535	hypothetical protein MGC10966	1.20	1.79	1.20
	424046 447233	AF027866 AW246333	Hs.138202 Hs.17901	serine (or cysteine) proteinase inhibito	1.20 1.20	2.34 1.93	1.20 1.20
	422565	BE259035	Hs.118400	Homo sapiens, clone IMAGE:3937015, mRNA, singed (Drosophila)-like (sea urchin fas	1.20	1.32	1.52
	446159	NM_013379	Hs.14089	dipeptidyl peptidase 7	1.19	1.64	1.22
50	434563	AW083994	Hs.9469	pteckstrin homology domain-containing, f	1.19	1.53	1.45
	421541	NM_003942	Hs.105584	ribosomal protein S6 kinase, 90kD, polyp	1.19	1.75	1.27
	450706	AW167578	Hs.14691	ESTs, Moderately similar to 138022 hypot	1.19	1.71	1.22
	430381 426329	NM_006411 AL389951	Hs.240534 Hs.271623	1-acytglycerol-3-phosphate O-acytransfe nucleoporin 50kD	1.19 1.19	1.66 1,17	1.21 1.55
55	421612	AF161254	Hs.106196	BD6 antigen	1.19	1.73	1.30
	410182	NM_001983	Hs.59544	excision repair cross-complementing rode	1.19	1.75	1.18
	434171	BE247688	Hs.347349	KIAA0948 protein	1.18	1.73	1.09
	424837	BE276113	Hs.333034	N-acetyltransferase, homolog of S. cerev	1.18	2.13	1.22
60	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	1.18	1.45	1.30
UU	453754 439012	AW972580 BE383814	Hs.172753 Hs.6455	ESTs RuvB (E coli homolog)-like 2	1.18 1.18	1.71 1.60	1.35 1.23
	422256	M64673	Hs.1499	heat shock transcription factor 1	1.18	1.51	1.28
	439863	BE547830	Hs.9408	paired immunoglobulin-like receptor beta	1.18	1.89	1.18
	430513	AJ012008	Hs.241586	G6C protein	1.18	2.07	0.81
65	427283	AL119796	Hs.174185	ectonucleofide pyrophosphatase/phosphodi	1.18	1.13	3.25
	441648	HU5/34	Hs.30559	ESTS	1.18	1.56	1.23
	418219 406422	AA731836	Hs.137319	ESTs Target Exon	1.18 1.18	1.77 1.43	1.23 1.31
	414823	AA156531	Hs.103902	ESTs, Weakly similar to A44861 keratin,	1.18	1.66	1.23
70	425720	AA352394	Hs.293984	hypothetical protein MGC13102	1.18	1.58	1.15
	419250	AW770185		US snRNP-specific protein, 116 kD	1.17	1.74	1.21
	454390	AB020713	Hs.56966	KIAA0906 protein	1.17	1.33	1.35
	428471	X57348	Hs.184510	stratifin	1.17	1.19	1.24
75	430200	BE613337	Hs.234896	geminin	1.17	1.13	1.96
13	412965 430122	L06419 NM_013342	Hs.75093 Hs.233765	procollagen-lysine, 2-oxoglutarate 5-dio TCF3 (E2A) fusion partner (in childhood	1,17 1,17	1.50 1.69	1.22 1.32
	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	1,17	1.12	2.44
	417080	BE392846	Hs. 1063	small nuclear ribonucleoprotein polypept	1,17	1.93	1.18
00	423102	AW067812	Hs.303025	chromosome 11 open reading frame 24	1,17	1.89	1.17
80	408393	AW015318	Hs.23165	ESTs	1.16	1.10	1.91
	424292	AA338432	He seree	gb:EST43554 Fetal brain I Homo sapiens c	1.16	1.61	1.21
	446759 427324	R61463 AA159587	Hs.16165 Hs.285932	expressed in activated T/LAX lymphocytes hypothetical protein FLJ23322	1.16 1.16	1.45 1.50	1.23 1.23
	721329	A-133001	13.203332	Hypothetical protein ( Carastra	1.10	1,50	1.43

	446055	AJ815981	Hs.12909	mucolipin 1	1.16	1.49	1.10
	414432	BE378174	Hs.26506	Homo sapiens clone CDABP0005 mRNA sequen	1.16	1.67	1.20
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1,16	1.66	1.32
_	411305	BE241596	Hs.69547	myelin basic protein	1.16	1.15	4.29
5	438930	AW843533	Hs.343261	hypothetical protein AL110115	1.16	1.37	1.34
	407239	AA076350	Hs.67846	teukocyte immunoglobufin-like receptor.	1.15	1.82	1.17
	427458	BE208364	Hs.29283	ESTs, Weakly similar to LKHU proteoglyca	1.15	1.46	1.32
	402160			Target Exon	1.14	1.23	1.12
10	416881	N32520	Hs.141358	ESTs	1.14	2.42	1.14
10	420223	N27807		ribosomal protein L4	1.14	1.23	1.14
	450778	U81375	Hs.25450	solute carrier family 29 (nucleoside tra	1.14	1.38	1.27
	429538	BE182592	Hs.139322	small proline-rich protein 2A	1.14	1.15	3.52
	428342	AI739168	11 40010-	Homo sapiens cDNA FLJ13458 fis, clone PL	1.13	1.13	1.13
15	436696	AA725678	Hs.120487	ESTs	1.13	1.22	1.13
13	448950 437696	AF288687 283844	Hs.9275	CGI-152 protein	1.12	1.52	1.19
	425009	X58288	Hs.5790 Hs.154151	hypothetical protein dJ37E16.5 protein tyrosine phosphalase, receptor t	1.12	1.31 1.08	1.08
	412099	U64198	Hs.73165		1.12 1.12	2.9	1.20 1.12
	407951	W77762	Hs.79015	interleukin 12 receptor, beta 2 antigen identified by monoclonal antibod	1.12	1.11	3.43
20	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cONA 5430	1,12	1.50	1.12
	450296	AL041949	Hs.24756	hepatocyte growth factor-regulated tyros	1.11	1.48	1.12
	420697	AA827705	Hs.26605	ESTs	1.11	2.19	1.11
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.11	2.73	1.11
	418399	AF131781	Hs.84753	hypothetical protein FLJ12442	1,10	1.43	1,14
25	450358	AB010098	Hs.24907	coronin, actin-binding protein, 2B	1.10	1.35	1.19
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	1.10	1.43	1.10
	408801	AI866590	Hs.63405	Homo sapiens, done IMAGE:3609337, mRNA,	1.10	1.53	1.14
	402622			C1003392":gij12314272 emb CAC00591.1  (A	1.10	1.59	1.06
20	418661	NM_001949	Hs.1189	E2F transcription factor 3	1.09	1.82	1.09
30	442680	BE270707	Hs.8583	similar to APOBEC1	1.09	1.49	1.24
	439702	AW085525	Hs.55964	ESTs	1.09	1.68	1.09
	423858 443759	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp43480650 (f	1.09	1,10	1.73
		BE390832	Hs.134729	FXYD domain-containing ion transport reg	1.09	1.23	1.25
35	414396 401558	BE548266	Hs.76057	galactose-4-epimerase, UDP-	1.09 1.08	1.07	1.23
55	428411	AW291464	Hs.10338	ENSP00000220478*:SECRETOGRANIN III. ESTs	1.08	1.54 1.07	1.08 6.19
	422051	AW327546	Hs.111024	solute carrier family 25 (mitochondrial	1.08	1.25	0.13
	414694	NM_015362	Hs.76907	HSPC002 protein	1.08	1.18	1.12
	453883	AI638516	Hs.347524	cofactor required for Sp1 transcriptiona	1.07	1,15	1.31
40	420856	BE513294	Hs.205736	HLA class II region expressed gene KE2	1.06	1.47	1.08
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	1.06	1.17	1.22
	429259	AA420450	Hs.292911	Plakophilin	1.06	1.08	0.73
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	1.05	1.04	0.84
AE	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	1.05	1.09	1.37
45	44443B	N32755	Hs.322489	ESTs	1.04	1.13	1.05
	407394	AF005081		gb:Homo sapiens skin-specific protein (x	1.04	1.22	0.78
	404960		11. 10030	eyes absent (Drosophila) homolog 3	1.04	1.06	1.04
	408972 414477	AL050100 U41635	Hs.49378	DKFZP586D0919 protein	1.04	1.09	1.13
50	409327	L41162	Hs.76228 Hs.53563	amplified in osteosarcoma	1.03 1.03	1.11	1.03
50	435056	AW023337	Hs.5422	collagen, type IX, alpha 3 glycoprotein M6B	1.03	1.02 1.02	2.33 3.56
	415314	N88802	Hs.5422	glycoprotein M6B	1.02	1.02	4.02
	408591	AF015224	Hs.46452	mammaglobin 1	1.00	1.41	0.05
	401203			Target Exon	1.00	1.02	0.98
55	400304	AF005082	Hs.113261	Homo sapiens skin-specific protein (xp33	1.00	1.49	0.56
	407395	AF005082		gb:Homo sapiens skin-specific protein (x	1.00	1.69	0.91
	411388	X72925	Hs.69752	desmocollin 1	1.00	3.12	1.00
	428618	AA885360		Target CAT	1.00	1.77	1.00
60	402860			ENSP00000239210:DJ50O24.4 (novel protein	1.00	1.53	1.00
60	437211	AA382207	Hs.5509	ecotropic viral integration site 28	1.00	1.39	1.00
	409269	AA576953	Hs.22972	steroid 5 alpha-reductase 2-like; H5AR g	1.00	1.46	1.00
	409190 416143	AU076536 AI955650	Hs.50984	sarcoma amplified sequence	1.00 1.00	0.60	1.00
	401588	NI333030		glutaminyl-peptide cyclotransferase (glu C15000180°:gij544344[spjQ05859]FOR4_MOUS	1.00	1.96 2.04	1.00 1.00
65	419519	A1198719	Hs.176376	ESTs	1.00	1.91	1.00
•••	448816	AB033052	Hs.22151	KIAA1226 protein C	1.00	1.82	1.00
	440270	NM_015986	Hs.7120	cytokine receptor-like molecule 9	1.00	1.15	1.00
	418518	U66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dy	1.00	1.66	0.74
	422836	AL037365	Hs.194093	AKAP-binding sperm protein ropportn	1.00	2.21	1.00
70	452461	N78223	Hs.108106	transcription factor	1.00	1.61	1.00
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	1.00	1.42	1.00
	422420	<b>U03398</b>	Hs.1524	tumor necrosis factor (ligand) superfami	1.00	1.81	1.00
	429477	AI275514	Hs.6658	ESTs	1.00	1.67	1.00
75	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	1.00	1.05	1.00
75	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	1.00	1.79	1.00
	451993	AA765776	Hs.122983	ESTs	1.00	2.15	1.00
	416947	N23282	Hs.184341	ESTs, Weakly similar to 834087 hypotheti	1.00	1.67	1.00
	441606 442590	R37263 AI002686	Hs.21065	ESTs, Moderately similar to PC4259 femi ESTs	1.00	1.87	1.00
80	404831	WAS TOO	Hs.130313	C1002937*:gi]7499208[pirl]T20993 hypothe	1.00 1.00	2.59 1.44	1.00
	428454	U55936	Hs.184376	synaptosomal-associated protein, 23kD	1.00	1.47	1.00 1.00
	419717	H07970	Hs.92458	G protein-coupled receptor 19	1.00	1.78	1.00
	408611	NM_004367	Hs.46468	chemokine (C-C motif) receptor 6	1.00	1.64	1.00

	421666	AL035250	Hs.1408	endothelin 3	1.00	0.63	1.00	
	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y7	1.00	1.60	1.00	
	423899	NM_001427	Hs.134989	engrailed homolog 2	1.00	2.91	1.00	
	423130	AW897586	Hs.21213	ESTs	1.00	1.65	1.00	
5	433843	AW021423	Hs.112819	ESTs	1.00	2.08	1.00	
,	458574	AW384436	Hs.135265	Homo sapiens clone FLB8436 PRO2277 mRNA,	1.00	1.00	1.00	
				carbonic anhydrase XIV	1.00	1.41	1.00	
	430205	AB025904	Hs.235168		1.00	1.15	1.00	
	427335	AA448542	Hs.251677	Gantigen 78	1.00	1.80	1.00	
10	439951	AI347067	Hs.124636	ESTs	1.00	2.15	1.00	
10	420248	Al377191	Hs.44714	ESTs		2.35	1,00	
	446259	AA425204	Hs.334721	hypothetical protein FLJ 13391	1.00		1.00	
	447164	AF026941	Hs.17518	vipirin; similar to inflammatory respon	1.00	1.53		
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1.00	1.73	1.00	
	408758	NM_003686	Hs.47504	exonuclease 1	1.00	1.59	1.00	
15	453745	AA952989	Hs.63908	hypothetical protein MGC14726	1.00	1.73	1.00	
	436609	AI022514	Hs.131380	ESTs	1.00	1.96	1.00	
	419308	N40321		gb:yx80g07.r1 Soares melanocyte 2NbHM Ho	1.00	2.28	1.00	
	421650	AA781795	Hs.122587	ESTs	1.00	1.74	1.00	
	459578	AW612538	Hs.304491	EST	1.00	2.16	1.00	
20	446152	Al292036	16.501151	ESTs	1.00	1.66	1.00	
20			Hs.134014	ESTs, Wealty similar to T46425 hypotheti	1.00	2.04	1.00	
	449579	AW207260		lymphocyte antigen 64 (mouse) homolog (	1.00	1.75	1.00	
	418573	NM_005582	Hs.87205	ESTs, Weakly similar to GBP1_HUMAN INTER	1.00	1.85	1.00	
	415004	AA158925	Hs.240849	ES15, 498Billy Stitute to GOT 1_1000-14 INTER	1.00	1.92	1.00	
25	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfami	1.00	1.72	1.00	
25	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	1.00	1.52	1.00	
	417791	AW965339	Hs.44269	ESTs		2.02	1.00	
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	1.00		1.00	
	416445	AL043004	Hs.79337	KIAA0135 protein	1.00	1.28		
	408375	AI224520	Hs.40930	ESTs	1.00	1.92	. 1.00	
30	406964	M21305		FGENES predicted novel secreted protein	1.00	0.46	1.00	
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	1.00	1.00	2.48	
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob	0.98	0.98	3.24	
	422270	AF114494	Hs.114062	protein tyrosine phosphatase-like (proli	0.95	0.96	3.06	
	446488	AB037782	Hs.15119	KIAA1361 protein	0.94	0.96	1.61	
35	433435	BE545277	Hs.340959	Ts translation elongation factor, mitoch	0.94	0.94	0.76	
55	409402	AF208234	Hs.695	cystatin B (stefin B)	0.93	0.91	1.55	
	423942	AF209704	Hs.169407	glycolipid transfer protein	0.92	0.93	2.09	
		W20010	Hs.75823	ALL1-fused gene from chromosome 1q	0.91	0.91	4.08	
	414219			gap junction protein, beta 5 (connexin 3	0.90	0.81	0.73	
40	429211	AF052693	Hs.198249		0.90	0.92	3.89	
	417632	R20855	Hs.5422	glycoprotein M6B	0.89	0.79	0.84	
	449092	U91641		atpha 2.8-sialyltransferase	0.89	0.92	3.70	
	426716	NM_006379		sema domain, immunoglobulin domain (lg),	0.88	0.90	2.02	
	445033	AV652402	Hs.72901	cyclin-dependent kinase inhibitor 28 (p1			0.73	
	408349	BE546947	Hs.44276	homeo box C10	0.88	0.87		
45	429345	R11141	Hs.199695	hypothetical protein	0.85	0.84	0.69	
	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	0.84	0.85	1.32	
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	0.84	0.88	3.37	
	405885	_		Target Exon	0.81	0.71	1.00	
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	0.78	0.78	0.90	
50	417515	L24203	Hs.B2237	ataxia-telangiectasia group D-associated	0.77	0.73	0.71	,
• •	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	0.75	0.78	4.69	
	440274	R24595	Hs.7122	scrapie responsive protein 1	0.74	0.78	5.42	
	425071	NM_013989		deiodinase, iodothyronine, type II	0.70	0.75	4.29	
	412719	AW016610	Hs.816	ESTs	0.70	0.77	3.99	
55	432467	T03667	Hs.239388	Human DNA sequence from clone RP1-304B14	0.69	0.73	3.79	
"	437191	NM_006846		serine protease inhibitor, Kazal type, 5	0.65	0.64	1.11	
			Hs.6630	Homo sapiens cDNA FLJ 13329 fis, clone OV	0.61	0.65	3.20	
	452487	AW207659		folate receptor 1 (adult)	0.61	0.22	0.49	
	448133	AA723157	Hs.73769	Homo sapiens cDNA FLJ14471 fis, clone MA	0.49	0.30	0.67	
<b>60</b>	439659				0.41	0.11	0.34	
60	419092		Hs.89603	mucin 1, transmembrane	0.23	0.30	0.35	
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	0.25	0.00		
							•	
	TABLE							
	Pkey:		rique Eos probeset	identifier number				
65	CAT nu	mber: Ge	ene cluster number					
	Access	ion: G	enbank accession r	numbers				
	Pkey	CAT Numb	er Accession					
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35	406827 443086	0_0 25669_4	AA971409 BE896316 BG819393 AA187888 AW753122
	400261	23110_1	BC006097 X03066 NM_002120 M26040 AW469119 AW469127 AI299772 AW518149 AI144456 AW628070 AI629032 AI358810 AI880433 AI440472
	412315	1163860_1	A357070 A1865365 AW014799 A1767973 AW518041 AA909398 AW768606 AW936678 AW936821 AW936683 AW93682 AW936781 AW936817 AW936811 AW936653 AW936823 AW936685 AW936815 AW936637 AW936812
40		4273_16	AW936730 AW936762 AW936682 AW936732 AW796921 AW798102 AW805749 AW805872 BF985060 AW794380 BF380449 AW794466 AW794538
40	454478 459345	919706_1	AUGIE221E AUGIEA2E73
	400214	9255_1	AKS5329 BE897640 BE907077 BC003059 BC017245 BC010733 BM423383 AL537826 AL580324 BG749884 BE910412 BI085225 BG830374 BG765711 BE513420 BE513706 AW249005 BE378229 BE250756 BG389441 BF998736 H61321 BF869238 BG979991 H49658 AA353290 D64154
45			BM468130 AL549088 BI765497 AL556922 BI833272 BM009270 BI546248 BG750170 BG480128 AL561553 BI559389 BG762029 BG741197 BI561200 BI259044 AL523216 BG333073 Bi838073 BE790691 AV762878 BF972560 Bi260209 BI333058 BI090606 BG468883 BI598273 BI826098 BE622086
43			01759051 DG751116 DE005428 DG764482 A1522174 DG761428 DB36634 DG749048 DG774512 BE280653 BG480630 BG/10/20 BI/00030
			BG573991 BG389395 BF971754 BG680599 BE795075 BG324709 AA984290 BE304564 BG283813 BE252914 BF872431 BE407696 BE264894 AL552517 BF872428 BF724779 BE279635 BF804329 BE764960 BF811388 D31335 AW951318 BF992435 BF811453 NM_007002 AL518634
50			AL57493A AL523534 AL520445 AL521785 AL547001 AL558522 B1829145 B1862487 B1753281 BE258642 AL039594 BG015181 BE925165 BF872433 AJ904540 AJ904495 AA776741 AA317533 BG476628 R13328 BG489456 BF102495 BF693420 AL526597 BG104181 BG740214 BE393189 A986312
50			H61596 AW051180 BI668762 AW938619 BI086232 AA053472 BE264345
	406851 448498	0_0 20078_4	AAG09784 R97304 BG167206 AAG77283 AAG77217 A1703389 A1051577 A1912137 H39571 AAG50047 A1399738 H24807 AA341614 BG945259 A1074162 AW960920
	410130	20070_4	AA528934 AA659499 AA699617 H14450 H21758 H39576 AA095608 AI049973 BG054505 BG319545 AI742408 AA421324 AI580138 AI375883 AI374848 AI367657 AI374762 AI304678 AA007357 BF477168 AI373751 AA779885 AI801494 BE349021 AI220937 AW338397 AA253409 AA418327
55			AAB72682 AI572030 AI521517 AI572944 AI418670 AI266089 W72413 W76492 AI809207 AI915747 H22230 H21951 H08513 H25154
	416929 419250	14596_3 249447_1	BC017849 BC005892 N42993 BF691239 N42991 N29240 N40292 N33322 N33330 N20535 BC355C78 B1225090 N41827 AWADA160 RIDSR921 H11253 AA461274 R05714 H00515 B1086965 A1032786 B1089613 BM171783 A1127382 A1660953
	413230	243441_1	AW206271 AISR2200 AA460965 AI376115 AI016900 BG055846 AI023644 AA767046 AA815039 AW403510 AI858663 AA815462 AA235654 AW232253
60	424292	892193_1	AW959582 AV725205 AW959578 AA300091 W24933 R05715 AW770185 H00465 N93714 H11254 T49555 AW966308 AA339512 AA338432
	420223 428342	191648_1 6712_1	AVOSCO LA ANTIGERA AATOANTO RITTOSTO ALGOTTOR AWOQOSRO ALGORIAN ALGOTANA ALGOSOSO AA731340 BM469629 AW968804 AA425658 AA769094
	420042	0712_1	BF446026 AW118719 A1332755 AW500888 AW576556 A1859571 AW499664 AW614573 AW629495 AW505314 W74704 A1356361 A1923640 AW070509 A1521500 AL042095 AA609309 AA761319 A1381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 A1392620 Z40708
65			AW070509 A1521500 ALMXU95 AA6U3309 AA761319 A1361469 M3700 AA761353 AW263522 AG05352 AG05351 AG05360 A1521500 A A1985564 AW263513 AA913892 A1693486 AW263502 A1806164 AW291137 B1061872 B1059498 AA134476 AW084888 AA036967 AW370823 T55263
	407204	27110_2	Bi002756 AA489664 BF827261 W74741 BF963166 AF005081 BG193848
70	407394 428618		BC017008 RIBOKEA3 RC715704 RC722697 RI460787 RC773459 H52859 AI652853 AI990773 AW665193 AW340601 AA913806 AI337099 BE045942
70	416143	40539_2	AW57Z790 AW515652 H15004 AA909115 BI465310 BI462024 BI561578 BI463075 BG722527 R86003 BG623286 H15003 BI562131 BG435272 BG218868 AV705271 N34158 AL538368 BG186620 BG188697 BG181900 AIZ00440 BG033721 BF968528 BF792647 AW204688 AA922311 F02735
	.,		AW142041 BG217293 BE619664 BE465887 AA745605 A1278924 A1278546 A1280994 AA809678 AA282134 T08599 AA732436 T05478 F04402 AA262267 A1969523 N25559 A1760218 BG217318 BF893160
	419308	249928_1	N40321 AA236322 AA236215
75	446152 449092		AKRS627D AV706896 A1692935 A1681140 AW162481 AW087114 AW157019 A1689795 AW251085 AW205911 BF 438207 AW134945 BEU41668
	-14436		BF111425 U91641 NM_013305 BF968902 U55966 AU130750 BE174853 AU929731 AW161524 R43753 BE779688
	TABLE	49C:	
80	Pkey: Ref:		Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
			sequence of human chromosome 22' Dunham, et at. (1999) <u>Nature</u> 402:489-495.
	Strand		Indicates DNA strand from which exons were predicted.

	Nt_position:	: Ind	ficates nucleotide	positions of predicted exons.			
	Pkey	Ref	Strand	Nt_position			
_	402075	8117407	Plus	121907-122035,122804-122921,124019-12416			
5	405451	7622517	Minus	145949-146227			
	401747	9789572	Minus	118596-118816,119119-119244,119609-11976			
	401454	9185923	Minus	114559-114832			
	405545	1054740	Phrs	118677-118807,119091-119296,121626-12182			
10	401780	7249190	Minus Minus	28397-28617,28920-29045,29135-29296,2941 120428-120703			
10	403328 405547	8469085 1054740	Plus	124361-124520,124914-125050			
	403532	8076842	Minus	81750-81901			
	400750	8119067	Plus	198991-199168,199316-199548			
	405506	6466489	Plus	80014-80401,80593-81125			
15	400533	6981826	Minus	277132-277595			
	405779	7280331	Minus	33048-33856			
	402994	2996643	Minus	4727-4969			
	401781 401994	7249190 4153858	Minus Minus	83215-83435,83531-83656,83740-83901,8423 42904-43124,43211-43336,44607-44763,4519			
20	403969	8569909	Plus	31237-31375,32405-32506			
	401760	9929699	Plus	83126-83250,85320-85540,94719-95287			
	401797	6730720	Plus	6973-7118			
	401151	9438288	Ptus	30848-31228			
26	404872	9650523	Minus	18540-18718			
25	402876	9864669	Plus	5679-6027,7485-7584			
	405204 402294	7230116 2282012	Ptus Minus	126569-126754 2575-3000			
	400991	8096825	Plus	159197-159320			
	401284	9800819	Minus	101307-101421			•
30	402474	7547175	Minus	53526-53628,55755-55920,57530-57757			
	403022	3132351	Plus	92097-92864			
	402542	9801558	Minus	67076-67594			
	403409 403506	9438598 7596863	Plus Plus	6860-7054,12573-12771 105008-105650			
35	406016	8272661	Ptus	41341-41940			
	405268	4156151	Minus	24404-24521			
	401106	8568931	Plus	122694-122893			
	404186	4481839	Ptus	829-1110			
40	403817 406422	8962065 9256411	Plus Plus	110297-111052 163003-163311			
40	402160	8516165	Plus	166063-166354			
	402622	9930984	Minus	129861-130099			
	401558	7139678	Plus	103510-104090			
40	404960	7408010	Minus	146186-146377,147747-147943			
45	401203	9743387	Minus	172961-173056,173868-173928			
	402860 401588	9588237 7230871	Minus Plus	76423-76560 46412-46561			
	404831	6624702	Minus	16833-17020,20007-20120,21605-21799,2333			
	405885	7677703	Minus	42574-42998			
50							<i>t</i>
55	Table 50/ Eos/Affyr	A fists about netrix Hu03 ( evel of mRN/	398 genes upreg Genechip array. A expression. Unique Eos probi	REGULATED IN PRIMARY MELANOMAS OR MELANO ulated in primary melanoma or melanoma metastases re Gene expression data for each probeset obtained from the eset identifier number ion number, Genbank accession number	lative to benign nevi.	Genes wer	re selected from 59680 probesets on the
	Unigene	Tite:	Unigene gene tit	e			
60	R1:		70th percentile of	primary melanoma and melanoma metastasis Als divide primary melanoma and melanoma metastasis Als divide	d by the maximum Al	of benign (	NEVI.
	R2:			rom both the numerator and denominator	o by the meaning re	or occurgin	tion, whose are root personal or normal accounts
					•		
65	Pkey	ExAccn	Unigenell		R1 13.		R2 16.82
U.S	422424	A118643		8 prostate differentiation factor secreted phosphoprolain 1 (osteopontin,	11.		11.84
	446619 407846	AU07664 AA42620			9.3		7.59
	444381	BE3873			8.6		7.90
	417880	BE24159			8.2	21	4.09
70	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	7.1		6.10
	447210	AF03526			6.7		6.26
	417693	AW9597			6.5		6.36
	429500	X78565	Hs.28911		6.4 6.4		7.11 7.51
75	414812 451736	X72755 AW0803	Hs.77367 156 Hs.23889				4.28
,,	418870	AF1472			6.3		4.32
	428291	AA5340			6.0	03	4.52
	417308	H60720	Hs.81892	KIAA0101 gene product	6.0		6.78
90	448569				5.9		7.51
80	439310				5.5	95 95	4.79 5.55
	452838 422241	U65011 Y00062				33 76	4.82
	442379					76	2.19
		-					

	409274	NM_003930	Hs.52644		SKAP55 homologue	5.65	4.63
	442739	NM_007274	Hs.8679		cytosolic acyl coenzyme A thioester hydr	5.58	3.41
	442711	AF151073	Hs.8645		hypothetical protein	5.45	5.79
5	425118	AU076611	Hs.154672		methylene tetrahydrofolate dehydrogenase	5.42	5.56
,	412918	BE563957	11- 400000		activated RNA polymerase II transcriptio	5.35	4.31
	428125 446921	AA393071	Hs. 182579		leucine aminopeptidase	5.33	4.83
	431183	AB012113 NM_006855	Hs.16530 Hs.250696		smail inducible cytokine subfamily A (Cy KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	5.33 5.30	5.13 · 6.27
	414219	W20010	Hs.75823		ALL1-fused gene from chromosome 1q	5.30 5.16	5.13
10	426600	NM_003378	Hs.171014		VGF nerve growth factor inducible	5.05	13.72
	415444	BE247295	Hs.78452		solute carrier family 20 (phosphate tran	5.03	4.93
	436701	AW959032			ESTs, Moderately similar to 178885 serin	5.03	3.42
	406648	AA563730	Hs.277477		major histocompatibility complex, class	4.99	3.36
16	410850	AW362867	Hs.302738		Homo sapiens cDNA: FLJ21425 fis, clone C	4.98	5.30
15	418299	AA279530	Hs.83968		integrin, beta 2 (antigen CD18 (p95), ly	4.98	4.85
	432469	AL080084			CGI-100 protein	4.97	4.46
	404854	MIL 003030	Hs.78619		Target Exon	4.85	3.49
	415701 425397	NM_003878 J04088	Hs. 156346		gamma-glutamyl hydrolase (conjugase, fol	4.82	4.5)
20	408958	T99607	Hs.49346		topoisomerase (DNA) II alpha (170kD) signal recognition particle 54kD	4.81 4.78	5.26 2.34
20	453949	AU077146	Hs.36927		heat shock 105kD	4.78	5.18
	458079	AI796870	Hs.54277		DNA segment on chromosome X (unique) 992	4.77	4.13
	440245	AK001913	Hs.7100		hypothetical protein	4.74	3.32
~ -	412228	AW503785	Hs.73792		complement component (3d/Epstein Barr vi	4.74	1.55
25	417834	BE172058	Hs.82689		tumor rejection antigen (gp96) 1	4.73	4.25
	451003	AF058696	Hs.25812		Nijmegen breakage syndrome 1 (nibrin)	4.67	4.69
	424571	BE379766			polymerase (RNA) II (DNA directed) polyp	4.62	3.02
	434203	8E262677	Hs.283558		hypothetical protein PRO1855	4.61	5.45
30	452268	NM_003512	Hs.28777		H2A histone family, member L	4.60	2.68
20	421311 410491	N71848 AA465131	Hs.283609 Hs.64001		hypothetical protein PRO2032	4.60 4.60	3.24
	425706	AW406678	Hs.122559		Homo sapiens clone 25218 mRNA sequence hypothetical protein FLJ22570	4.59	4.34 3.58
	450293	N35754	Hs.171118		hypothetical protein FLI00026	4.57	3.82
	406836	AW514501	Hs.156110		immunoglobulin kappa constant	4.57	9.27
35	413441	AI929374	Hs.75367		Src-like-adapter	4.53	3.60
	431129	AL137751	Hs.263671		Homo sapiens mRNA; cDNA DKFZp434I0812 (f	4.48	4.89
	418506	AA084248	Hs.85339		G protein-coupled receptor 39	4.47	3.72
	411060	NM_006074	Hs.318501		Homo sapiens mRNA full length insert cDN	4.47	3.96
40	417501	AL041219	Hs.82222		sema domain, immunoglobulin domain (lg),	4.45	2.40
40	437763	AA469369	Hs.5831		tissue inhibitor of metalloproteinase 1	4.43	4.27
	448883	BE614989	Hs.7503		hypothetical protein FLJ14153	4.42	3.91
	417274 419285	N92036 D31687	Hs.81848		RAD21 (S. pombe) homolog	4.41	3.80
	418321	063477	Hs.89868 Hs.84087		KIAA0062 protein	4.40	3.20
45	430154	AW583058	Hs.234726		KIAA0143 protein serine (or cysteine) proteinase inhibito	4.38 4.37	2.79 3.86
	428450	NM_014791	Hs.184339		KIAA0175 gene product	4.36	4.65
	428297	AA236291	Hs.183583		serine (or cysteine) proteinase inhibito	4.36	3.42
	447232	AW499834	Hs.327		interleukin 10 receptor, alpha	4.36	3.31
50	409598	NM_014018	Hs.55097		mitochondrial ribosomal protein S28	4.35	3.10
50	442432	BE093589	Hs.38178		hypothetical protein FLJ23468	4.34	5.61
	407047	X65965			gb:H.sapiens SOD-2 gene for manganese su	4.33	3.31
	443991	NM_002250	Hs.10082		potassium intermediate/small conductance	4.33	3.57
	452322 420991	BE566343 AW504814	Hs.28988 Hs.287379		glutaredoxin (thioltransferase)	4.32	2.20
55	449722	BE280074	Hs.23960		Homo sapiens mRNA for FLJ00111 protein, cyclin B1	4.32 4.31	3.60 5.79
	408380	AF123050	Hs.44532		diubiquitin	4.30	3.62
	427127	AW802282	Hs.22265		pyruvate dehydrogenase phosphatase	4.28	4.18
	417933	X02308	Hs.82962		thymidylate synthetase	4.28	5.06
<b>CO</b>	432828	AB042326	Hs.287402		chondroitin 4-sulfotransferase	4.25	4.15
60	450306	AL080080	Hs.24766		thioredoxin domain-containing	4.24	3.15
	440266	AA088809	Hs.19525		hypothetical protein FLJ22794	4.23	3.65
	407951	W77762	Hs.79015		antigen identified by monoclonal antibod	4.22	4.21
	427337 408989	Z46223 AW361666	Hs.176663 Hs.49500		Fc fragment of IgG, low affinity IIIb, r	4.20	4.11
65	449626	AA774247	Hs.301637		KIAA0746 protein	4.20 4.19	4.26 2.65
05	422846	BE513934	Hs.1583		zinc finger protein 258 neutrophil cytosolic factor 1 (47kD, dC		
	415726	T89844	Hs.78712		aminolevulinate, delta-, synthase 1	4.18 4.16	6.80 4.28
	444207	A1565004			cathepsin D (lysosomal aspartyl protease	4.16	1.89
	416980	AA381133	Hs.80684		high-mobility group (nonhistone chromoso	4.14	3.32
70	438718	AL040058	Hs.6375		uncharacterized hypothalamus protein HTO	4.14	3.02
	437802	AI475995	Hs.122910		ESTs	4.12	4.18
	446392	AF142419	Hs.15020		homolog of mouse quaking QKI (KH domain	4.12	3.87
	409461	AA382169	Hs.54483		N-myc (and STAT) interactor	4.11	3.80
75	427247	AW504221	Hs.174103		integrin, alpha L (antigen CD11A (p180),	4.11	5.71
13	414359	M62194	Hs.75929		cadherin 11, type 2, OB-cadherin (osteob	4.10	4.25
	450071 452882	AA018283 AW972990	Hs.24359 Hs.196270		Homo sapiens cONA FLJ11174 fis, clone PL	4.10	2.91
	414522	AW518944	Hs.76325		folate transporter/carrier Immunoglobulin J chain	4.10 4.09	4.25 3.99
	407756	AA116021	Hs.38260		ubiquitin specific protease 18	4.09	4.60
80	405506				Target Exon	4.08	3.64
	444677	AL110212	Hs.301005		purine-rich eternent binding protein B	4.07	2.43
	417497	AW402482	Hs.82212		CD53 antigen	4.07	6.55
	413715	AW851121	Hs.75497	•	Homo sapiens cDNA: FLJ22139 fis, clone H	4.06	3.27

	421508 408688	NM_004833 A1634522	Hs.105115 Hs.152925	absent in melanoma 2	4.05	4.39
	439453	BE264974	Hs.6566	KIAA1268 protein thyroid hormone receptor interactor 13	. 4.05 4.04	3.32 3.53
_	445701	AF055581	Hs.13131	lymphocyte adaptor protein	4.02	4.20
5	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A figase, long-chain	4.01	3.96
	449291 443071	BE176893 AL080021	Hs.23440 Hs.8986	KIAA1105 protein	4.01	2.34
	417615	BE548641	Hs.82314	complement component 1, q subcomponent, hypoxanthine phosphoribosyltransferase 1	4.00 3.99	6.97 4.27
••	408246	N55669	Hs.333823	mitochondrial ribosomal protein L13	3.98	3.66
10	408819	AW1634B3	Hs.48320	doubte ring-finger protein, Dorfin	3.98	3.76
	424058 418942	AL121516	Hs.138617 Hs.141269	thyroid hormone receptor interactor 12	3.97	2.38
	424756	AJ566004 AW504657	Hs.152931	Horno sapiens cDNA: FLJ21550 fis, clone C tamin B receptor	3.97 3.93	3.40 2.67
	421958	AA357185	Hs.109918	ras homolog gene family, member H	3.89	2.39
15	440692	AL031591	Hs.7370	phosphotidytinositol transfer protein, b	3.88	3.23
	433001 418255	AF217513 AW135405	Hs.279905 Hs.37251	dane H00310 PR00310p1 ESTs	3.88	4.24 2.53
	444371	BE540274	Hs.239	forkhead box M1	3.87 3.86	4.29
	450515	AW304226		biphenyl hydrolase-like (serine hydrolas	3.85	3.73
20	416114	AI695549	Hs.183868	glucuronidase, beta	3.65	3.74
	440598 417020	H13032 T78413	Hs.103378	hypothetical protein MGC11034 heterogeneous nuclear ribonucleoprotein	3.84 3.82	1.90 2.04
	448503	BE243146	Hs.21332	BTB (POZ) domain containing 1	3.81	3.07
25	446506	Al123118	Hs.15159	chemokine-like factor, alternatively spl	3.81	3.69
25	417059	AL037672	Hs.81071	extracellular matrix protein 1	3.80	6.01
	410668 420107	BE379794 AL043980	Hs.159651 Hs.7886	hypothetical protein pellino (Drosophila) homolog 1	3.80 3.79	5.22 3.93
	446071	N51527	Hs.13659	hypothetical protein DKFZo586F2423	3.79	2.74
20	419731	S47242	Hs.92909	SON DNA binding protein	3.77	1.85
30	443710	AI928136	Hs.9691	Homo sapiens cDNA: FLJ23249 fis, clone C	3.77	4.98
	406837 436481	R70292 AA379597	Hs.156110 Hs.5199	immunoglobulin kappa constant HSPC150 protein similar to ubiquitin-con	3.77 3.76	7.42 3.55
	419381	AB023420	Hs.90093	heat shock 70kD protein 4	3.76	3.81
26	423979	AF229181	Hs.136644	CS box-containing WD protein	3.76	3.97
35	402474	41 122200	14- 74004	NM_004079:Homo sapiens cathepsin S (CTSS	3.76	4.01
	412828 454080	AL133396 Al199711	Hs.74621 Hs.576	prion protein (p27-30) (Creutzfeld-Jakob fucosidase, alpha-L- 1, tissue	3.75 3.74	3.77 6.15
	408085	N25929	Hs.342849	ADP-ribosylation factor-like 5	3.74	2.92
40	426096	D87436	Hs.166318	lipin 2	3.72	2.98
40	417105 418322	X60992	Hs.81226	CD6 antigen	3.72	2.78
	447735	AA284166 AA775268	Hs.84113 Hs.6127	cyclin-dependent kinase inhibitor 3 (CDK Homo sapiens cDNA: FLJ23020 fis, clone L	3.72 3.70	3.37 4.09
	409264	NM_014937	Hs.52463	KIAA0966 protein	3.69	4.79
45	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	3.69	2.94
43	428398 423494	AI249368 AW504365	Hs.98558 Hs.24143	ESTs Wirkett Aldrich gradenma gestein interna	3.68	3.82
	413235	BE243445	Hs.75248	Wiskoti-Aldrich syndrome protein interac lopoisomerase (DNA) II beta (180kD)	3.67 3.67	3.52 2.79
	423712	W46802	Hs.81988	disabled (Drosophila) hornolog 2 (mitogen	3.66	3.42
50	409703	NM_006187	Hs.56009	Z-5-oligoadenylate synthetase 3 (100 k	3.66	6.44
20	447225 414829	R62676 AA321568	Hs.17820 Hs.77436	Rho-associated, coiled-coil containing p pleckstrin	3.65 3.65	2.93 2.30
	400219	74021000	113.11400	Eas Control	3.64	2.76
	437239	AW503395	Hs.5541	ATPase, Ca transporting, ubiquitous	3.63	2.73
55	422445	M23114	Hs.1526	ATPase, Ca transporting, cardiac muscle,	3.52	3.60
"	449971 424460	AA807346 BE275979	Hs.288581 Hs.296014	Homo sapiens cDNA FLJ14296 fis, clone PL polymerase (RNA) II (DNA directed) polyp	3.62 3.62	3.62 3.06
	427609	AK000436	Hs.179791	hypothetical protein FLJ20429	3.62	2.31
	400750			Target Exon	3.61	2.74
60	424541 427051	AW392551 BE178110	Hs.180559 Hs.173374	ESTs, Weakly similar to A56194 thromboxa	3.61	2.25
00	433867	AK000596	Hs.3618	Homo sapiens cDNA FLJ10500 fis, clone NT hippocatcin-like 1	3.60 3.59	4.20 4.19
	421986	AL137438	Hs.110454	SEC15 (S. cerevisiae)-like	3.59	1.58
	414841	H55601	Hs.77490	glutathione S-transferase theta 1	3.58	1.00
65	429693 425204	BE254962 NM_002436	Hs.211612 Hs.1861	SEC24 (S. cerevisiae) related gene famil membrane protein, palmitoylated 1 (55kD)	3.57 3.56	3.00 3.09
	441669	R78195	Hs.29692	Homo sapiens cDNA FLJ11436 fis, clone HE	3.56	3.26
	442043	BE567620	Hs.99210	ESTs	3.55	3.56
	406636	L12064		gb:Homo sapiens (clone WR4.12VL) enti-th	3.55	3.83
70	445341 432485	AL040763 N90866	Hs.310735 Hs.276770	ESTs, Moderately similar to ALU7_HUMAN A CDW52 antigen (CAMPATH-1 antigen)	3.54 3.54	3.52 4.66
. •	422765	AW409701	Hs.1578	baculoviral IAP repeal-containing 5 (sur	3.54	3.25
	412630	AA738437	Hs.26226	Homo sapiens cDNA: FLJ21286 fis, clone C	3.54	1.87
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	3.53	3.96
75	425177 426643	AF127577 AA857131	Hs.155017 Hs.171595	nuclear receptor interacting protein 1 HIV TAT specific factor 1	3.53 3.51	3.40 2.21
-	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TiT3 co	3.51	2.51
	429248	U96759	Hs.198307	von Hippel-Lindau binding protein 1	3.51	2.85
	452852 451791	AK001972 278407	Hs.30822	hypothetical protein FLJ11110	3.51	2.71
80	418310	AA814100	Hs.27023 Hs.86693	vesicle transport-related protein ESTs	3.49 3.49	2.91 1.45
_	406868	AA505445	Hs.300597	immunoglobulin heavy constant gamma 3 (G	3.48	6.81
	400200	A1005045	14- 40-202	NM_002788*:Homo sapiens proteasome (pros	3.48	2.51
	438746	AI885815	Hs.184727	Human melanoma-associated antigen p97 (m	3.47	6.94

	44546	AB023169	Hs.7935	KIAA0952 protein	3.47	3.38
	441646 427968	AI857607	Hs.181301	cathepsin S	3.45	2.71
	440201	AL359588	Hs.7041	hypothetical protein DKFZp7628226	3.45	3.45
-	434608	AAB05443	Hs.179909	hypothetical protein FLJ22995	3.44 3.44	3.68 6.70
5	427527	AI809057	Hs.153261	immunoglobulin heavy constant mu indoleamine-pyrrole 2,3 dioxygenase	3.44	2.72
	413385 435550	M34455 A1224456	Hs.840 Hs.324507	H.sapiens polyA site DNA	3.43	2.76
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	3.43	3.64
	423392	AA195037	Hs.169341	HTPAP protein	3.43	2.29
10	418460	M26315	Hs.85258	CD8 antigen, atpha polypeptide (p32)	3.43 3.41	2.78 3.06
	453915	AA588721	Hs.286218	ribosomal protein L44 hypothelical protein FLJ13187	3.41	4.23
	442485 432606	BE092285 NM_002104	Hs.29724 Hs.3066	granzyme K (serine protease, granzyme 3;	3.40	3.93
	417410	AF063020	Hs.82110	PC4 and SFRS1 interacting protein 1	3.40	2.12
15	436810	AA353044	Hs.5321	ARP3 (actin-related protein 3, yeast) ho	3.40	4.70
	422545	X02761	Hs.287820	fibronectin 1	3.39 3.36	7.58 4.12
	409142	AL136877 AF155661	Hs.50758 Hs.22265	SMC4 (structural maintenance of chromoso pyruvate dehydrogenase phosphatase	3.34	5.05
	434826 448410	AK000227	Hs.21126	hypothetical protein FLJ20220	3.33	4.31
20	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.33	4.60
	432642	BE297635	Hs.3069	heat shock 70kD protein 98 (mortalin-2)	3.32 3.24	4.49 4.22
	425234	AW152225	Hs.165909	ESTs, Wealthy similar to 138022 hypotheti	3.23	12.31
	443623 426490	AA345519 NM_001621	Hs.9641 Hs.170087	complement component 1, q subcomponent, aryl hydrocarbon receptor	3.23	5.07
25	443958	BE241880	Hs.10029	cathepsin C	3.16	4.97
	412577	Z22968	Hs.74076	CD163 antigen	3.14	4.75
	414050	NM_004766	Hs.75724	coatomer protein complex, subunit beta 2	3.13 3.12	4.00 4.45
	421633	AF121860	Hs.106260	sorting nexin 10 serine (or cysteine) proteinase inhibito	3.11	4.00
30	413936 428797	AF113676 AA496205	Hs.297681 Hs.193700	Homo sapiens mRNA; cDNA DKFZp58610324 (f	3.10	4.03
50	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	3.06	4.49
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	3.04	4.98
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	3.03 3.01	4.49 4.75
35	452139	AA099969 AW408158	Hs.16331 Hs.318893	Horno sapiens cDNA: FLJ21482 fis, clone C ESTs, Wealdy similar to A47582 B-cell gr	2.95	5.55
. 33	439237 422684	BE561617	Hs.119192	H2A histone family, member Z	2.94	4.64
	406782	AA430373	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	gb:zw20f11.s1 Soares ovary tumor NbHOT H	2.93	10.28
	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	2.91	5.40 4.86
40	450455	AL117424	Hs.25035	chloride intracellular channel 4 minichromosome maintenance deficient (S.	2.90 2.89	4.04
40	427528 422530	AU077143 AW972300	Hs.179565 Hs.118110	bone marrow stromal cell antigen 2	2.87	9.61
	423605	AF047826	Hs.129887	cadherin 19, type 2	2.83	4.86
	410231	AA314163	Hs.61153	proteasome (prosome, macropain) 26S subu	2.82	5.02
45	419956	AL137939	Hs.40096	cadherin 19, type 2	2.80 2.79	4.30 5.80
45	416511	NM_006762	! Hs.79356 Hs.2488	Lysosomal-associated multispanning membr tymphocyte cytosolic protein 2 (SH2 doma	2.78	4.21
	429732 448517	U20158 AA082750	Hs.42194	hypothetical protein FLJ22649 similar to	2.78	4.23
	416784	AA334592	Hs.79914	tumican	2.78	4.40
50	427792	M63928	Hs.180841	tumor necrosis factor receptor superfami	2.77 2.77	4.23 4.17
50	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines ras-related C3 botulinum toxin substrate	2.76	4.43
	427080 446272	AW068287 BE268912	Hs.301175 Hs.14601	hematopoietic cell-specific Lyn substrat	2.75	4.20
	437179	AA393508		serologically defined colon cancer antig	2.74	4.07
	429402	AF116571	Hs.201671	SRY (sex determining region Y)-box 13	2.72 2.71	4.63 4.93
55	421360	AA297012	Hs.103839	erythrocyte membrane protein band 4.1-li hexosaminidase B (beta polypeptide)	2.68	4.15
	409202 426124		Hs.51043 Hs.250697	phosphatidylinositol glycan, class F	2.68	4.00
	422672		Hs.119129	collagen, type IV, alpha 1	2.67	4.72
	417389		Hs.82045	midkine (neurite growth-promoting factor	2.65 2.65	7.77 4,47
60	409415		Hs.6083 Hs.42915	Homo sapiens cDNA: FLJ21028 fis, clone C ARP2 (actin-related protein 2, yeast) ho	2.64	5.61
	410341 433027		Hs.279923	putative nucleotide binding protein, est	2.63	4.34
	424687		Hs.151738	matrix metalloproleinase 9 (gelatinase 8	2.62	4.95
	409430	R21945	Hs.346735	splicing factor, arginine/serine-rich 5	2.60 2.60	6.00 4.27
65	424779		Hs.153053	CD37 antigen Homo sagiens cONA: FLJ22224 fis, clone H	2.60	4.64
	409354 427550		Hs.159472 Hs.311609	nuclear RNA helicase, DECD variant of DE	2.57	4.27
	426143			proteasome (prosome, macropain) subunit,	2.56	4.20
	421563			granutysin	2.56	4.13
70	425593			proteoglycan 1, secretory granule	2.55 2.54	5.46 5.78
	428169		Hs.182793 Hs.223014	golgi phosphoprotein 2 antizyme inhibitor	2.50	5.15
	429800 407241		IIS.223014	gb:Human omega light chain protein 14.1	2.50	4.98
	42173		Hs.107526	UDP-Gal:betaGicNAc beta 1,4- galactosyll	2.45	5.58
75	412819	9 T25829	Hs.24048	FK506 binding protein precursor	2.45 2.44	7.20 4.11
	41202		Hs.24143	Wiskott-Aldrich syndrome protein interac membrane-spanning 4-domains, subfamily A	2.44	4.11
	43552 44535		Hs.11090 Hs.12540	hysophospholipase I	2.44	5.44
	44929			Homo sapiens cDNA: FLJ23015 fis, clone L.	2.41	4.31
80	44006	5 W03476	Hs.266331	hypothetical protein MGC4595	2.41	4.25
	40022			Eos Control	2.39 2.39	5.68 6.62
	42265 43162			homolog of yeast long chain polyunsatura interferon, alpha-inducible protein (clo	2.38	7.22

	414622	AI752666	Hs.76669	nicotinamide N-methyltransferase	2.38	5.21
	415149 435099	X12451	Hs.78056	cathepsin L	2.37 2.37	7.71
	427407	AC004770 BE268649	Hs.4756 Hs.177766	flap structure-specific endonuclease 1 ADP-ribosyttransferase (NAD; poly (ADP-r	2.31	5.68 4.89
5	426432	AF001601	Hs.169857	paraoxonase 2	2.29	4.83
	430555	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE	2.27	5.03
	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	2.25	4.14
	412617 447547	AK001364 NM_007229	Hs.808 Hs.18842	heterogeneous nuclear ribonucleoprotein	2.21 2.19	4.31 4.62
10	416232	AW502678	Hs.79090	protein kinase C and casein kinase subst exportin 1 (CRM1, yeast, homolog)	2.18	4.84
- •	420842	AI083668	Hs.50601	hypothetical protein MGC10986	2.14	4.22
	411358	R47479	Hs.94761	KIAA1691 protein	2.13	4.65
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	2.13	4.03
15	406687 417331	M31126 AW411297	Hs.81972	matrix metalloproteinase 11 (stromelysin	21i 211	4.16 4.25
13	450344	AW994032	Hs.8768	SHC (Src homology 2 domain-containing) t hypothetical protein FLJ10849	211	4.09
	429642	X68264	Hs.211579	melanoma cell adhesion molecule (MCAM) (	2.11	5.42
	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	2.10	6.42
20	418613	AA744529	Hs.86575	mitogen-activated protein kinase kinase	2.10	4.00
20	453352 409220	T10446 BE243323	Hs.51233	ESTs	2.09 2.09	4.48 4.98
	414045	NM_002951	Hs.75722	tumor necrosis factor receptor superfami ribophorin ()	2.07	4.59
	422451	AA310753	Hs.42491	ESTs, Wealdy similar to S65657 alpha-1C-	2.07	4.09
25	414085	AA114016	Hs.75746	addehyde dehydrogenase 1 family, member	2.06	5.06
25	452363	AI582743	Hs.94953	Homo sapiens, Similar to complement comp	2.04	11.17
	438393 413313	AA351815 NM_002047	Hs.50740 Hs.283108	Homo sapiens cDNA: FLJ22272 fis, clone H glycyl-IRNA synthelase	2.03 2.02	4.36 4.79
	412994	032257	Hs.75113	general transcription factor IIIA	2.00	4.67
20	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	1.98	4.79
30	421897	AW583693	Hs.109253	N-terminal acetyltransferase complex ard	1.98	4.17
	442159 429451	AW163390	Hs.278554	heterochromatin-like protein 1	1.95	7.53
	416967	BE409861 BE616731	Hs.202833 Hs.80645	heme oxygenase (decycling) 1 Interferon regulatory factor 1	1.95 1.95	4.63 4.31
	400203	02010101	113.00013	Eos Control	1,94	5.03
35	437317	AA748613	Hs.311977	ESTs, Highly similar to SWVSNF related,	1.94	4.03
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.93	4.68
	416224	NM_002902	Hs.79088	reticulocalbin 2, EF-hand calcium bindin	1.92	4.12 4.23
	445411 413945	AL137255 NM_000591	Hs.12646 Hs.75627	hypothetical protein FLJ22693 CD14 antigen	1.91 1.90	5.00
40	413317	U53225	Hs.75283	sorting nexin 1	1.89	4.20
	448719	AA033527	Hs.21858	trinucleotide repeat containing 3	1.89	4.26
	430838	N46664	Hs.169395	hypothetical protein FLJ12015	1.88	4.15
	427239 450440	BE270447 AB024334	Hs.25001	ubiquitin carrier protein	1.87 1.87	5.72 5.81
45	433671	AW138797	Hs.132906	tyrosine 3-monooxygenase/tryptophan 5-mo 19A24 protein	1.85	4.27
	413190	AA151802	Hs.40368	adaptor-related protein complex 1, sigma	1.85	5.19
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	1.85	4.31
	430040	AW503115	Hs.227823	pM5 protein	1.83	5.57
50	417929 414570	R27219 Y00285	Hs.74647 Hs.76473	Human T-cell receptor active alpha-chain insulin-like growth factor 2 receptor	1,82 1,81	4.29 4.39
•	414416	AW409985	Hs.76084	hypothetical protein MGC2721	1.80	4.20
	428977	AK001404	Hs.194698	cyclin B2	1.79	4.17
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	1.78	4.30
55	425367 425811	BE271188 AL039104	Hs.155975 Hs.159557	protein tyrosine phosphatase, receptor t	1.78 1.77	5.44 5.11
33	422009	A1742845	Hs.110713	karyopherin alpha 2 (RAG cohort 1, impor DEK oncogene (DNA binding)	1.77	4.37
	424909	S78187	Hs.153752	cell division cycle 258	1.74	5.00
	409154	U72882	Hs.50842	interferon-induced protein 35	1.74	4.85
60	413892	AI878921	Hs.75607	myristoylated alanine-rich protein kinas	1.73	4.37
00	444954 424263	AW247076 M77640	Hs.12163 Hs.1757	eukaryotic translation initiation factor L1 cell adhesion molecule (hydrocephalus	1,71 1,70	5.02 4.68
	424825	AF207069	Hs.153357	procollagen-lysine, 2-oxoglutarate 5-dio	1.70	4.59
	427378	BE515037	Hs.177556	melanoma antigen, family D, 1	1.67	5.59
65	413322	AA380158	Hs.75290	ADP-ribosylation factor 4	1.67	4.39
03	442414	BE408758	Hs.8297	ribonuclease 6 precursor	1.65	4.03
	410129 422976	BE244074 AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e	1.64 1.64	4.24 4.91
	443051	AA333660	Hs.71331	hypothetical protein MGC5350	1.64	4.08
70	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	1.63	4,41
70	446143	BE245342	Hs.306079	sec61 homolog	1.62	4.70
	431142 407752	AA852596 AA573581	Hs.250641 Hs.13328	tropomyosin 4 ESTs	1.62 1.62	4.86 4.19
	416322	BE019494	Hs.79217	pyrrofine-5-carboxylate reductase 1	1.61	4.51
7.	414572	AU077174	Hs.288181	cathepsin H	1.50	5.25
75	415017	F06434	Hs.77805	ATPase, H transporting, lysosomal (vacuo	1.60	4.56
	452056	AW955065	Hs.101150	Homo sapiens, clone IMAGE:4054156, mRNA,	1.58	5.46
	413976 414420	BE295452 AA043424	Hs.75655 Hs.76095	procollagen-proline, 2-oxoglutarate 4-di immediate early response 3	1.58 1.58	4.05 4.00
	419638	N46504	Hs.91747	profilin 2	1.57	5.57
80	422624	BE616678	Hs.76152	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	1.57	4.44
	415819	AU077330	14. 04	transcription elongation factor A (SII).	1.55	4.89
	439627 425243	BE621702 N89487	Hs.29076 Hs.155291	hypothetical protein FLJ21841 KIAA0005 gene product	1.55 1.54	6.66 4.38
	CFACAF		(15.153251	rovadous gens product	1.54	4.30
				F97		

	424799	BE550723	Hs.153179	fatty acid binding protein 5 (psoriasis-	1.53	4.22	
	416971	R34657	Hs.80658	uncoupling protein 2 (mitochondriat, pro	1.53	7.41	
	426059	BE292842	Hs.166120	interferon regulatory factor 7	1.51	4.12	
_	418879	AW162087	Hs.5437	Tax1 (human T-cell leukemia virus type I	1.50	4.02	
5	432999	BE294029	Hs.279903	Ras homolog enriched in brain 2	1.50	4.18	
	415661	AF057307	Hs.78575	prosaposin (variant Gaucher disease and	1.49	4.19	
	428098 452264	AU077258	Hs.182429	protein disuffide isomerase-related prot transmembrane 9 superfamily member 2	1.49 1.48	5.74 4.53	
	415198	AU077013 AW009480	Hs.28757 Hs.943	natural killer cell transcript 4	1.47	4.95	
10	411794	AL118577	Hs.75658	phosphorylase, glycogen; brain	1.45	4.61	
10	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (HV	1.45	4.15	
	421416	BE302950	Hs.104125	adenylyl cyclase-associated protein	1.42	4.67	
	415089	N25117	Hs.299465	ribosomal protein S26	1.41	5.19	
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.41	4.03	
15	400202			NM_002795°:Homo sapiens proteasome (pros	1.41	4.44	
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.41	4.57	
	412968	AW500508	Hs.75102	alanyl-IRNA synthetase	1.40	4.25	
	440704	M69241	Hs.162	insufin-like growth factor binding prote	1.39	4.11	
20	447099	AB030656	Hs.17377	coronin, actin-binding protein, 1C	1.39	4.51	
20	428511	AA019912	Hs.184693	transcription elongation factor 8 (SIII)	1.38	4.90	
	413825 441737	BE299181	Hs.75564	CD151 antigen	1.37 1.36	4.44 4.29	
	440087	X79449 W28969	Hs.7957 Hs.7718	adenosine deaminase, RNA-specific hypothetical protein FLJ22678	1.36	4.29	
	413566	AW604451	Hs.285814	sprouty (Dresophila) homolog 4	1.35	4.50	
25	413019	BE281604	Hs.75140	low density lipoprotein-related protein-	1.35	5.14	
	433026	AW160616	Hs.279921	HSPC035 protein	1.35	4.14	
	427380	NM_005534	Hs.177559	interferon gamma receptor 2 (interferon	1.34	4.35	
	428289	M26301	Hs.2253	complement component 2	1.33	4.23	
	419715	AF070523	Hs.92384	vitamin A responsive; cytoskeleton relat	1.32	4.61	
30	425299	AW505214	Hs.155560	calnexin	1.31	4.76	
	422242	AJ251760	Hs.273385	guanine nucleotide binding protein (G pr	1.30	5.30	
	448483	AA356392	Hs.21321	Homo sapiens clone FLB9213 PRO2474 mRNA,	1.29	6.09	
	407143	C14076	Hs.332329	EST	1.29	4.56	
35	413125	BE244589	Hs.75207	glyoxalase I chaperonin containing TCP1, subunit 2 (b	1.26 1.26	5.56	
22	439053 413929	BE244588 BE501689	Hs.6456 Hs.75617	collagen, type IV, alpha 2	1.25	4.98 4.76	
	419663	AA394208	Hs.92198	calcium-regulated heat-stable protein (2	1.24	4.56	
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	1,21	8.96	
	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	1.21	4.02	
40	425335	BE394327	Hs.296267	follistatin-like 1	1.18	4.29	
	446211	AI021993	Hs.14331	S100 calcium-binding protein A13	1.17	4.32	
	428542	NM_014899	Hs.10432	KIAA0878 protein	1.13	4.17	
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	1.10	4.00	
40	428216	M18468	Hs.183037	protein kinase, cAMP-dependent, regulato	1.09	4.40	
45	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	1.00	4.70	
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	0.98	4.40	
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	0.90	4.78	
	740155	00.					
50	TABLE 5		nua Eas ambasat ida	atifar numbar			
50	CAT num		que Eos probeset ide le cluster number	munes number			
	Accessio		bank accession num	there			1
			OO IN OOCLASION HOL	<b></b>			
	Pkey	CAT Number	Accession				
55	412918	2764_3		9009 AV755430 AV756363 AV711927 BI523434 AI52145	3 AA846815 AW02	4829 AW949702	BG218926 AA626658 AI445621 AI452815
		<b>-</b>		3580 AA612925 BG105326 BG532618 AW513994 AW60			
			BE774875 BG19	0378 AA483698 BE066066 BE066067 BE066062 AW304	207 BE939351 AV	795569 BG21059	92 AW795644 BE939358 AW102886
			BE065977 BG18	2971 H97042 D58090 BI046351 H81248 AI750112 AW37	2079 C05492 D58	287 D57835 AA9:	35095 BF700910 BG215802 BG195459
				95535 BG533177 BI087962 BE541579 BF130753			
60	436701	28142_1		33 BM353155 Al473754 Al147901 Al803109 AA843296 A			
				234 AA394157 BF378047 BE467036 AA319724 AW2909			
				02 N36920 H50440 A1919034 A1004399 A1383862 A11238			
				1911 AW 194733 AA213447 AI290291 BF437165 AA7575	32 BF086904 AW9	59032 AW992466	i BF 446888 AI936337 BE938849
65	432469	58644_1	AW149064 AI70		7407 DE340402 D	C010CC0 AWG70	C44 ANIACODOE ANIAZO122 DIA1CO101
05	432403	30044_1		6365 NM_016040 AF 151858 BI561037 AW966873 AW96 4135 AI632346 AI129838 BM147664 AI292112 BE244667			
				100 AW087624 AA668793 AL080084 BI335866 BI820940			
				54201 BM145846 BG111760 AI750065 BG655794 AA56			
				4602 AI343932 AW136586 AW029464 AI708651 AAB242			
70				1537 AA609603 A1873901 A1859995 AA833589 AA76581			
				85 AA282179 AA831098 AA112676 AI702407 BG621752			
			AW966879 AA3	93405 BF115146 AA910851 AA013099 N28878 AA28771	3 BE348728 BG61	6446 AL599953 A	AL599952 BF381073 AW505056 AA094735
			H03613 AA2877	14 H27168 R54718 BF792697 AV693603 AV685883 BG	19956 BF541504	BF216789 AA319	1751 BM452652 BF335838 AA280397
				1997 AA490239 AW388161 BE842126 BG165309 N719			
75			BE241414 AA01	3098 H00297 AW576477 AW150918 AW591371 AI3827	11 N71926 H72497	AI285602 AA745	5055 AI281647 BF377670 T65207
				21680 AA285143 H27167 AW500235 BG494497 BF6688			
	424571	9758_1	BE379766 AW1	52643 A1803450 A1564343 A1092711 A1140525 AW15215	6 A1620740 A15541	89 Al161209 Al2	90242 AJ339745 AJ374611 AJ347388
				529 Al366124 AA493912 AA406235 AA493889 Al057160			
90				63 N70628 AA424577 AA983537 BF003004 AA626688 A			
80			AI3/5272 AW57	1777 AI359198 AA993793 BE614394 BE738239 AA1278	AIU34344 I 595	USAA 50015U FU	5/4 AWUS 065 944564 07504649
				15 BE244980 AA548596 AW449675 AI191008 BF223749 4968 BE858217 BF793358 AV756758 BG483603 AI0937			
			6G34Z330 AI4/	4500 0E000217 DE150000 AV100100 DO400003 AU0001	4-4 DL 0333333 DQ3		15555 0011113 00433131

	444207	9172_3	BE739425 AA514221 AA865491 AI828293 AA470456 AI276739 AA169357 BE932464 AA514889 AW819039 AW819083 BE843048 AI432496 AI470335 AI247243 BG533994 AA513783 AI887309 AA528036 AW972006 AW873028 AI924914 AI818810 AW152378 AW084946 AI521413 AI669583 BE932521 AI581370 BE180238 AW089750 AW771461 AW089714 AI590949 AI819148 AA731056 BF815234 BF911506 AA235803 AA485373 AI735658
5			AW393133 AW073980 AV707637 BF35320 BE843111 AW819936 AW393135 BG697291 AV648570 AV554332 AV687539 BC566964 AI807430 AI876072 AA837010 A452482 AI62817 AW214750 BE048616 AI290928 AI680714 AA485530 BE175687 AV648513 AW130312 A1000556 AA632893 BE674169 BF001208 AA948166 BE175650 AA524664 AA490345 AI244948 AA602956 AA483492 AA918178 AVV602049 BG675859 AV568871 BC678060 AI555004 AW819026 BEB43092 AV586437 AV723049 BC616948 AI911647 AI743490 AU091096 BEB57251 AI9562074 AA040027 AW769317 AA343477 AA640112 BF876213 R82948 H26425 H82976 BEB43095 BEB43140 BG536641 BC617830 AA235802 BE774985 BE006682 BF342375 AA903144 BF332003 BF394258 AV557996 AI749532 BE768614 BE657252 BE932516 BE768573 AV65793 AV657777 AV752631 BE774974 T55847
10	450515	13638_2	BE095761 BF911511 BE710793 BE180119 BG617338 H45942 T55897 AV657718 BG563497 BE29966 ALS89870 AA847598 A4470122 BF933895 ALS04355 BE233045 BF435800 ALS94207 A4708171 AW025415 A0079409 AW008420 AW304226 N34543 AW603578 AA526951 AA983631 N99134 AA626645 R45023 AA902417 AW672925 AA449985 AA953982 AW675471 AA010062 N80194
15	417020	74857_1	H14620 H28475 H26247 BF333581 AWR32369 H06848 H05608 H81745 H15016 R51905 AA860423 A4860904 AA876023 AK024824 B1089104 AL596792 A1880004 BF969921 BE349489 AA843097 A4475644 AWS76123 AW731676 A1339951 A1128503 AW243903 BC231992 BC057353 AA987811 AA575927 A1889162 N68847 AA64693 AA962541 AA844233 A1969578 A1890997 AW731626 H77926 A1338984 R24078 A1128953 T88696 AA808038 AA694545 H02091 BF439007 A1188805 A1278912 AA730423 R26552 AA455017 A1264219 A4446015 R19187 D51331 T24484 AL522034 AV721528 B1056340 BC0008879 AW371368 Z36733 BE707682 BC5071334 BG180238 BE177547 H48381 BF055495 A1948528 AW594256 BF109394 A1817046 W588756 H48807 H01994 T78413 BG750345 R24132 M92009 R2538.
20	400219	8366_1	BC003552 L10284 NIM_001746 AJ271880 BIB34281 BI597016 AU133331 BI568332 BI463073 BG720694 AL046729 BI460138 BI461052 AV647588 BC623268 AW889757 BE001258 AA312566 AA476446 AU089976 AA312196 BF749977 M94859 AF070646 BC564195 BC623397 AU117332 BC608053 BI667083 AU134542 AU138830 A/761769 BC670828 AA30406 AW512644 AW514813 AJ570535 BE547592 BC6555418 AJ459204 BF725673 BE870032 BF001968 AL047245 BF72470 BF058818 H18415 BE976849 BE076857 BE076848 BE076857 BE076856 AV708897 AA380923 BE076851 F03118 L18887 BF795701 AU128383 BE903383 AW673350 AW500108 BE079837 BE929419 BF868758 AW503373 AW580528 BE005524
25			BI917505 BI457781 BE883312 BI668159 AA213643 AA374821 BF969974 BIMB07200 AU136152 BE395635 X0465066 AV593755 AL040984 AA676820 BIG896408 BE082272 BE082312 C05287 BE082264 AA374821 BF96992 AI652955 BF033526 AW296557 AA728815 BE077058 AW081700 AA911707 AA365640 BE707179 BC913228 BG116191 BG752367 AA074678 AL036937 BG113706 H03524 BG581802 AJ554888 AU149556 BE178600 A813488 AJ452433 AZ069989 AA599392 AA580385 AA466274 AA623899 AA555929 AA114046 AA094752 BM450328 BG529968 R68320 BE076782 BE090073 BE076855 BE0766859 BE076682 AA361719 AA379164 AJ202712 BG223315 BE122741 BG534531 AA603494 H24976 BF032674 BF085150 BE739158 AA352904 C21593 BG587597 AA134969 AA374612 BE566182 BE871838 BE076911 AW579175 BF966390 BI548594 BG386452 BG311195
30	406636	0_0	BMA56787 N40286 T80096 N39642 H42119 BC483861 AW381621 R69347 AW128895 AJ367416 AL095285 AA099344 BE568161 AA180109 BF246488 BI561938 AW579170 BC567212 L12064 L12083 L12065 L12075 L12066 L12085 L12072 L12082 L12081 L12062 L12080
35	400200	3806_1	BC005265 BG176720 AW006027 BM352064 AW026316 AI635822 AI880584 AI693769 AI092211 BI492387 AI400449 AW166297 BF939910 AA232282 AW021432 AI333893 AA465389 AA458498 AIA8595 AW069256 AA682373 AI092748 AA933184 AI126077 AI081768 AI240686 AI261863 AI378423 AA465237 AI376096 AA035579 AI087306 AA466527 AI376096 AA035579 AI087306 AA466526 AA29977 AI090903 AI080686 AI288939 N33004 AI801240 AW021546 AI370773 AI086064 AA669528 AI258033 AI870113 AA853181 AA658014 BG055562 BG939559 AW080765 AA032283 AW467587 H40506 D00762 NM_002788 AA641134 AIS82295 AI417525 AIS65975 AI093566 AI707743 AI280741 AW073417 BE875418 BN264076 BG876884 AI680535 AW854219 BE774635 AW854212 BG952443 AW854221 AW854220 AW854208 BE156348 BE843056 AW858991 BE937569 BG878291 BG876450 AW819099 AI908570 AA449871 AU135228 BM478404 BF126296 AA375499 AA248473
40	406782 437179	0_0 12239_1	AA430373 AA968771 AK055109 BC019085 AA187684 BCG556226 BM023227 AI932311 AW264381 AA398371 BM021483 AI432433 AI375777 AI129580 AW262782 AA134107 BM023515 AA977504 AI859222 AI348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 AI092259 AI028416 AI074114 BCG565538 BES01677 AW193419 AA917040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF476021 R41226
45	426143	3806_1	R59631 F0H125 C02343 AA115589 R56480 A400988 R54266 R31422 BC005255 BG176720 AW006027 BM352064 AW026316 Al635822 Al880584 Al693769 A092211 BI492387 Al400449 AW166297 BF939910 AA232282 AW021432 A333893 AA494308 AA854899 A436795 AW069256 AA682373 Al092748 AA993184 Al128077 Al081758 Al240686 Al251853 AJ378423 AA465237 AJ376096 AA035579 Al087306 AA48162 AA129977 Al098903 Al080686 Al288393 N33004 Al801240 AW021546 AJ370773 Al086064 AA669528 Al250053 Al870113 AA853181 AA858014 BG0555562 BG939559 AW080765 AA032283 AW467587 H40506 D00762 NM_002788 AA641134 AL582295 Al417525 AL563975 Al093366 A707743 JA290741 AW073417 BE875418 BW264076 BG876884 AL680335 AW854219 BE774635 AW053212
50	400223	2368_1	BG952443 AW854221 AW854208 BE156348 BE843056 AW858991 BE937569 BG878291 BG876450 AW819099 AI908570 AA449871 AU135228 BM478404 BF126296 AA375499 AA248473 NM_005648 BC013809 L34587 BF103775 BG702618 BG716553 BI667090 BG505863 BF983483 BG718195 BI857891 BG501016 BM043599 AL521812 BG705730 BI495545 BM95546 BF112248 BM023182 BM023123 AI075173 AW051799 BF058224 BI324885 BF436008 AA398446 BG822375
55			BM019558 BM023302 BG164174 N56909 BH67064 BM02346A AL207475 BM311415 BG758430 BG758807 AN334826 N90351 BG422026 BE910312 AM027778 AL081950 AJ360890 BM009115 A1191829 BG759697 A138728 AA399403 AJ355589 AJ364577 AA58702 AA393560 AA025127 BG027630 AA9672774 AA631224 BG940967 BE791007 AA57315 W81685 AA393525 BG944103 AJ359125 A1149864 AA977655 N90014 BE612839 BG491847 AI129091 AA461234 AA781198 AA759256 AA888954 AA975984 AJ184099 AJ018025 AA398353 M003331 AJ193380 AA626020 AJ244476 AJ601114 AW135664 AJ206607 AW263399 AA813219 AJ684453 AA878526 AA772222 AJ085496 AJ630226 BG940966 AJ022010 AA770649 AA887624 AA491739 AA974295 BG530040 AA037091 AA019912 BI60457 H64512 BG503896
60	406687 453352	0_0 12299_2	M31126 BG619646 AA367158 BI850421 AW998556 BF107010 BF969630 BF185964 AA361080 AW960026 AA147486 AIB07023 AW770262 BI492178 BM145577 AA829932 AW021238 AW629477 AJ337862 AI457141 BI712705 BM194542 BI712465 AJ380070 N27407 AI609764 AJ274152 AI206228 AU076874 AJ261827 AI610382 AI469158 AI420690 A168768 AA491675 C16249 C16232 C16209 C16275 C16247 C16243 R23287 BF246254 R66738
65	400203	11774_1	R23212 C14593 NM_002794 D26599 BM469989 BF305151 BG821966 BI089030 AW007738 BI222910 BM049422 BG028749 A1189162 A1831230 AW131497 BM272215 BE791105 AW778828 AA479594 AA480133 \$\incredxed{\text{131997}}\text{A284572 AA453009 BF928258 AA152127 AA333918 BF755307 BE247542} BF934697 BF341798 BE253409 AA470620 A1828932 AW378902 AV762678 AV741784 AV760892 AW025755 AA678562 AA630630 AA761708 AA862518 AA865831 AA862947 N53065 AA131821 AA293499 N23342 N26856 A1147346 AW951549 AA772963 BE245986 BG208493 AI831666
70	427239	20459_2	BGA74873 BI023168 AU149647 BG197069 BG191102 BF304178 BE536135 AA706900 AA443583 AI002710 AW276192 AU149842 BG214797 BG188193 AW197923 AW627799 T88663 BG194788 BG214656 BF345258 BG716363 AI066528 BI546220 AA393815 AA132004 AA353826 H97858 BG187823 BF841463 AI351714 AV735968 BG196439 BG216840 BG198438 BG400765 AL532360 BF794750 AA582906 AU015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881 AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478 AI251789
75			AW302327 AW072520 AJ312145 AW073656 AW072513 AW071289 AJ307559 AAB76186 T29587 AJ307493 AJ255068 AJ252668 AJ25268 AW074809 AJ252926 AJ252160 AJ251662 AJ251262 AJ610913 AJ270787 AJ270156 AJ252075 AW073469 AW072901 AW072496 AW071420 AJ305762 AJ254764 AJ802837 AJ251264 AW073049 AW071311 AJ30643 BE138965 BE138950 AW073456 AJ334733 AJ054335 BE139260 AJ054302 AJ054060 AJ054057 AJ053722 AJ289711 BE139228 AW470478 AW271039 AW302085 BE041872 AJ254454 AJ271439 AJ252427 BF718773 BF718645 AW074866 BE857822
80	415819	40015_1	BE739429 BM460292 AL549095 BF752457 BE783002 BG035869 AW601528 AI880413 BF593762 AA974415 AW305318 AA716501 AI938239 AB09486 AI744171 AW804992 BF108747 AW804693 BE219333 AI807707 AA306963 BG012140 BF741651 BF741618 BF741619 AW052543 AA155832 AU151381 AU158043 AU150410 AU145605 AU150252 AA188205 AU153035 AI147293 AA084507 AA886165 AI887120 AI468336 AW023112 H46035 F01513 AA747672 AW779630 AA757298 R77738 AU150931 R38473 AA189022 H96984 AL550490 AW949737 AU150194 AU149258 AI749453 AW172950 AW276160 AI753604 AI421762 AW575512 AI275633 AW516120 AI340167 AI567728 AI797326 AI471532 AI074080 AIG33122 AW674646 AW316571 AA258187 AA102780 AA258186 AI363307 AA862862 AI206836 AA629555 AA486287 AI185097 AI872389 BE465687

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ESTs

A1246746 A1351453 A1189679 AA594582 A1038639 AA862764 AA544332 AA912423 AA601552 AW014502 AA694605 AW068949 BF941650 ANZ97886 BF941649 ANJ7565A ANJ75462 ANJ76602 ANZ97678 H91731 AA977135 AA559973 BI522334 AA398723 ANZ9803 AN19671 ANX99199
AA498011 AU144081 AI538440 BF741690 BF741680 H41990 AV724108 AN955578 BE698790 T29312 BG954488 R33179 BI832621 BF742040 AA49011 AU144081 ALSA4400 PA1699 B-716890 R-71690 R-71690 B-71690 R-71690 00202 11771_2 BEGATZRO BIG 13/14/10533 A316042 PAZO43 AW040246 AW392054 A379398 AW301110 AW06917 A3737931 BG91889 BEO76254 A3560459
A379385 AA320056 BG942618 D31230 A308300 A3560371 AA3711733 AA732937 AA494241 W32225 BF745937 A1383690 BG202360 10 TABLE 50C: Plusy: Ref: Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Gentrank Identifier (GI) numbers. "Durtham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Durtham, et al. (1999) Nature 402:489-495. 15 Indicates DNA strand from which exons were predicted. Strand: Nt_position: Indicates nucleotide positions of predicted exons. Strand Nt_position Pkey 404854 20 14260-14537 7143420 Plus 80014-80401,80593-81125 53526-53628,55755-55920,57530-57757 402474 7547175 Minus 198991-199168,199316-199548 8119067 400750 25 TABLE 51A: ABOUT 453 GENES UPREGULATED IN PRIMARY MELANOMAS RELATIVE TO NORMAL SKIN Table 11A fix about 43 genes upregulated in primary melanomas relative to normal skin. Cenes were selected from 59680 probesets on the Eos/Affymetrix Hu/03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. Unique Eos probeset identifier number Pkev: 30 Exemplar Accession number, Genbank accession number UnigenelD: Unigene number Unigene gene title Unigene Title: uniques generous 90th percentile of primary metanoma Als divided by 90th percentile of normal skin Als 90th percentile of primary metanoma Als divided by 90th percentile of normal skin Als, where the 15th percentile of normal tissue Als was subtracted from both R2 35 the numerator and denominator UnigenelD Hs.30743 Unigene Title preferentially expressed antigen in mela Pkay 452838 ExAcon U65011 14.06 13.64 15.56 11.62 NM_001922 NM_000372 Hs.301865 Hs.2053 dopachrome tautomerase (dopachrome delta tyrosinase (oculocutaneous albinism IA) 430377 40 7.98 426555 BE386801 Al186431 trinucleotide repeat containing 3 prostate differentiation factor 12.78 13.80 438549 Hs.21858 15.56 Hs 295638 422424 426600 Hs.171014 VGF nerve growth factor inducible 10.14 22,46 glyceraldehyde-3-phosphate dehydrogenase ESTs, Weakly similar to S51797 vasodilal chondrollin sulfate proteoglycan BEHAB/b 9.33 8.66 7.87 7.25 9.62 430822 AJ005371 Hs.248017 45 Hs.32399 457211 AW972565 438380 T06430 Hs.6194 D13168 Hs.82002 endothelin receptor type B 7.66 7.38 4.63 417355 9.04 phosphatidylserine-specific phospholipas secretogranin II (chromogranin C) 447210 AF035269 AA319146 Hs.17752 Hs.75426 7.32 4.65 413554 50 6.46 415752 BE314524 Hs.78776 putative transmembrane protein 7.00 absent in metanoma 2 NM 004833 Hs.105115 421508 AW960707 AF026939 Hs.148324 Hs.181874 **ESTs** 6.43 6.27 5.92 interferon-induced protein with tetratri 426312 small inducible cytokine sublamily A (Cy hexabrachion (tenascin C, cytotactin) AB012113 6.17 3.70 446921 3.92 7.73 55 Hs.289114 429500 X78565 X72755 6.04 6.04 414812 Hs.77367 monokine induced by gamma interferon 5.89 452973 H88409 Hs.40527 **FSTs** 5.96 5.72 2.50 5.29 ENSP00000251056°:Plasma membrane calcium 402075 436856 A1469355 Hs.127310 **ESTs** 5.68 5.62 5.88 6.30 60 AA663372 Hs.169395 hypothetical protein FLJ12015 425088 AF086120 NM_001394 439310 Hs.102793 FSTe 5.62 5.36 5.36 5.35 5.28 5.23 5.20 5.14 5.09 5.04 4.94 4.88 4.87 4.74 4.74 4.72 4.68 3.30 Hs.2359 dual specificity phosphatase 4 429170 AB000115 AW979187 hypothetical protein, expressed in osteo melanorna differentiation associated prot 4.28 413670 Hs.75470 Hs.293591 409512 65 Homo sapiens cDNA: FLJ22105 fis, clone H 4.64 Hs.27935 hypothetical protein MGC4837 4.31 BF390513 436315 hypothetical protein MGC48370 glycoprotein M6B Hs.332938 Hs.5422 442426 AI373062 4 03 435056 AW023337 Hs.287402 chondroitin 4-sullatransferase 5.52 432828 AB042326 70 AI538226 AK000680 Hs.32976 Hs.266175 guanine nucleotide binding protein 4 phosphoprotein associated with GEMs 4.82 430294 4.35 431639 430838 N46664 Hs.169395 Hs.7155 hypothetical protein FLJ12015 ESTs, Moderately similar to 2115357A TYK 3.68 AA737033 414004 gb:Homo sapiens cig33 mRNA, partial sequifis485 AF026942 AA305159 Hs.17518 Hs.113019 6.29 75 422192 silver (mouse homolog) like 6.00 420208 BE276055 deafness, autosomal dominant 5 hypothetical protein MGC4595 NM_004403 W03476 446006 Hs.13530 Hs.266331 Hs.105924 9.85 5.75 440065 421574 440274 AJ000152 R24595 defensin, beta 2 80 Hs.7122 scrapie responsive protein 1 2.78 AA431323 N88802 Hs.42146 Hs.5422 417166 **ESTs** 4.29

	432642	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	4.62	2.87
	437179	AA393508		serologically defined colon cancer antig	4.62	5.08
	417933	X02308	Hs.82962	thymidylate synthetase	4.58 4.50	3.02 4.37
5	431620 431629	AA126109 AU077025	Hs.264981 Hs.265827	2-5-oligoadenylate synthetase 2 (69-71 interferon, alpha-inducible protein (clo	4.49	16.82
•	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cON	4.44	5.96
	409264	NIM_014937	Hs.52463	KIAA0966 protein	4,42	2.94
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	4.42 4.38	3.54 3.30
10	422309 449722	U79745 BE280074	Hs.114924 Hs.23960	solute carrier family 16 (monocarboxylic cyclin B1	4.32	4.07
10	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.30	3.82
	450065	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	4.28	4.36
	424247	X14008	Hs.234734	lysozyme (renal amytoidosis)	4.27 4.25	3.05 4.68
15	413916 420267	N49813 N37030	Hs.75615 Hs.173337	apolipoprotein C-II ESTs	4.24	4.24
13	442739	NM_007274	Hs.8679	cytosotic acyl coenzyme A thioester hydr	4.21	3.00
	433576	BE080715	Hs.161091	ESTs	4.20	6.31
	412652	AI801777		ESTs	4.20	2.73 5.18
20	438209 441553	AL120659 AA281219	Hs.6111 Hs.121296	aryl-hydrocarbon receptor nuclear transl ESTs	4.20 4.14	4.94
20	407856	AA045281	Hs.266175	phosphoprotein associated with GEMs	4.14	3.14
	439926	AW014875	Hs.137007	ESTs	4.12	4.76
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.12	4.85
25	400860	AAE302E0	EL- E003	Target Exon	4.10 4.08	5.20 6.02
23	409415 416636	AA579258 N32536	Hs.6083 Hs.42645	Homo sapiens cDNA: FLJ21028 fis, clone C solute carrier family 16 (monocarboxylic	4.08	2.42
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	4.06	2.96
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	4.06	2.28
20	417632	R20855	Hs.5422	glycoprotein M6B	4.01 4.00	2.96 4.62
30	418064 448111	BE387287 AA053486	Hs.83384 Hs.20315	\$100 calcium-binding protein, beta (neur interferon-induced protein with tetratri	4.00	2.82
	420674	NM_000055	Hs.1327	bulyrylcholinesterase	4.00	2.90
	451668	Z43948	Hs.326444	cartilage acidic protein 1	3.99	5.17
26	430015	AW768399		ESTs	3.96	3.89
35	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.94 3.93	2.91 3.89
	430223 433364	NM_002514 AI075407	Hs.235935 Hs.296083	nephroblastoma overexpressed gene ESTs, Moderately similar to 154374 gene	3.93	4.70
	448719	AA033627	Hs.21858	trinucleotide repeat containing 3	3.92	7.78
40	419381	AB023420	Hs.90093	heat shock 70kD protein 4	3.87	3.34
40	402609	0500000		KIAA1209 protein	3.87 3.86	3.69 4.04
	408083 409703	BE383668 NM_006187	Hs.42484 Hs.56009	typothetical protein FLJ 10518 2-5'-oligoadenylate synthetase 3 (100 k	3.85	3.64
	420218	AW958037	113.50003	ribosomal protein L4	3.84	3.20
4.5	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	3.84	5.19
45	410600	AW575742		ESTs, Moderately similar to S65657 alpha	3.82	5.74 2.96
	442117 428513	AW664964 BE220806	Hs.128899 Hs.184697	ESTs; hypothetical protein for IMAGE:447 Homo sapiens clone 23785 mRNA sequence	3.82 3.82	4.03
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	3.80	3.56
	432094	AI658580	Hs.61426	Homo sapiens mesenchymal stem cell prote	3.79	3.23
50	443105	X96753	Hs.9004	chondroitin sulfate proteoglycan 4 (mela	3.77	3.66 2.28
	423605 407846	AF047826 AA426202	Hs.129887 Hs.40403	cadherin 19, type 2 Cbp/p300-interacting transactivator, wit	3.72 3.72	5.34
	442578	AK001643	Hs.8395	hypothetical protein FLJ10781	3.71	3.42
	448965	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.68	3.31
55	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	3.68 3.68	4.24 2.74
	400750 447217	BE465754	Hs.17778	Target Exon neuropilin 2	3.66	3.60
	459373	BE408266	Hs.301406		3.66	3.48
	419628	H67546	Hs.49768	ESTs	3.62	4.13
60	406868	AA505445	Hs.300697		3.61	4.40
	421866 421709	M24470 AA159394	Hs.1435 Hs.107056	guanosine monophosphate reductase 6 CED-6 protein	3.59 3.57	3.53 2.63
	438501	Z44110	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.56	3.54
	408962	8E386436	Hs.44317	SRY (sex determining region Y)-box 10	3.55	2.70
65	425139	AW630488	Hs.25338	protease, serine, 23	3.50 3.49	2.80 2.58
	428411 452744	AW291464 AJ267652	Hs.10338 Hs.246107	ESTs Homo sapiens mRNA; cDNA DKFZp434E082 (fr	3.48	4.61
	411305		Hs.69547	myelin basic protein	3.48	3.37
	447343		Hs.23589		3.47	2.68
70	429954		Hs.21374		3.47	2.63
	417621		Hs.82316		3.46 3.46	2.34 2.47
	435256 450534		Hs.13872 Hs.25132		3.42	3.65
	421100				3.41	2.63
75	418506	AA084248	Hs.85339	G protein-coupled receptor 39	3.40	4.02
	442711		Hs.8645	hypothetical protein	3.39	2.95 2.38
	453344 435700		Hs.44571 Hs.30140		3.38 3.36	4.60
	418007		Hs.83169		3.36	2.61
80	433867			hippocalcin-like 1	3.36	4.26
	408393				3.36	2.10
	447484 412828				3.36 3.35	2.49 2.27
	412020		Hs.74621	from harm, they and forentiern down		

					2.00	3.00
	426158			v-erb-b2 avian erythroblastic leukemia v	3.35 3.34	2.58 2.55
	440325 420602	NM_003812 AF060877	Hs.7164 Hs.99236	a disintegrin and metalloproteinase doma regulator of G-protein signalling 20	3.34	5.96
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.34	273
5	406663	U24683		immunoglobulin heavy constant mu	3.31	5.21
	427540	R12014	Hs.20976	ESTs	3.30	3.40
	412141	AI183838	Hs.48938	hypothetical protein FLJ21802 NM 005313:Homo sapiens glucose regulated	3.29 3.29	2.80 3.46
	400282 419870	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.28	5.20
10	416539	Y07909	Hs.79368	epithelial membrane protein 1	3.28	2.79
	431518	AA743462	Hs.165337	ESTs	3.27	2.51
	402994			NM_002463°:Homo sapiens myxovirus (influ	3.26	6.38
	419956	AL137939	Hs.40096	cadherin 19, type 2	3.26 3.26	4.48 3.71
15	421379	Y15221	Hs.103982 Hs.239	small inducible cytokine subfamily 8 (Cy forkhead box M1	3.25	3.72
13	444371 432874	BE540274 W94322	Hs.279651	metanoma inhibitory activity	3.25	5.33
	417282	AA195203		RAB5C, member RAS oncogene family	3.24	3.20
	439569	AW602166	Hs.222399	CEGP1 protein	3.24	2.32
20	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	3.24 3.23	6.20 3.70
20	403817 407857	A1928445	Hs.92254	NM_015271:Homo sapiens tripartite motif- synaptotagmin-like 2	3.22	2.49
	426334	BE305081	Hs.169358	hypothetical protein	3.21	2.46
	453837	AL138387	Hs.256126	baculoviral IAP repeat-containing 7 (liv	3.19	5.50
0.0	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	3.18	2.04
25	437379	AL359575	Hs.23765	Homo sapiens mRNA; cDNA DKFZp547M123 (fr	3.18 3.18	3.73 4.44
	424090 410491	X99699 AA465131	Hs.139262 Hs.64001	XIAP associated factor-1 Homo sapiens clone 25218 mRNA sequence	3.18	3.26
	408418	AW963897	Hs.44743	KIAA1435 protein	3.16	2.21
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	3.16	4.04
30	402829			C1002500:gij6754254 ref[NP_034610.1  hea	3.15	4.57
	437852	AW978107	Hs.5884	Homo sapiens mRNA; cDNA DKFZp586C0224 (f	3.15 3.14	3.07 3.08
	425935 417124	Z98200 BE122762	Hs.163724 Hs.25338	HSPC019 protein ESTs	3.14	2.73
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.11	2.16
35	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	3.10	2.43
	442271	AF000652	Hs.8180	syndecan binding protein (syntenin)	3.10	2.83
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	3.10 3.10	1.78 3.17
	429083 437673	Y09397 AW665665	Hs.227817 Hs.153034	BCL2-related protein A1 ESTs	3.10	3.32
40	407813	AL120247	Hs.40109	KIAA0872 protein	3.10	3.90
	445745	AB007924	Hs.13245	KIAA0455 gene product	3.10	3.35
	451537	R56631	Hs.26550	retinoid X receptor, gamma	3.09	4.45
	408654	BE018882	Hs.46721	UCC1 protein	3.08 3.08	3.65 2.12
45	444484 446019	AK002126 AI362520	Hs.11260	hypothetical protein FLJ 11264 histone deacetylase 3	3.08	2.26
43	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	3.08	5.29
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.06	3.36
	403532			NM_024638.Homo sapiens hypothetical prot	3.06	3,37 3.17
50	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens ESTs, Moderately similar to ALU7_HUMAN A	3.04 3.03	2.98
50	446341 426501	AL040763 AW043782	Hs.310735 Hs.293616		3.03	2.01
	450325	AJ935962	Hs.91973	ESTs	3.02	2.19
	418941	AA452970	Hs.239527	E18-55kDa-associated protein 5	3.02	3.29
55	431797	BE169641	Hs.270134		3.02 3.00	2.54 1.96
23	442064 405451	A1422867	Hs.88594	ESTs dihydropyrimidinase-like 3	3.00	2.98
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	2.99	6.41
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	2.98	3.25
60	452958	AA883929	Hs.40527	ESTs	2.98	4.14 3.30
60	427647	W19744	Hs.180059		2.96 2.96	2.47
	409190 428819	AU076536 AL135623	Hs.50984 Hs.193914	sarcoma amplified sequence KIAA0575 gene product	2.96	4.16
	428450	NM_014791			2.96	2.41
	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	2.95	2.79
65	411358	R47479	Hs.94761	KIAA1691 protein	2.95 2.94	4.70 2.65
	432467 400222	T03667	Hs.239388	Human DNA sequence from clone RP1-304814 NM_002082*:Homo sapiens G protein-couple	2.94	2.69
	405785			NM_025184*:Homo sapiens hypothetical pro	2.94	2.55
	409760			gb:EST10534 Adipose tissue, white I Homo	2.94	2.57
70	418113		Hs.83484	SRY (sex determining region Y)-box 4	2.93	2.52
	409038		Hs.50002		2.93 2.92	2.43 3.20
	456760 459710		Hs.12782 Hs.12159		2.91	4.45
	411395		Hs.7542	KIAA1802 protein	2.90	2.72
75	427528		Hs.17956	5 minichromosome maintenance deficient (S.	2.90	2.27
	406964	M21305		FGENES predicted novel secreted protein	2.90	2.03
	428834		Hs.33931		2.89 2.89	3.55 3.87
	413190 438619		Hs.40368	adaptor-related protein complex 1, sigma TU1281-TY protein	2.88	2.37
80	442432		Hs.38178		2.87	2.00
	428782	X12830	Hs.19340	0 interleukin 6 receptor	2.86	2.51
	454027		Hs.21527		2.86	3.07 5.58
	453107	MM_01611	3 Hs.27974	6 vanilloid receptor-like protein 1	2.86	3.36

	414737	AI160386	Hs.125087	ESTs	2.84	2.79
	412140	AA219691		RAB6 interacting, kinesin-like (rabkines	2.84 2.83	3.80
	447735	AA775268		Homo sapiens cDNA: FLJ23020 fis, clone L defensin, beta 3	2.83	2.11 3.32
5	416091 442445	AF295370 AA082665		KIAA1715 protein	2.81	2.17
•	408208	BE018717		ESTs	2.81	2.43
	430066	A1929659	Hs.237825	signal recognition particle 72kD	2.80 2.80	2.25 2.74
	424755 422616	AB033094	Hs.152925 Hs.118725	KIAA1268 protein selenophosphate synthetase 2	2.79	201
10	405506	BE300330	13.110123	Target Exon	2.78	2.65
	411619	AJ418609	Hs.71040	hypothetical protein FLJ20425	2.78	3.10
	400236			Eos Control	2.78 2.78	2.21 3.15
	452698 446488	NM_001295 AB037782	Hs.301921 Hs.15119	chemokine (C-C motif) receptor 1 KIAA1361 protein	278	2.80
15	439778	AL109729	Hs.99364	putative transmembrane protein	2.78	3.78
	420005	AW271106	Hs.133294	ESTs	2.78	2.86 .
	428642	NM_014899	Hs.10432	KIAA0878 protein 28kD interferon responsive protein	2.77 2.76	3.07 4.56
	453779 425289	N35187 AW139342	Hs.43388 Hs.155530	interferon, garrina-inducible protein 16	2.76	1.83
20	437723	AI672731	Hs.13256	ESTs	2.76	4.23
	416730	T99937		gb:ye72d04.r1 Soares fetal liver spleen	2.76	2.98 3.21
	426153 444670	AF057169 H58373	Hs.182771 Hs.332938	vitelliform macular dystrophy (Best dise hypothetical protein MGCS370	2.76 2.76	3.97
	421351	AU076667	Hs.103755	receptor-interacting serine-threonine ki	2.74	3.50
25	406673	M34996	Hs.198253	major histocompatibility complex, class	2.74	3.24
	427268	X78520	Hs.174139	chloride channel 3	2.74 2.74	2.82 1.95
	428403 409417	AI393048 AA156247	Hs.326159 Hs.104879	leucine rich repeat (in FUI) interactin serine (or cysteine) proteinase inhibito	2.74	2.99
	419705	AW368634	Hs.154331	ESTs	2.74	2.28
30	440457	BE387593	Hs.21321	Homo sapiens clone FLB9213 PRO2474 mRNA,	2.72	3.60
	413599	AJ006239	Hs.75438	quinoid dihydropteridine reductase	2.72 2.72	2.43 4.77
	447164 430594	AF026941 AK000790	Hs.17518 Hs.246885	vipirin; similar to inflammatory respon hypothetical protein FLJ20783	2.72	3.67
	413278	BE563085	Hs.833	Interferon-stimulated protein, 15 kDa	2.71	12.06
35	424572	M19650	Hs.179600	2,3-cyclic nucleotide 3 phosphodieste	270	2.40
•	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	2.70 2.69	3.81 3.85
	425996 430441	W57330 BE398091		hypothetical protein AL110115 desmoplakin (DPI, DPII)	2.68	2.55
	442355	AA456539	Hs.8262	lysosomal-associated membrane protein 2	2.68	1.67
40	421362	AK000050	Hs.103853	hypothetical protein FLJ20043	2.68	2.94 1.89
	437158	AW090198		KIAA1150 protein gb:PM2-DT0023-080300-004-a04 DT0023 Homo	2.68 2.68	2.80
	412315 432878	AW936678 BE386490	Hs.279663	Pirin	2.68	2.58
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	2.68	2.74
45	426759	AI590401	Hs.21213	ESTs	2.68 2.67	2.35 2.70
	405486 410326	AI368909	Hs.47650	Target Exon ESTs	2.67	3.33
	434040	AW444613	Hs.288809	hypothetical protein FLJ20159	2.66	2.54
50	437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	2.66	1.91
50	412719	AW016610	Hs.816 Hs.60975	ESTs ESTs	2.66 2.66	4.21 5.69
	451708 418299	A1306536 AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	2.66	2.31
	425017	AL119305	Hs.26409	ESTs	2.66	2.73
55	400235	DE007500	000040	NM_005336:Homo sapiens high density lipo	2.66 2.64	2.29 2.86
55	444809 436291	BE207568 BE568452	Hs.208219 Hs.344037	oculospanin protein regulator of cylokinesis 1	2.64	2.33
	406382	DEGGGTGE	113.0-1-001	C16001275":gij12698037 dbj BAB21837.11 (	2.64	2.48
	432241	AI937060	Hs.6298	KIAA1151 protein	2.63	3.16
60	417308	H60720	Hs.81892 Hs.198793	KIAA0101 gane product Homo sapiens cDNA: FLJ22463 fis, clone H	2.63 2.62	2.10 2.43
00	429294 453935	AA095971 AI633770	Hs.42572	ESTs	2.62	1,99
	401454			NM_014226":Horno sapiens renal turnor anti	2.62	3.01
	436456	AW292677	Hs.248122		2.62 2.61	5.94 3.02
65	418478 453256	U38945 Al565587	Hs.1174 Hs.32556	cyclin-dependent kinase inhibitor 2A (me KIAA0379 protein	2.60	2.68
05	451622		Hs.30579	Homo sapiens cDNA: FLJ23070 fis, clone L	2.60	2.51
	424006	AF054815	Hs. 137548		2.60	2.56
	409354		Hs.159472		2.59 2.58	3.00 3.52
70	425392 427286		Hs.15220 Hs.2132	zinc finger protein 106 epidermal growth factor receptor pathway	2.58	1.86
. •	418166			Cdc42 effector protein 3	2.58	2.15
	413794		Hs.61638	myosin X	2.58 2.58	2.54 1.95
	445707		Hs.114390 Hs.79404	ESTs neuron-specific protein	2.57	2.46
75	416640 427982				2.56	1.74
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.56	2.22
	455839		16- 40404	gb:MR0-HT0208-101299-202-a04 HT0208 Homo	2.55 2.55	2.34 2.31
	447737		Hs.19404 Hs.13290	DKFZP564L0862 protein 5 19A24 protein	2.54	2.31
80	442762		Hs.8700	deleted in liver cancer 1	2.54	2.47
	432888	BE159028	Hs.27970	chromatin accessibility complex 1	2.54	3.99
	440676		7 Hs.11237 Hs.1787	3 UM and senescent cell antigen-like doma oroteolipid protein 1 (Pelizaeus-Merzbac	2.54 2.53	2.96 6.98
	424481	R19453	113.170/	morecular broken i la cuescoamerence		

	422340	AW296219		RAB7, member RAS oncogene family-like 1	2.53 2.53	3.06 3.13
	428844	AW972635	Hs.301904	hypothetical protein FLJ12671 ESTs	2.53	1.63
	458997 419591	AW937420 AF090900	Hs.91393	Homo sapiens cDNA; FLJ21887 fis, clone H	2.52	2.30
5	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	2.52	1.60
	429238	NM_002849	Hs.198288	protein tyrosine phosphatase, receptor I	2.52 2.52	3.02 3.05
	432882 407260	NM_013257 L09095	Hs.279696	serum/glucocorticoid regulated kinase-li abd-tomo sapiens mRNA fragment.	2.50	5.00
	431186	NM_012249	Hs.250697	ras-like protein	2.49	6.16
10	417542	J04129	Hs.82269	progestagen-associated endometrial prote	2.49	4.71
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	2.48 2.48	5.77 3.77
	408209	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	2.46	3.11
	405885 406837	R70292	Hs.156110	Target Exon immunoglobulin kappa constant	2.44	3.10
15	412609	Z48804	Hs.74124	ocular albinism 1 (Nettleship-Falls)	2.44	4.90
	421633	AF121860	Hs.106260	sorting nexin 10	244	4.31 3.19
	415929	AA724373	Hs.49344 Hs.75219	hypothetical protein FLJ11006 tyrosinase-related protein 1	2.42 2.37	3.55
	413171 406621	AA318325 X57809	Hs.8997	immunoglobulin lambda locus	2.36	5.87
20	414142	AW368397	Hs.334485	hemicentin (fibufin 6)	2.36	3.04
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	2.36	3.66
	414283	AW960011	Hs.154993	ESTs	2.34 2.34	4.95 4.18
	453931 422515	AL121278 AW500470	Hs.25144 Hs.117950	ESTs multifunctional polypeptide similar to S	2.32	3.45
25	435292	N20514	Hs.172965	ESTs	2.32	4.94
	412926	A1879076	Hs.75061	macrophage myristoylated alanine-rich C	2.31	3.78
	440197	AW340708	Hs.317714	pallid (mouse) homolog, pallidin	2.30 2.29	3.96 5.08
	425262 439979	D87119 AW600291	Hs.155418 Hs.6823	GS3955 protein hypothetical protein FLJ 10430	2.28	4.05
30	403969	**********		ENSP0000034663:Zinc finger protein 131	2.28	3.64
	421686	AB011156	Hs.106794	KIAA0584 protein	2.26	3.31
	432800	BE391046	Hs.278962	AIM-1 protein gb:zw20f11.s1 Soares ovary tumor NbHOT H	2.24 2.24	4.08 3.47
	406782 415539	AA430373 AI733881	Hs.72472	BMP-R1B	2.22	3.66
35	447523	BE613328	Hs.21938	hypothetical protein FLJ12492	2.20	3.43
	433180	AB038651	Hs.31854	K562 cell-derived leucine-zipper-like pr	2.20	3.52
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	2.19 2.18	3.76 3.17
	407241 422243	M34516 AW803733	Hs.23585	gb:Human omega light chain protein 14.1 hypothetical protein MGC12250	2.18	3.28
40	417324	AW265494		ESTs	2.16	5.85
-	412819	T25829	Hs.24048	FK506 binding protein precursor	2.14	3.49
	432342	AL036128	Hs.274404	plasminogen activator, tissue	2.13 2.13	4.39 5.48
	427923 417437	AW274357 U52682	Hs.301406 Hs.82132	hypothetical protein PP3501 interferon regulatory factor 4	2.13	3.08
45	425535	AB007937	Hs.158287	KIAA0468 gene product	2.13	8.66
	429638	AI916662	Hs.211577	kinectin 1 (kinesin receptor)	2.12	3.01
	409154	U72882	Hs.50842	interferon-induced protein 35	2.12 2.12	4.66 3.71
	429951 418918	AL040521 X07871	Hs.15220 Hs.89476	zinc finger protein 106 CD2 antigen (p50), sheep red blood cell	211	4.27
50	419200	AW966405	16.65416	EST	2.11	3.58
	415448	L13210	Hs.79339	tectin, galactoside-binding, soluble, 3	2.10	5.34
	425069	AA687465	Hs.298184		2.07 2.06	7.86 3.68
	445133 411492	AW157646 T46848	Hs.198689 Hs.70337	ESTs immunoglobulin superfamily, member 4	2.04	3.36
55	408015	AW136771	Hs.244349		2.03	3.41
	424412	H15512	Hs.10043	hypothetical protein FLJ13074	2.03	3.82
	431657	AI345227	Hs.105448 Hs.115803		2.02 2.02	3.03 3.09
	427536 400533	BE277141	ns.1130W	ENSP0000209376*:PRED65 protein (Fragmen	2.00	3.29
60	432680	T47364	Hs.278613		1.99	3.07
	410129	BE244074	Hs.58831	regulator of Fas-induced apoptosis	1.97	4.52
	417312	AW888411	Hs.250811 Hs.136102		1.97 1.94	3.26 3.79
	423952 455705	AW877787 AW161061	PLS. 130 104	! KIAA0853 protein ESTs, Weakly similar to zinc finger prot	1.93	3.16
65	419723	AL120193	Hs.339810		1.93	3.11
	438866	U44385	Hs.325495	issue inhibitor of metalloproteinase 2	1.93	3.47
	448410		Hs.21126		1.92 1.92	3.00 4.07
	400292 436797		Hs.72472 Hs.334477		1.90	3.04
70	406851		163.55741	major histocompatibility complex, class	1.90	6.53
	428437		Hs.18432		1.89	3.39
	431836		Hs.27141		1.89	4.04 3.64
	424687		Hs.15173	B matrix metalloproteinase 9 (gelatinase B transcobatamin 1 (vitamin B12 binding pr	1.87 1.85	4.21
75	426322 425221		Hs.2012 Hs.15518		1.85	3.13
15	420162		Hs.95577		1.85	3.04
	443530	BE563088	Hs.9552	binder of Arl Two	1.85	3.20
	433671				1.84 1.82	3.39 3.22
80	424415		5 Hs.14658	0 enolase 2, (gamma, neuronal) Target Exon	1.82	4.11
30	400991 418677		Hs.87224		1.82	3.43
	424441	X14850	Hs.14709	7 H2A histone family, member X	1.81	3.12
	424825	AF207069	Hs.15335	7 procollagen-lysine, 2-oxoglutarate 5-dio	1.79	5.31

	425818	AB021225	Hs.159581	matrix metalloproteinase 17 (membrane-in	1.79	3.40
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	1.78	3.38
	414945	BE076358	Hs.77667	tymphocyte antigen 6 comptex, locus E	1.77	3.69
_	440942	AW246547	Hs. 17901	Homo sapiens, clone IMAGE:3937015, mRNA,	1.77	3.12
5	401591			Target Exon	1.75	4.30
	425923	NM_005026	Hs.162808	phosphoinositide-3-kinase, catalytic, de	1.75	3.68
	412844	AI828045	Hs. 18016	Homo sapiens mRNA; cDNA DKFZp586H0324 (f	1.74	3.53
	417237	H86385	Hs.81737	palmitoyl-protein thioesterase 2	1.73 1.72	3.06 4.38
10	419849 454429	BE041436 BE273437	Hs.93379 Hs.301406	eukaryotic translation initiation factor hypothetical protein PP3501	1.72	4.38
10	440672	AF083811	Hs.7345	MAD1 (mitotic arrest deficient, yeast, h	1.72	3.61
	408204	AA454501	Hs.43666	protein tyrosine phosphatase type IVA, m	1.72	3.06
	430148	BE387620	Hs.234489	lactate dehydrogenase B	1.71	4.38
	426502	Y07759	Hs.170157	myosin VA (heavy polypeptide 12, myoxin)	1.70	3.13
15	413317	U53225	Hs.75283	sorting nextin 1	1.70	3.08
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	1.68	3.15
	407223	H96850	11- 005044	gb:yw03b12.s1 Soares metanocyte 2NbHM Ho	1.68	4.19
	413566 404067	AW604451	Hs.285814	sprouty (Drosophila) homolog 4	1.67 1.67	5.74 4.73
20	447630	AJ660149	Hs.44865	Target Exon lymphoid enhancer-binding factor 1	1.66	3.22
20	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	1,65	3.17
	427747	AW411425	Hs.180655	serine/threonine kinase 12	1.64	3.35
	437912	BE278594	Hs.5912	F-box only protein 7	1.64	3.24
0.5	404140			NM_006510:Homo sapiens ret finger protei	1.64	3.10
25	414214	D49958	Hs.75819	gtycoprotein M6A	1.64	3.45
	427239	BE270447		ubiquitin carrier protein	1.62	3.58
	427289	AI097346	11- 200045	phosphoserine aminotransferase	1.62	5.89
	452923 426020	BE276018 AL110195	Hs.288940 Hs.166017	five-span transmembrane protein M83 microphthalmia-associated transcription	1.62 1.62	3.23 4.00
30	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	1.61	5.00
50	451489	NM 005503	Hs.26468	amyloid beta (A4) precursor protein-bind	1.60	3.06
	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	1.58	3.34
	411825	AK000334		hypothetical protein FLJ20327	1.56	3.18
25	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	1.56	3.23
35	428081	AA421048	Hs.95011	syntrophin, beta 1 (dystrophin-associate	1.55	3.10
•	401914		11- 450000	Target Exon	1.54	3.33
	424902	NM_003866	Hs.153687 Hs.30559	inositol polyphosphate-4-phosphatase, ty	1.54 1.52	3.15 3.36
	441648 439769	H05734 AA448828	Hs.30596	ESTs Homo sapiens mRNA full length insert cDN	1.52	3.17
40	437696	Z83844	Hs.5790	hypothetical protein dJ37E16.5	1.52	4.93
. •	413019	BE281604	Hs.75140	low density fipoprotein-related protein-	1.52	3.01
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.52	3.83
	422596	AF063611	Hs.118633	2-5-oligoadenylate synthetase-like	1.50	3.04
45	421851	R18686	Hs.108896	lambda-crystallin	1.47	3.10
45	448499	BE613280	Hs.77550	hypothetical protein MGC1780	1.44	3.07
	427378	BE515037	Hs.177556	melanoma antigen, family D, 1	1.44	3.00
	412641 448143	M16660 AF039704	Hs.74335 Hs.20478	heat shock 90kD protein 1, beta ceroid-lipofuscinosis, neuronal 2, late	1,42 1,42	3.66 4.16
	413291	NM_006278	Hs.75268	siatyltransferase 4C (beta-galactosidase	1.41	3.30
50	435968	AW161481	Hs.111577	integral membrane protein 3	1.41	3.30
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	1.40	3.01
	443759	8E390832	Hs.134729	FXYO domain-containing ion transport reg	1.39	3.82
	444441	AW613841	Hs.301394	hypothetical protein MGC3101	1.39	3.43
55	430205	AB025904	Hs.235168	carbonic anhydrase XIV	1.36	3.32
33	406827 406906	AA971409 Z25424		gb:op92c04.s1 NCI_CGAP_Lu5 Homo sapiens	1.35 1.34	3.03 6.25
	426890	AA393167	Hs.41294	gb:H.sapiens protein-serine/threonine ki ESTs	1,34	3.66
	433320	D60647	Hs.250879	ESTs, Highly similar to CTXN RAT CORTEXI	1.34	3.18
	450358	AB010098	Hs.24907	coronin, actin-binding protein, 28	1.33	3.19
60	421612	AF161254	Hs.106196	806 antigen	1.33	3.03
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.32	3.68
	428342	AI739168		Homo sapiens cDNA FLI13458 fis, clone PL	1.32	3.10
	449444	AW818436		solute carrier lamily 16 (monocarboxylic	1.30	3.30
65	404700			Target Exon	1.30	3.14
U)	403043 409858	NM_006586	Hs.56828	Target Exon trinucleotide repeat containing 5	1.30 1.29	4.22 3.09
	424679	AL117477	Hs.119960		1.27	3.13
	406908	Z25437	115.113300	gb:H.sapiens protein-tyrosine kinase gen	1.27	3.66
	432665	AW603880		ATPase, H transporting, lysosomal (vacuo	1.26	3.09
70	423130	AW897586	Hs.21213	ESTs	1.24	3.34
	453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	1.24	3.15
	442680	BE270707	Hs.8583	similar to APOBEC1	1.22	3.94
	422319	AW403342	Hs.115232		1.21	3.36
75	402408			NM_030920*:Homo sapiens hypothetical pro	1.04	3.37
13	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	1.00	3.02

## TABLE 51B:

Pkpy: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT Number Accession

	430540	713_2	BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM48810 AU120387 BG770228 BG866740 BG913323 B1759980 BG395988 BM48875 BE881070 BE313889 BE879144 BM03834 AW245847 AH770171 BF196861 BE856897 AA463876 AJ375927 AA648810 AA948193 AA490916 AJ455893 AJ458188 AJ424008 A191843 A1137029 AW768399 AJ365196 AW337984 AW026150 BE466591 BE674599 AJ818438 AA772197 AJ651927 AW151143 BI198825 BG819083 BM458764 BE903567
5			AUSD/198 AVXIV.26130 DE369331 BE493391 A01926 BE731937 BE390023 BE637534 BF998405 BF988330 BM475542 AWX26215 BE591697 BE900610 BE731715 BW004200 BE900765 BE731097 BE390023 BG637534 BF998405 BF988330 BM475542 AWX26215 BE591697 BE900610 BE561530 BE561537 BE903182 BE732947 B1272704 BG761305 BE263420 BE391848 BE392475 BC008258 BI547991 BM50999 BE391391 BE259420 BE298109 AWX245422 A4423847 A4914618 H80534 BE30104 AL531791 A4435581 BF793112 AL577303 AA373365 BE748953 BF478303 BE879296 A451939 BM018598 A6893260 AW072450 F20201 AW151405 AW511572 AA773468 BG259639 BE391163 BC6621529 A4421728 BG767231 BM462953
10			BC340524 W52648 AA113434 BE785431 BI041981 BC332385 BC253168 BC759470 BF363229 BF981332 BE2599418 BE785738 BI091658 N72512 W58732 W58590 BC355399 A1205266 H19721 W17051 W770598 BI262010 AA844319 W74143 W772214 N85194 BC734033 BC164099 AA931069 F13645 R41394 AK025758 BC180917 BC349455 AA812018 AA740241 A1027722 A1150356 AA886395 AW977627 BE220225 AA884082 AW518114 A243844 AA809493 AA481029 AA825718 A1347856 A4431670 AA814436 A1251109 R07704 AA755505 AA724533 AU918399 AL537550 AA491103 AW008188 R07703 AA989120 AA746235 AW028933 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BC077936 B1860809
15	437179	12239_1	BE002760 BG746251 BE962912 BMA54584 AL134894 BF104082 H80591 AK055109 BC019985 AA187684 BC656226 BMR23227 AI932311 AW264381 AA398371 BM021483 AW32433 AI375777 Al129580 AW262782 AA134107 BMD23515 AA977504 AI859222 AI348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 AI092259 AI028416 AI074114 BG656536 BE501677 AW193419 AA917040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF476021 R41226 R69631 F04125 C02343 AA115589 R56480 AI400988 R54266 R31422
20	412652	18858_2	ABD1777 BE677762 AW008210 AW009441 BE350994 BE207949 AU091475 AI802774 AI827533 AI075363 AI659979 AA687855 AU078125 AU090285 AA670058 AA602411 AA683472 AI435058 AA612826 AU038932 BC057726 A167355 BF449023 AI289476 AW074381 BF972912 AI991780 AA889919 AI537472 Z39730 AI668953 AI192337 BE812978 BE812939 AA115248 H99006 AI915784 F08973 T16748 D20468 AA609899 BF081234 AA115336 BE812876 BE812972 BE812982 BE813006 BE813019 R43883 BE812981
	430015	713_2	BC017171 BC012195 NM, 007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 B1759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847
25			AIT70171 BF 196861 BEB56897 AA463876 AI375927 AA648810 AA948193 AA499316 A445993 AA458188 A2240408 AI191843 A1131029 AW768399 AI365196 AW337984 AW026150 BE466991 BE574599 AIB18438 AA772197 AI651927 AW151143 BI19826 BG819083 BMA59764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG675384 BF996406 BF988390 BMA75542 AW246215 BE501887 BE903610 BF541570 BF567437 BF903787 BF737947 B1777204 BG781305 BF262642 BE391848 BE382475 BG008258 BI647991 B4459099 BE391391 BE259420
30			BE298109 AW245422 A423847 A1914518 H80534 BE301004 AL531791 A1435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 A1359493 BM018598 A1689260 AW072450 F20201 AW151405 AW517572 AA773468 BG255694 BE391163 BG621529 A421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 B57853929 BF93132 BE259418 BE785738 B1091658 N72512 W536732 W35690 BG958989 A1205206 H19721 W17051 W77958 B1262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 A1027722 A150336 AA886395 AW977627 BE220225 AA884082 AW518114 A1243844 AA809493 A4481029 AA825718 A1347866 A1431670 AA814436 A1251109 R07704 AA765606 AA724593 A1918399 A1537550 AA491103
35	420218	191547_1	AW008188 R07703 AA989120 AA745235 AW02983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612085 BE077936 BI860809 BE002760 BC746251 BE962912 BM454584 AL134894 BF104082 H80591 AW958017 R42557 AL337047 AA948360 AI633005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756
	410000	497855_1	AW779380 AA609879 AI634791 A1493770 A1565211 Z41145 AI627952 AA303734 BE349457 AW195765 AA256527 BE089727 BF347859 AW499616 AA191322 AW499617 AL601010 AW575742 AA729043 BE463447 AA086179 BE549623 A1335824 AW408712 BM149172
40	410600 400282	497635_1 7778_2	BC014433 Z49835 D16224 U42068 D63465 NM, 005313 AL535156 AL533202 AL533596 AL531770 AL547267 AL551080 AL5442510 AL542531 AL5442531 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 BIS56431 BIB52264 AL045490 BE407948 BI668702 BI713725 BE547233 BM312673 BG822625 AW239512 BM312658 BE296719 BM312059 BI712618 BM309832 BI712639 BE713678 BM3164261 AL5442631 BE726661 BG326781 BF726662 BM3161034 BM316135 BG472541 BM316136 BG745678 AL54472541 BM316135 BG74678541 BM316135 BG74678541 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL5442631 AL544263
45	417282	2142_2	AW991405 BG739837 AA287804 AW801855 AL568814 AW384099 AW384058 AW754178 AU01019 R33917 BE814037 AI557164 AK025474 U11293 AF141304 BM424202 AL539879 AL564793 AL543707 BIR53328 BG756797 BIB55494 BE901116 AL556989 AU133347 RI825805 AW949559 BM012604 BG773980 BG661309 B1260149 BF435764 BG983060 BF822225 BI059728 BF917866 BF917609 BF914374 O31003 AA734218 AL470466 BM283921 BE566788 BE669957 BF430992 AW514978 AW705958 BF110763 BF222758 AA195232 AU341353 AI698676
50			A093230 A172322 A1656594 A1208758 AA975916 A1089224 A1264922 AA256604 AA659637 BE218707 AA195203 AW999239 AW139706 N31717 AW205941 R95955 N39147 BM015411 A1576975 BF689524 A1563130 B1658155 AA417889 AL513995 AL568815 AU150693 AA8366028 H84388 AL517078 AL564680 AL535907 AL551042 A020435 W47314 A1680613 AA456116 BF836679 AW975173 H24039 AW105059 BE548113 AW370257 BM011139 AW675130 BE276045 BF933396 AL517903 AA886367 B1030598 BC477193 BF973867
	446019	658727_1	A362520 D25917 N570784 A1742347 AW269789 A1270700 AW610541 AW793036 AW793035 AW610540 AW362220 AW362166 AW362214 AW362225 AW362228 AL 119827
55	400222	9287_3 865166_1	NM_002082 L16862 BG828886 BE795217 BE904064 BE294526 BE297283 BE394617 BE935127 BE935106 F12351 BG823182 H16710 AA302840 T93016 T92950 AU184997 AA077551
	409760 438619	35124_1	NM_016575 AB032773 A1765521 BF593742 A1897757 A1761233 AW467938 BF000670 AB18496 N24761 AL043306 BF476138 BF593836 AA132787 A147248 AU86795 AA151317 T95298 AW083548 AA058371 N27951 A1769860 A1784548 AW205506 A1800679 A1041733 A459902 BE327641 A1868679 A1524738 A1374333 A1744176 A1241825 AA027842 AL524933 AL524932 BF947764 BF340737 BF948700 BG996395 N53455 N21027
60	408208	642734_1	A1127616 NJ5901 AA682443 AA678249 AA719371 AA132582 T15881 H99958 N40717 XW959402 A1267251 BF909329 A1142035 T95379 H29420 R59502 H17318 H17331 H29327 R40829 R43395 R59573 A1749561 R56599 H16755 A1694500 AA0277907 RJ757877 AWA39843 AW172765 BE018717 BE464329 BE302285 H96902 BF477981 BE674208 BE670755 H95980 T15387
	400236	231_3	MB0359 NM_002376 AU132239 AU120606 AU124963 A065116 BE900808 BF968374 A1806648 BG774205 AW250728 BE265845 AA290719 AU125196 BG428863 AA333580 AA604551 W73300 A1932646 AA082201 AA627618 BF038887 BF337051 B1021159 AW057581 A1983156 A1268004
65	416730	1988296_1	T71931 T90093 AW194009 H93969 A1742843 A1935080 BEO41751 H93970 AW797399 W05032 T87824 T82912 AW129639 A1221821 AJ911810 AA703093 AA160135 AW779124 AA102559 AA969546 D29560 BI915937 AA707716 BI085679 AA700887 AA081085
<b>70</b>	425996		BM006551 AA367152 AW953705 AI631833 AW237429 AW027804 AA729038 BE503409 AI521935 BF739953 AA702982 AA557633 AA780065 AI218139 AW194264 D20120 AI082715 AI959980 BE857686 BE326711 AW953706 AI393749 AI383821 W67199 AH31759 AI796526 AI521794
70	430441	1438_6	AI796380 AW117545 AI749657 AI537634 N50122 BG108218 BE50048 AW380115 BE2769629 AI911518 AW380113 AA902964 AA455001 AI276529 AI685597 AA970496 DG1084 AW380068 AW380080
	437158	59575_1	R00283 C15238 AW327776 D80759 AL050068 AA160485 AW173544 AW296506 AW439860 AI521563 AI702529 AI393606 AW138323 AA570109 H19504 BM021968 BF063327 BF593552 AA530766 AI597717 AI807128 AA523012 AI356250 AW451857 AA974203 AI762577 BF512552 AW007307 BE675286 AW450602 AA962057
75			AWS16069 AIS82546 BF221924 BF222543 AI801808 AW468599 AW000736 AI856625 AW235356 BM021837 AA911956 AI680606 W06516 103370
	412315	1163860_1	AWG2673A AWG26762 AWG26682 AWG26732
80	400235	3084_1	BC001179 NM_005336 M64098 BC014305 BI827845 BI918183 AU124191 AU125604 AU140930 AL043307 BG763670 BG824279 AU125959 BI518466 BE271867 BM264138 BE314823 BM996533 BE273657 BG418930 BM048338 AU134388 BE163486 BE163483 BG421880 BG768130 AW500482 AI910107 AW668323 BF0813770 AW460290 BM466817 BG255224 BE394282 AU140278 BE887348 AL042675 BI195986 BE883385 BE544751 BE270148 BM011334 AI093482 AA029803 AI610706 BE386809 F06628 AW408605 BF814085 BC007961 BM451548 BG768053 BM452488 AU140330 BG489566 BI870474 BM014013 AU131264 BG679824 BI225752 BI457400 BE410173 BM044254 BG763690 BE251495 BG179862 BE513489
			• • •

	Pkey 402075	Ref 8117407	Strand Plus	NL_position 121907-122035, 122804-122921,124019-12416
80	Strand: Nt_posit	ion:	Indicates DNA stra	in chromosome 22° Dunham, et al. (1999) <u>Nature</u> 402:489-495. and from which exons were predicted. te positions of predicted exons.
75	TABLE S Pkey: Ref:	i1C:	Sequence source.	rresponding to an Eos probeset The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
70	432665	27095_3	BG165971	SICA(SSIS) BESISSOS DE FOTTOS BE143233 AL.577712 AI400326 AA769318 AA427866 AW088714 AI150755 AI924874 AI186243 AA804195 AA768972 AW574769 AW204520 AA235326 AI005076 BE826687 AW004816 AW007235 BE826639 BE826634 BF222941 BE826631 BE826643 AA292639 AI690331 AI673409 AA627727 AI923685 AA931499 AI249783 AI810663 AA548622 AA702095 AA832395 BI259508 AA262993 AW075840
_	449444	2735_1	BI002756 A U59185 NN AU155762	A489664 BF827261 W74741 BF963166 L004656 AV734324 A1245349 AA359517 H88760 D79128 AA970406 HD1059 H88761 H03446 BG620383 AU135008 AU136895 AU158158 R73508 R55751 R23756 N74630 AW078687 BE439761 BE786351 R68994 BE785867 AW297502 AW297553 BG431545 AW814843 3G429539 BE928862 BF811258
65	406827 428342	0_0 6712_1	BF446026 / AW070509	NO15524 AA724079 BI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW966804 AA425658 AA769094 NW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW629495 AW506314 W74704 AI356361 AI923640 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 AI392620 Z40708 W263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036967 AW370823 T55263
60	411825	7891_1	AK000695 / BE272330 / AK000334 (	11953 BF93333 BF932671 N00357 R14072 BF9362 15061 B6950000 1505000 150500 150500 150500 150500 150500 150500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 160500 16050
55	427289	1820_2	BC007350 E AW512968 AW512240 AV703420 F	(G756159 BG769338 BG761999 BG744385 BG770572 AW370610 AW370581 AA978353 AW327973 AW402425 Al889380 AA868504 AA630644 AI751211 N26980 A1394506 AA747849 BF154926 BF477185 AA69647 R9135 AI750216 T33536 W36278 AW079375 AA505485 AA515380 BG760793 AW370651 BG766029 AW370595 BF229885 BG762422 BG764907 T50662 AA025671 AW815715 BG5047 AA485582 R55186 H90385 R55913 BI261497 BI018403 BF376945 T75578 BF933325 BF 932853 BG502266 AW868934 AV683504 AW3693 BG764943 BG764943 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494 BG76494
50			AW075006 A AW302327 A AI252926 AI AI802837 AI	(NOD75181 AA464019 AVV302733 AW075100 AW072433 AI802854 AI334999 AI802853 AI345036 AJ485921 AJ307274 AJ307478 AI251289 (NOD72520 AJ312145 AW073656 AW072531 AW071289 AJ307559 AA876186 T29587 AJ307493 AI255068 AI252868 AI25288 AW07899 252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073459 AW072901 AW072496 AW071470 AJ305762 AI254764 251264 AW073049 AW071311 AJ340643 BE138955 BE138502 AW073456 AJ334733 AI054335 BE13950 AI054302 AI054060 AI054057 259311 BE139278 AW0771031 AW771039 AW320058 BED41872 AI254444 AI271496 AI252427 BF718773 BF718845 AW074866 BE857822
45	406851 427239	0_0 20459_2	BF355591 B AA609784 R	F336596 AA360497 H26072 BG198352 AW364709 H40926 H44214 AA836538 BI059563 97304 F704750 AAS92906 AID15067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI3348B1
10	455705	77478_2	AA625761 A AI863860 HC	AB72090 AB26790 AA328366 BE827416 R75951 D56918 R68122 BE827384 AL118797 A184164 AA164411 BI495332 BE858113 0660 T69849 AW780398 C14667 BE934995 BI016652 R92801 AA164410 H00752 AW373305 AW373299 AW373329 AW78039 5513812 AA133359 AW581719 BF434402 AL600619 BG699731 B1551395 AW027136 AW055130 BF93912 AU76048 H18584 AW161061 B16101 BE049456 AW064012 AA554079 A1274682 AI370526 AW131990 AA853195 AA853191 BG118295 AA761620 BG705371
40			BE827256 R BE093545 A' BE702099 B AV724531 D RM128728 A	16550 R39478 R39479 R94368 BG540916 BM314745 AA251087 D54231 D55274 BF085805 D31589 AM966405 AW994425 D81879 M901107 AA383529 BD021552 R56420 N39976 AA573281 H82595 AA23455 BE093539 AW367006 BF386697 BF366318 AA663856 C035969 A1267384 A1267232 BE348320 AA621574 AA861212 BF083343 BF083341 AV745131 D53074 AW954476 AW954472 AA376836 53063 C14928 AA093287 AA062638 BG483558 BE940050 AA765954 T70171 BE938775 BE940057 D53502 AW373300 AL118798 A19411 AW444708 AW952455 A1887612 BF431948 B1496876 A1264159 BM128481 A1624657 A1689301 A1969467 AA861685 AA251595
35	419200	9531_1	BF036043 AV AA937302 AV AW028637 A	V190446 BG 194731 AW662036 AI445021 BE937550 AW818972 AW393132 AA834685 BF112058 AV721682 H16423 AIZ70167 AI857345 W318444 BE929780 BG498678 BF155010 BI598271 BI599811 BE161728 AW578737 AW753711 AW379707 AW381918 BG506608 W994240 BF887392 BF790073 AW381624 AV727105 BF49618 AA443174 AU18009 AW2850 AW573242 AI417258 AA85483 AI676131 B36627 AA443828 AW7592922 AA233129 AA730278 AW439062 AW474332 BI043239 AW474342 BG708553 AW362422 BF090028
30	406782 417324	0_0 292720_1	AA430373 AA BG775668 B	3680336 AW991605 AA455904 AW265494 AW265432 BF911380 AA456370 BF911379 AA195677 BF914311 BF913866 BG775059
25	455839 458997	1518842_1 11847_4	AI096810 AW R93989 AA37 AA249732 BE145823 BE BM453041 A	183016 AIG35738 NZ7524 BE645916 AI247842 AW991230 AI754277 H16814 AI766892 BF108422 AI800361 195129 F11313 N37946 5242 BF109388 AI860939 AI680060 AW953899 BF971486 AI972337 AW953841 AA372437 AI216746 H11384 R38484 AA249043 145830 BE145884 BE145814 BE145905 BE145833 BE145834 BE145833 BE145889 A760783 BE218582 AI340046 AW166131 BF515854 AIG30296 AA461307 AI090881 AW023059 AA155797 AA115486 AL597396
20	418166	18858_1	AA102142 BG AI673786 BF6 BE613627 AA AK065915 BE	749978 BI770417 BI862544 A111687 AFG63562 BE740347 BE874854 A3305113 BE513675 BE091369 BR045680 BE091463 BI046548 68704 A025179 BF355840 BF886357 BF886313 BG951884 A3347880 AW627563 BF932536 AW820377 BF739372 BF831620 BE068264 641745 W01130 H28252 867252 A1523348 AA765350 BF446858 Z43675 R19529 AL133837 BG389444 AW382942 BE702596 AA081961 BE835247 BE835308 7787279 BE64570 AA 376590 AA376592 AW9542473 M87727 AA248770 AJ754416 AA213316 BF592044 AA811729 AW514842 AI633486
15			AW374086 BC H45012 R107 W80749 BF23	4 T78959 W01317 H45860 W80837 N53985 BG757202 BE838055 BE072895 BE072668 BE857012 BM042833 AA083591 BG745462 831126 BE715757 BG767243 BG763272 AA113402 A1024044 BF818501 BE081938 BF353818 AA746336 BM019086 BE772894 H16977 33 BE708619 BF570432 AA593338 AA064637 T28082 AA852845 T78907 AA346590 F00017 BE966368 N85726 AA732431 T54379 8314 BE279768 AA325106 T19241 BE409939 BF852119 W23803 T54011 AW392638 B1465185 AW516784 AA211335 B1159846 9615 W49576 BF851406 R88120 AA4340728 H44546 T61029 N44804 AA114948 H25950 B1261965 AA582599 BG469385 BF818172 87470 AW362633 BE883122 BM470779 BE935760 AW856056 AW856103 BE826607 AW381799 AL121058 BE828618 BE769545
10			A1720319 A186 AW082909 A19 BG479797 BE W25087 BM49 BE948864 BE	6190 AA047013 AA039525 BC049622 AA369065 AA025686 AIS70198 AA7U6304 AW439251 IN54551 AW16800 AW16909 AW16909 AS 51490 BEBSGA1 AW591246 A199143 A1151074 A1499514 A1050394 AW02167 AA382409 F16207 T02399 A1922691 AW761663 408436 B1450153 BC386046 BE616601 AW151629 BC236164 BF852743 BF852046 T57801 W37981 AA482668 H43740 W58142 9862 AU125403 BC767992 BC286516 A1114509 BC39514 BE385905 AA450315 BC750593 AA557855 BC766487 BC766998 707077 PRF7070010 AA577089 BT36851 A1745058 AY39517 AI625038 AA641801 AA846174 H26335 AA025658 BF690282 R57845
5			8E712976 8E7 BE713043 8E7 BE712984 BE7 BE712902 BE7 BENEGRAD RC	54815 BF569858 BI712614 BG655891 BG424940 BE175180 BM313160 BG471936 BM091124 BF885884 BF870522 BE004490 12862 AA401033 BF569477 BE712936 BF353839 BE713042 AA316561 BE712974 BE712977 BE712938 BE712937 BE712867 13022 M42463 BE712901 BE713041 BE712994 BE712895 BE713049 BE713049 BE713098 BE712988 BE712988 BE712986 13022 M42463 BE712901 BE713043 BE712949 BE712895 BE713049 BE713049 BE713040 BE713040 BE713040 BE712865 12982 BE712975 BE712970 BE712950 BE764799 BE715723 BE715745 BE712915 AAA41839 BE713040 BE715755 BF872528 12897 BE712912 BG984910 BE7142003 BE764799 BE715723 BE715745 BE712915 AAA41839 BE713040 BE715755 BF872528 195104 BG744878 AU124081 AI889823 AI801072 AI633102 AI678670 AI433608 AW194294 AI354559 AI686736 AW152477 AI419496

	400850	9757499	Minus	151830-152104,152649-152744
	402609	9926445	Minus	113464-113633,114264-114654
	400750	81 19067	Ptus	198991-199168,199316-199548
_	402994	2996643	Minus	4727-4969
5	403817	8962065	Plus	110297-111052
	402829	8918414	Plus	101532-101852,102006-102263
	403532	8076842	Minus	81750-81901
	405451	7622517	Minus	145949-146227
_	405785	9581533	Minus	98702-98925
10	405506	6466489	Plus	80014-80401,80593-81125
• •	405486	6651379	Plus	179441-179598
	406382	9256148	Plus	122336-122851
	401454	9186923	Minus	114659-114832
	405885	7677703	Minus	42574-42998
15	403969	8569909	Plus	31237-31375,32405-32506
	400533	6981826	Minus	277132-277595
	400991	8096825	Plus	159197-159320
	401591	9966977	Minus	55410-55835
	404067	3282162	Plus	1415-2071
20	404140	9843520	Plus	37761-38147
	401914	9369520	Plus	62537-62945,63155-63308
	404700	9800123	Minus	159621-160203
	403043	7768753	Minus	314423-316252
25	402408	9796239	Minus	110326-110491

TABLE 52A: ABOUT 204 GENES UPREGULATED IN PRIMARY MELANOMAS RELATIVE TO MELANOMA METASTASES
Table 52A lists about 204 genes upregutated in primary metanomas relative to melanoma metastases. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03
Genechtip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey:

ExAcon:

Unique Eos probeset identifier number

Exemplar Accession number, Genbank accession number

Uniquenel Title:

Unique File:

Vingene gene title

R1:

90th percentile of primary metanoma Als divided by the 90th percentile of metanoma metastasis Als, where the 15th percentile of normal tissue Als was subtracted from both the numerator and denominator

35

30

Unique Eos probeset identifier number
Exemplar Accession number, Genbank accession number
Unigene number
Unigene gene tite
90th percentile of primary metanoma Als divided by the 90th percentile of metanoma metastasis Als
90th percentile of primary metanoma Als divided by the 90th percentile of metanoma metastasis Als, where the 15th percentile of normal tissue Als was subtracted from both the numerator and denominator

	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
40	421948	L42583	Hs.334309	keratin 6A	21.90	16.66
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	21.36	43.65
	401781			Target Exon	18.70	18.58
	401780			NM_005557°:Homo sapiens keratin 16 (foca	15.34	16.00
	431350	NM 000427	Hs.251680	loricrin	12.34	9.86
45	409632	W74001	Hs.55279	serine (or cysteine) proteinase Inhibito	11.24	8.73
	412636	NM 004415		desmoplakin (OPI, DPII)	11.20	6.62
	417366	BE185289	Hs.1076	small proline-rich protein 18 (comifin)	10.46	12.75
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	10.41	25.49
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	9.20	8.63
50	420783	AI659838	Hs.99923	tectin, galactoside-binding, soluble, 7	8.11	11.14
•	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	7.90	8.92
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	7.14	22.14
	427666	A1791495	Hs.180142	calmodutin-like skin protein (CLSP)	7.03	8.90
	430686	NM_001942	Hs.2633	desmoglein 1	6.88	5.39
55	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	6.60	12.79
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	6.44	6.19
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	6.34	7.77
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	6.15	8.91
	418067	AJ127958	Hs.83393	cystatin E/M	6.08	9.24
60	408535	AW381532	Hs.135188	ESTs	6.04	17.40
00	402075	7111001002	12.100.00	ENSP00000251056*:Plasma membrane calcium	5.96	8.41
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	5.46	3.32
	410001	AB041036	Hs.57771	katikrein 11	5.38	5.36
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	5.32	3.84
65	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	5.19	5.30
-	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	5.03	7.94
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	4.86	5.22
	421773	W69233	Hs.112457	ESTs	4.82	12.41
	442577	AA292998	Hs.163900	ESTs	4.82	4.40
70	401760	1445230	13.100300	Target Exon	4.60	11.03
, 0	408522	AI541214	Hs.46320	Small profine-rich protein SPRK (human,	4.50	11.35
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	4.47	12.43
	431211	MB6849	Hs.323733	gap junction protein, beta 2, 26kD (conn	4.45	2.99
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	4.39	4.23
75	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	4.38	4.55
15	418663	AK001100	Hs.41690	desmocollin 3	4.36	5.16
	424620			kallikrein 7 (chymotrypic, stratum com	4.29	5.19
		AA101043	Hs.151254		4.28	5.41
	401747	4/3300+0	11- 77240	Homo sapiens keratin 17 (KRT17) hydroxyprostaglandin dehydrogenase 15-(N	4.24	2.30
80	414807	AI738616	Hs.77348		4.22	4.82
οU	411274	NM_002776 BE616501		katilitrein 10 Homo sapiens, Similar to RIKEN cDNA 1110	4.22	8.26
	439496		Hs.32343		4.18	4.73
	420039	NM_004605		sulfotransferase family, cytosolic, 2B, small profine-rich profein 2A	4.16	7.30
	429538	BE182592	Hs.139322	Strail from particulation of	4.10	7.30

	418686	236830	Hs.87268	annexin A8	4.12	4.09
	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	4.08 4.08	2.13 4.38
	421733	AL119671	Hs.1420 Hs.283082	fibroblast growth factor receptor 3 (ach defension, beta 3	4.05	5.38
5	416091 442757	AF295370 AI739528	Hs.28345	ESTs	3.94	4.28
•	427318	AF 186081	Hs.175783	zinc transporter	3.92	3.07
	453309	A1791809	Hs.32949	defensin, beta 1	3.90	4.30
,	422192	AA305159	Hs.113019 Hs.137569	fis485 tumor protein 63 kDa with strong hornolog	3.88 3.86	2.81 5.03
10	424012 429365	AW368377 AA451798	Hs.99249	ESTs	3.76	4.05
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	3.72	6.35
	425580	L11144	Hs.1907	galanin	3.68	3.65
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot hypothetical protein FLJ22408	3.68 3.59	2.75 5.72
15	444946 408591	AW139205 AF015224	Hs.156457 Hs.46452	mammaglobin 1	3.58	4.73
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	3.58	2.62
	438501	Z44110	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.56	2.61
	421574	AJ000152	Hs.105924	defensin, beta 2	3.56 3.48	4.0~′ 4.38
20	402294 428666	AL080190	Hs.189242	Target Exon Homo sapiens mRNA; cDNA DKFZp434A202 (fr	3.44	2.95
20	401785	AL000130	15.103242	NM_002275°:Homo sapiens keratin 15 (KRT1	3.42	4.92
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	3.36	4.24
	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	3.31	5.42
25	452392	L20815 AB007877	Hs.507 Hs.12385	comeodesmosin KIAA0417 gene product	3.30 3.30	8.56 2.35
23	445183 433124	U51712	Hs.13775	hypothetical protein SMAP31	3.26	2.15
	419098	AA234041	Hs.87271	ESTs	3.25	4.34
	421978	AJ243862	Hs.110196	NICE-1 protein	3.17	5.86
20	445493	AJ915771	11- 00215	metallothionein 1E (functional)	3.16 3.14	2.98 2.07
30	448111 445745	AA053486 AB007924	Hs.20315 Hs.13245	interferon-induced protein with tetratri KIAA0455 gene product	3.10	2.39
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.06	2.71
	407839	AA045144	Hs.161566	ESTs	3.06	3.54
25	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	3.04	4.64 2.78
35	439706 452240	AW872527 AI591147	Hs.59761 Hs.61232	ESTs, Wealdy similar to DAP1_HUMAN DEATH ESTs	3.04 3.00	4.79
	409190	AU076536	Hs.50984	sarcoma amplified sequence	2.96	3.05
	408015	AW136771	Hs.244349	epidermal differentiation complex protei	2.94	10.53
40	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	2.91	3.01
40	406964	M21305	Hs.26557	FGENES predicted novel secreted protein	2.90 2.89	5.34 6.64
	451541 454027	BE279383 R40192	Hs.21527	plakophilin 3 Human DNA sequence from clone GS1-115M3	2.86	2.81
	414737	A1160386	Hs.125087	ESTs	2.84	1.76
45	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	2.82	1.83
45	405542	AE147070	Un 150953	Target Exon	2.80 2.78	2.77 5.17
	442503 402970	AF147078	Hs.150853	p53-responsive gene 5 C20000886*:gi]9280563 gb AAF86472.1  (AF	2.78	3.37
	416730	T99937		gb:ye72d04.r1 Soares letal liver spleen	2.76	2.76
	433435	BE545277	Hs.340959	Ts translation elongation factor, mitoch	2.75	2.76
50	447164	AF026941	Hs.17518	vipirin; similar to inflammatory respon ESTs	2.72 2.70	2.86 6.68
	409453 428824	AI885516 W23624	Hs.95612 Hs.173059	ESTS	2.67	2.75
	437233	D81448	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	2.65	3.07
<i>E E</i>	430630	AW269920	Hs.2621	cystatin A (stefin A)	2.63	2.38
55	433339	AF019226	· Hs.8036	glioblastoma overexpressed	2.61 2.57	2.44 1.74
	444670 414602	H58373 AW630088	Hs.332938 Hs.76550	hypothetical protein MGC5370 Horno sapiens mRNA; cDNA DKFZp564B1264 (f	2.54	3.66
	400995	,,,,,,,,,,,		C11000295*:gij12737279peffXP_012163.1[	2.54	2.93
<b>CO</b>	423515	AA327017	Hs.176594	ESTs	2.53	7.36
60	417359	T99264	Hs.191117	ESTs	2.53 2.52	2.54 2.15
	432426 413822	AW973152 R08950	Hs.31050 Hs.272044	ESTs ESTs, Weakly similar to ALU1_HUMAN ALU S	2.52	3.05
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.52	3.85
65	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	2.48	1.76
65	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	2.47 2.47	1.92 2.56
	413392 442762	AW021404 AF035119	Hs.13021 Hs.8700	ESTs deteted in fiver cancer 1	2.46	1.90
	444781	NM_014400		GPI-anchored metastasis-associated prote	2.46	7.90
~^	424364	AW383226	Hs.163834	ESTs, Weakly similar to G01763 atrophin-	2.46	2.66
70	420568	F09247	Hs.247735	protocadherin alpha 10	2.45 2.46	3.01 2.82
	405885 412633		Hs.74304	Target Exon periplakin	246	5.01
	429852		Hs.225948	small inducible cytokine subfamily A (Cy	2.45	3.35
	429624		Hs.99476	ESTs, Wealdy similar to 13131848 alpha1	2.44	2.33
75	407325	AA291180	Hs.328476	ESTs, Wealdy similar to alternatively so	244	211
	431441		Hs.2794	sodium channel, nonvoltage-gated 1 alpha Homo sapiens cDNA: FLJ21274 fis, clone C	2.43 2.42	3.66 3.12
	432543 430168		Hs.152423 Hs.145582	DKFZP43411735 protein	241	2.75
	408000		Hs.198689	butlous pemphigoid antigen 1 (230/240kD)	2.40	3.67
80	404049	l .		NM_018937":Homo sapiens protocadherin be	2.39	1.89
	433576 444083		Hs.161091	ESTs gb::co17a10.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.39 2.38	1.59 2.59
	444083			gb.to1/a10.t1 soates_NSF_F0_9W_O1_FA_F_3 ESTs	2.37	2.12
	~~~~					

	431842	NIM_005764	Hs.271473	epithelial protein up-regulated in carci	2.36 2.34	2.23 1.99
	453931 452308	AL121278 AJ167560	Hs.25144 Hs.61297	ESTs ESTs	2.31	3.82
	431048	R50253	Hs.249129	cell death-inducing OFFA-like effector a	2.31	2.18
5	403752			NM_002753*:Homo sapiens mitogen-activate	2.30	2.38
	402525			NM_002699*:Homo sapiens POU domain, clas	2.30 2.30	2.36 1.73
	420223 452023	N27807 AB032999	Hs.27566	ribosomat protein L4 KIAA1173 protein	2.29	4.54
	443172	AW662964	Hs.199061	p300/C8P-associated factor	2.28	2.02
10	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	2.28	1.71
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	2.27 2.26	1.81 2.17
	429554 436895	NM_012275	Hs.207224 Hs.5338	interleutin 1, delta carbonic anhydrase XII	2.26	2.51
	404029	AF037335	ns.3330	NM_018936":Homo sapiens protocadherin be	2.26	2.19
15	424049	AB014524	Hs.138380	KIAA0624 protein	2.26	2.99
	442423	BE326264	Hs.246842	ESTs	2.26	1.75
	408452	AA054683	Hs.192455	ESTs, Wealdy similar to ALU7_HUMAN ALU S stratitin	2.26 2.25	2.29 2.40
	428471 410541	X57348 AA065003	Hs.184510 Hs.64179	syntenin-2 protein	2.24	2.46
20	415539	AI733881	Hs.72472	BMP-R1B	2.22	1.64
	425701	AA361850	Hs.240443	Human clone 137308 mRNA, partial cds	2.22	3.04
	423973	AF038461	Hs.136574	arechidonate 12-lipoxygenase, 12R type	2.22 2.19	3.24 4.74
	409178 433091	BE393948 Y12642	Hs.50915 Hs.3185	katilivein 5 lymphocyte antigen 6 complex, locus D	2.19	7.96
25	430171	AF086289	Hs.234766	skin-specific protein	2.17	3.56
	401994			Target Exon	2.14	3.34
	449228	AJ403107	Hs.148590	protein related with psoriasis	2.11	5.52
	446292	AF081497	Hs.279682	Rh type C glycoprotein	2.11 2.05	5.78 2.96
30	426150 452554	NM_003658 AW452434	Hs.167218 Hs.58006	BarH-like homeobox 2 ESTs, Weakly similar to ALU5_HUMAN ALU S	2.04	4.17
50	443162	T49951	Hs.9029	DKFZP434G032 protein	1.98	3.20
	400304	AF005082	Hs.113261	Homo sapiens skin-specific protein (xp33	1.94	3.20
	407395	AF005082		gb:Homo sapiens skin-specific protein (x	1.92	3.24
35	412507	L36645	Hs.73964	EphA4	1.92 1.90	3.06 3.18
22	410310 425415	J02931 M13903	Hs.62192 Hs.157091	coagulation factor III (thromboplastin, involucrin	1.89	5.26
	417324	AW265494	113.131031	ESTs	1.88	3.82
	412446	AI768015		ESTs	1.88	3.36
40	451092	AI207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein,	1.87	3.75
40	444726	NM_006147		interferon regulatory factor 6 Al905687:IL-BT095-190199-019 BT095 Homo	1.86 1.85	4,11 4,20
	424399 434346	AI905687 AA630445		ESTs	1.84	3.08
	446051	BE048061	Hs.37054	ephrin-A3	1.83	3.44
4-	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	1.78	3.45
45	413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	1.76	2.99 3.60
	411908	L27943	Hs.72924 Hs.21299	cytidine deaminase ESTs, Wealdy similar to AF151840 1 CGI-8	1.74 1.71	3.56
	445656 413966	W22050 AA133935	Hs.173704	ESTs, Moderately similar to A53959 throm	1.71	3.38
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.70	3.92
50	425650	NM_001944		desmoglein 3 (pemphigus vulgaris antigen	• 1.68	3.25
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	1.67 1.66	2.92 3.35
	429002 421335	AW248439 X99977	Hs.2340 Hs.103506	junction ptakoglobin ARS component B	1.66	4.31
	433662	W07162	Hs.150826	RAB25 RAB25, member RAS oncogene family	1.65	3.55
55	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.64	4.04
	414214	D49958	Hs.75819	glycoprotein M6A	1,64 1,62	3.59 3.13
	437897		Hs.146170 5 Hs.2022	hypothetical protein FLJ22959 transglutaminase 3 (E polypeptide, prote	1.62	2.92
	426350 413163		Hs.75216	protein tyrosine phosphatase, receptor (1.57	3.09
60	422106		Hs.111732	Fc tragment of IgG binding protein	1.53	3.39
	427751			conserved gene amplified in osteosarcoma	1.52	3.53
	416881		Hs.141358	ESTS	1.52 1.49	3.06 2.91
	435013 434574		Hs.110024 Hs.33470	NM_020142:Homo sapiens NAOH:ubiquinone o ESTs	1.48	3.05
65	454478			superoxide dismutase 2, mitochondrial	1.48	3.54
	447330			tadinin 1	1.46	4.48
	414583			proline arginine-rich end leucine-rich r	1.41	2.99
	433640			Horno sapiens cDNA: FLJ23538 fis, clone L	1.40 1.36	3.71 2.98
70	427461 430205			hypothetical protein MGC13010 carbonic anhydrase XIV	1,36	3.14
. •	450796			envoplakin	1.34	3.74
	407394	AF005081		gb:Homo sapiens skin-specific protein (x	1.30	3.26
	430513			G6C protein	1.28	3.26
75	411388		Hs.69752	desmocollin 1 ESTs, Weakly similar to unknown protein	1.22 1.14	3.64 3.71
13	431089 444107		Hs.10319	UDP glycosyltransferase 2 family, polype	1.00	3.20
	443672			butyrobetaine (gamma), 2-oxoglutarate di	1.00	3.26
80	TABLE		lainna Fan anat	d identifies aurabas		
٥Ų	Pkey: CAT n		Inique Eos probese Sene cluster numbe			
	Acces		Senbank accession			

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	Pkey 412636	1438_1	Accession	004415 AF 139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813
	472000	1430_1	J05211 BG69	BB65 BG740734 BG680618 BG739778 B1765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164
			BF149266 BE	940187 B1060445 B1060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 B1039774 BE713818
5			BE713548 AV	V170253 BE 160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW354859
			BF993352 BG	223489 BE819009 BF381184 BE715956 R58704 AA852212 AW365566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467
			BE819069 BE	819048 BI036306 BC990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 E814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BC436319 BE182166 AW365175
			AVVSSOUD BE	E818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693
10			AW068840 AV	W847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254
			RF698470 BE	931048 RF999889 BF368816 RE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124
			BE865341 AV	V799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115
			BE696084 AV	VB48371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 E713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396
15			8E/1329/ BI	113296 BE 173915 AW 99309 BF072305 BF080076 BE170553 AW 750539 BC005797 BF 350000 BE775750 BF 349467 831190 BF752409 BE006561 BG9559922 BF094833 BF094748 BF094583 AW 3777699 AW 607238 BE082519 AW 377700 BF349467
13			AI190590 AIS	:54403 Al397926 AU158477 BI467252 AU159919 Al760816 BF082516 Al439101 AA451923 Al340326 Al590975 Bl791553 Al700963
			Al142882 AA	039975 AA946936 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702
			AW166807 A	1346078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 BI458589 AI860584 AI025932 AA026047
20			AA703232 A	ASSISA AAS 15500 AW 192085 AA9 18281 T77851 A1927207 A1205263 BF082491 AW 021347 A1568096 BE939862 AA088866 D12062 A782109 W 19287 W 02156 AW 150038 AA022701 T87181 H44405 A1910434 BF082513 A1494069 A1270027 A1635878 AA128330
20			RG681425 R	E706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 B1762796 BG287391 AW798780 BE706045 BE926470
			AW799118 P	F087996 RF002273 AW879451 AI571075 RF067786 AV721320 AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290
			A1686869 A15	568892 A)915596 AW105614 A)887259 A)538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173
25			AW850878 B	E339707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 J905927 BF992780 AW853812 BG954443 B1770853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210
23			AVVJOD148 A	1905927 BF992780 AW833812 BG939443 BI710633 BG879408 BG740832 BG881081 BG939433 AW83108 107207 BC88808 BC706273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291
			BG961498 B	G678984 BIO40941 AA337270 AW384371 AW847442 B1058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837
			BG949393 B	E714441 AW996245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292
20				W365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 Al498487
30	445493	423456_1		1809938 A1808768 A1240593 A1915771 ·
	416730 444083	1988296_ 10908_12		
	408208	642734_1		N339843 AW172765 BE018717 BE464329 BE302285 H96902 BF477981 BE674508 BE670755 H95980 T15387
25	420223	191648_1	N27807 AA2	55634 BE276324
35	417324	292720_1		IG680336 AW991605 AA455904 AW265494 AW265432 BF911380 AA456370 BF911379 AA195677 BF914311 BF913866 BG775059
	412446	63467_1	BG951874 A	US/2109 U669212 AL 120184 AI769949 BE701002 BE 184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245
	412440	03401_1	BF960659 A	A987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 Bf035538 BF908052 BF908057
40			BF090026 B	F943158 Al632924 BF512340 BF952021 BF960776 BF943437 BF942847 Al768015 F09778 F04816 F02721 AA102645 Al633838
40			AA617929 E	F947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815
	444726	3503_2	BG285809 8	8E940673 BC432524 BE157554 BC676980 AU144284 A1745383 AU159045 A1693500 AW293668 AW371408 BE856107 A1338042 A1698246 BE673290 AW297653 AA156532 A1017342 A1916754 A1190644 A1184302 AA857671 BE857018 A1307420 A1318157 AW204327
			AW664668	AW274339 AA582788 AI345741 AW301433 AI873468 AW137388 BF718731 BF718413 AA877495 BF001575 AI824693 AW849604
			AWRA9405	AWR49396 AWR49173 RE673179 A1611327 AA705753 RE715478 AW849414 AW849399 A1085759 A1140849 T67412 A1889885 AW104647
45			AI912495 A	I889874 AI744241 BE717113 BE717108 BE715564 AI872527 AA029457 C00338 AI469558 BE715577 AA045413 BF843813
	424399	2196_1	NM_058173	AF414087 W72837 BF742809 AW070916 BE092421 AI905687 AA340069 BE074512 AI905623 AI905633 BG202312 W72838 AI139456 BE926938 BE186013 AW176044 AW291950 BG185269 BG197186 BG192597 BG183176 BG207535 AI127172 BE815819 AI905624
				202313 AI905837 BE815853
	434346	MH1094	14 AK056896 /	N924216 Al660493 Al984141 Al991272 AA593860 Al983793 Al346155 Al274929 Al281211 Al821178 BC020841 BF352476 BF843140
50			BF917041 V	N80832 AA630445 BF350167 BE162052 BE931808 AI572329 BG536379
	427751	15028_1	8E875818 /	AW751975 W39241 BF808798 W22600 BF082190 AA031290 R42801 H98235 H17925 Al631236 Al933786 H42736 AF000152 AU123911 BM354207 BF800492 BM142340 BE019322 AL597008 AW327818 BI041915 AW504825 AW504941 BF987969 NM_005730 U81556
			A1422R31 A	U154008 AA147822 AA873109 A1089244 A1360868 AW168024 A1819848 AA811327 A1355616 AA281629 A1880578 A1274316 AW014622
			A1268660 A	IZ70283 AA171981 AI349410 AA402469 AI421985 AI004864 AI423497 AI361503 AI363096 AW805345 AL539979 AA553967 AW50ZZ64
55			A1290698 N	122420 A1281054 A1500699 AW342095 C75122 AW504577 A1130811 A1423567 R79086 A1860451 BE222885 A1697830 A1279575 BF438693
			AW576277	BE218210 A1952376 AA506609 A1147566 A1391690 AA991622 A1696368 A1784664 AA741555 A1002681 AW474554 AW474508 D25623 A179800 W73566 AW411368 AA147971 AA088581 BF804510 AU145809 AU148108 AA223219 AU157840 AW169757 A1537862 N42341
			A1493929 A	M327853 AA713915 W15255 W56743 AA058322 H81878 AA723464 N27523 R37745 AA613566 AL526353 Al905211 BF802713 N40338
			AA249397	RE752020 RE250441 H64761 RER53011 HR1R77 H96088 AL576453 W73585 H39990 AW438965 BE899684 AI040299 AL561879 AA293821
60			H27760 BC	x018922 ALS33396 BE513580 BF432649 Al884985 AA404264 AW024396 AW167863 AW027036 Al302177 Al660487 AW026086 BF432564
			BF091011	A193156 AA744623 A1859510 B1063081 B1061541 AA777036 BG058486 B1063555 A1349411 BF874521 AW139801 A1268585 AA401267 364276 N72043 AF022231 B1256540 AU134437 BG826972 BE298386 AW134499 AW206089 BF846730 AW500331 BF849336 B1041697
			A1905209 F	W192840 AW410527 AI69743S AW006631 AW504124 AL048926 AI085476 AW327855 AA459344 AW207516 AW204875 BM142514
			BF436650	AA96098D AW242609 BI012363 AW837102 BE703126 BE814612 BE837981 BE703141 BF343101 R47375 AA031413 N40264 BG027363
65			BF526360	BE391263 AA280192 BE294042 BE250630 AU147734 AU146610 AA196787 N59465 AW575791 H16738 H96089 H64762 AW006603
				A1719393 AU155418 BG770385 AA339673 BG337748 H42694 BE834346 AA090896 BE619985 BM006968 R46008 BF304621 AA172280
	454478	4273_16		8F304885 BF933455 BF809973 BG386280 AW079808 T51091 AL520569 BE694350 T06360 BF347780 BE560703 BE296629 AW798102 AW805749 AW805872 BF985060 AW794380 BF380449 AW794466 AW794538
	407394	27110_2		
70	431089	125941		AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826
	TABLE	52C:	I lainua aventus	programment in a to the probability
	Pkey: Ref:		Sequence source	presponding to an Eos probeset . The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
75	, usi.		sequence of hum	an chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
	Strand:		Indicates DNA str	and from which exons were predicted.
•	Nt_posi	tion:	Indicates nucleoti	de positions of predicted exons.
	Pkey	Ref	Strand	N1_position
80	401781	724919) Minus	83215-83435,83531-83656,83740-83901,8423
	401780	724919		28397-28617,28920-29045,29135-29296,2941
	402075 401760			121907-122035,122804-122921,124019-12416 83126-83250,85320-85540,94719-95287
	401700	532303	1105	MATER ANTONIO ANTAINI IN MEN.



	401747	9789672	Minus	118596-118816,119119-119244,119609-11976
	402294	2282012	Minus	2575-3000
	401785	7249190	Minus	165776-165996,166189-166314,166408-16656
_	405542	9857564	Plus	71331-72183
5	402970	9650703	Minus	124891-125049
	400995	8099094	Plus	141186-141601
	405885	7677703	Minus	42574-42998
	404049	3688074	Minus	75765-78155
	403752	7678B57	Plus	33704-33828
10	402525	9800048	Minus	19748-20683
	404029	7671252	Plus	108716-111112
	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,4519

TABLE 53A: ABOUT 298 GENES UPREGULATED IN MELANOMA METASTASES RELATIVE TO PRIMARY MELANOMAS
Table 53A fists about 298 genes upregulated in melanoma metastases relative to primary melanomas. Genes were selected from 59680 probesets on the Eos/Affymetrix Hut03
Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of
mRNA expression. 15

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Unique Eos probeset identifier number
Exemplar Accession number, Genbank accession number
Unigene number
Unigene number
Unigene gene tite
90th percentile of melanoma metastasis Als divided by the 90th percentile of primary melanoma Als
90th percentile of melanoma metastasis Als divided by the 90th percentile of primary melanoma Als, where the 15th percentile of normal tissue Als was subtracted from both the numerator and denominator mRNA express Pkey: ExAcon: UnigeneID: Unigene Title: R1 R2

25

		•				
	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2
	407245	X90568	Hs.172004	titin	10.56	11.32 6.14
20	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	9.22	10.44
30	426752	X69490	Hs.172004	tiin	8.78 8.65	6.49
	418310	AA814100	Hs.86693	ESTs	8.37	4.39
	414522	AW518944	Hs.76325	Immunoglobulin J chain		
	433447	U29195	Hs.3281	neuronal pentraxin II	8.27	7.25
25	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	7.78	6.70
35	425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	7.49	9.02
	428087	AA100573	Hs.182421	troponin C2, fast	7.45	7.65
	436485	X59135	Hs.156110	Immunoglobulin kappa constant	7.35	6.18
	414546	AA353776	Hs.901	CD48 antigen (8-cell membrane protein)	6.97	5.75
40	412519	AA196241	Hs.73980	troponin T1, skeletal, slow	6.15	6.33
40	430280	AA361258	Hs.237868	interleukin 7 receptor	6.07	3.11
	449078	AK001256	Hs.22975	KIAA1576 protein	6.05	8.55
	437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled	6.03	5.36
	412561	NM_002286	Hs.74011	lymphocyte-activation gene 3	5.85	5.57
4.5	431574	AW572659	Hs.261373	hypothetical protein dJ434O14.3	5.74	6.40
45	458079	A1796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.72	4.76
	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	5.71	5.00
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	5.69	3.84
	420338	AA825595	Hs.88269	Homo sapiens, clone MGC:17339, mRNA, com	5.37	4.12
	430580	AA806105	Hs.300697	immunoglobulin heavy constant gamma 3 (G	5.31	6.02
50	428804	AK000713	Hs.193736	hypothetical protein FLJ20706	5.29	7.97
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	5.26	2.93
	445784	AI253155	Hs.146065	ESTs	5.12	3.10
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	5.05	3.41
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.59	4.00
55	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	4.47	3.92
	453857	AL080235	Hs.35861	OKFZP586E1621 protein	4.45	3.61
	428242	H55709	Hs.2250	leukernia inhibitory factor (cholinergic	4.37	3.22
	414829	AA321568	Hs.77436	pleckstrin	4.35	3.35
	417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	· 4.35	2.68
60	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	4.27	2.67
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	4.27	3.67
	441623	AA315805		desmoglein 2	4.24	3.66
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	4.22	3.60
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	4.20	2.58
65	426317	AA312350	Hs.169294	transcription factor 7 (T-cell specific,	4.15	5.82
	430770	AA765694	Hs.123296	ESTs	4.15	5.10
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.12	5.06
	406707	S73840	Hs.931	myosin, heavy polypeptide 2, skeletał mu	4.11	3.82
	444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibito	4.10	2.68
70	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	4.04	4.10
	417105	X60992	Hs.81226	CD6 antigen	4.03	4.51
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	4.02	3.72
	432485	N90866	Hs.276770		3.99	4.87
	415165	AW887604	Hs.78065	complement component 7	3.97	3.98
75	421181	NM_005574			3.96	3.19
	421712	AK000140	Hs.107139		3.95	7.34
	408380	AF123050	Hs.44532	diubiquifin	3.94	2.45
	422423	AF283777	Hs.116481	CD72 antigen	3.93	3.29
	408989	AW361666	Hs.49500	KIAA0746 protein	3.90	3.02
80	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	3.84	3.40
-	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TiT3 co	3.84	4.84
	424922	BE386547	Hs.217112		3.78	3.04
	400440	X83957	Hs.83870	nebulin	3.77	4.89
	400740					
				5	51	

		•				
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	3.74	3.91
	450293	N36754	Hs.171118	hypothetical protein FLJ00026	3.74	2.89
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.72 3.72	2.65 2.43
5	408548	AA055449	Hs.63187	ESTs, Wealdy similar to ALUC_HUMAN !!!! ESTs, Wealdy similar to ALU7_HUMAN ALU S	3.71	2.23
,	429490 414821	AJ971131 M53835	Hs.23889 Hs.77424	Fc tragment of IgG, high affinity ta, re	3.70	2.36
	419749	X73608	Hs.93029	sparofosteonectin, owov and kazal-like d	3.67	3.30
	410016	AA297977	Hs.57907	small inducible cytokine subfamily A (Cy	3.67	6.72
	433658	L03678	Hs.156110	immunoglobulin kappa constant	3.66	2.49
10	424153	AA451737	Hs.141496	MAGE-like 2	3.64	265
	421666	AL035250	Hs.1408	endothetin 3	3.64 3.61	5.92 2.69
	417696	BE241624	Hs.82401 Hs.2488	CD69 antigen (p60, early T-cell activation lymphocyte cytosotic protein 2 (SH2 doma	3.60	1.95
	429732 422173	U20158 BE385828	Hs.250619	phorbolin-like protein MDS019 (CEM15)	3.59	3.08
15	413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory.	3.57	11.26
	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	3.56	4.91
	439859	AW292872	Hs.124554	ESTs	3.53	4.15
	453064	R40334	Hs.89463	potassium large conductance calcium-acti	3.51	2.88
20	411252	AB018549	Hs.69328	MD-2 protein lymphotoxin beta (TNF superfamily, membe	3.46 3.45	1.82 4.65
20	414324 420286	Y14768 AJ796395	Hs.890 Hs.111377	ESTs	3.42	2.47
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	3.42	3.09
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	3.41	2.22
0.5	405545			Target Exon	3.40	2.46
25	416373	AA195845		ESTs, Wealdy similar to \$12658 cysteine-	3.40	5.64
	417410	AF063020	Hs.82110	PC4 and SFRS1 interacting protein 1	3.37 3.33	4.27 2.37
	418522 433470	AA605038 AW960564	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H transmembrane 4 superfamily member 1	3.33	3.13
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	3.32	2.51
30	442149	AB014550	Hs.8118	KIAA0650 protein	3.30	2.29
	411852	AA528140	Hs.107515	ESTs, Wealdy similar to T00329 hypotheti	3.29	3.85
	447023	AA356764	Hs.17109	integral membrane protein 2A	3.24	2.79
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	3.23 3.22	1.78 2.90
35	414176 447513	BE140638 AW955776	Hs.75794 Hs.313500	EDG-2 (endothelial differentiation, lys ESTs, Moderately similar to ALU7_HUMAN A	3.18	4.16
55	421893	NM_001078	Hs.109225	vascular cell adhesion molecule 1	3.17	3.59
	424148	BE242274	Hs.1741	integrin, beta 7	3.14	2.29
	406648	AA563730	Hs.277477	major histocompatibility complex, class	3.13	3.05
40	429505	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	3.13	2.36
40	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.12 3.12	2.55 5.54
	406704 443885	M21665 H91806	Hs.929 Hs.15284	myosin, heavy polypeptide 7, cardiac mus ESTs	3.08	3.55
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.08	2.20
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	3.06	3.21
45	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	3.05	3.36
	409103	AF251237	Hs.112208	XAGE-1 protein	3.04	2.07
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	3.04 3.03	2.24 1.91
	421834 444666	BE543205 BE293347	Hs.288771 Hs.11638	DKFZP586A0522 protein long-chain fatty acid coenzyme A ligase	3.01	3.43
50	425295	AA431366	Hs.37251	ESTs	3.01	3.07
• •	429109	AL008637	Hs.196352	neutrophil cytosofic factor 4 (40kD)	2.99	2.55
	420340	NM_000734	Hs.97087	CD3Z antigen, zeta polypeptide (TiT3 com	2.98	5.98
	418968	NM_000078		cholesteryl ester transfer protein, plas	2.97	2.68
55	438914	N93892	Hs.10727	ESTS	2.97 2.96	2.19 2.68
25	418391 419056	NM_003281 M89957	Hs.84673 Hs.89575	troponin I, skeletal, slow CD79B antigen (immunoglobulin-associated	2.96	3.94
	449523	NM_000579		chemokine (C-C motif) receptor 5	2.96	4.02
	450847	NM_003155		stanniocalcin 1	2.96	3.24
60	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	2.95	2.73
60	426711	AA383471	Hs.343800		2.94	2.36 2.17
	426559	AB001914 AW073971	Hs.170414 Hs.238954		2.93 2.93	2.70
	424528 408633	AW963372	Hs.46677	PRO2000 protein	2.92	2.16
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	2.92	2.92
65	425234	AW152225	Hs.165909		2.90	2.09
	437802	A1475995	Hs.122910		2.90	3.71
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	2.90	3.56
	438000	AI825880	Hs.5985	non-kinase Cdc42 effector protein SPEC2	2.90 2.87	2.60 2.07
70	414555 421958	N98569 AA357185	Hs.76422 Hs.109918	phospholipase A2, group IIA (platelets, ras homolog gene family, member H	2.87	3.48
, 0	420224		Hs.96023	CD19 antigen	2.86	4.77
	434883	AW381538	Hs.19807	hypothetical protein MGC12959	2.85	5.44
	452852		Hs.30822	hypothetical protein FLJ11110	2.84	2.55
76	427527		Hs.153261		2.84	4.16
75	446231			interferon consensus sequence binding pr	2.83 2.82	2.97 1.82
	408838		Hs.40369 Hs.19691	ESTs	2.82	4.21
	429124 425023		Hs.15421		2.79	4.00
	425388		Hs.156110		2.79	2.28
80	414290	AI568801	Hs.71721	ESTs	2.78	3.19
	418255	AW135405		ESTs	2.76	3.27
	451952		Hs.301663		2.75 2.75	1.74 3.10
	424865	AF011333	Hs.15356	3 lymphocyte antigen 75	213	J. 10

	409245	AA361037		tRNA isopentenylpyrophosphate transferas	2.74	212
	453920	AI133148	Hs.36602	i factor (complement)	2.74 2.74	3.08 2.34
	443958	AA287702	Hs.10031	KIAA0955 protein hypothetical protein PRO2013	2.73	1.67
5	434094 436476	AA305599 AA326108	Hs.238205 Hs.33829	bHLH protein DEC2	2.72	1.70
-	428398	A1249368	Hs.98558	ESTs	2.72	2.06
	417141	U22662		nuclear receptor subfamily 1, group H, m	2.70	2.55
	427080	AW068287	Hs.301175	ras-related C3 botulinum toxin substrate	2.69 2.69	3.15 1.99
10	442485	BE092285	Hs.29724 Hs.268016	hypothetical protein FLJ13187 Homo sapiens cDNA: FLJ21243 fis; clone C	2.69	1.70
10	429317 443998	AA831552 AI620661	Hs.296276	ESTs	2.69	2.30
	417542	J04129	Hs.82269	progestagen-associated endometrial prote	2.68	3.23
	414291	AJ289619	Hs.13040	G protein-coupled receptor 86	2.68	3.01
1.5	448861	AL049951	Hs.22370	Homo sapiens mRNA; cDNA DXFZp56400122 (I	2.66	2.51
15	432435	BE218886	Hs.282070	ESTs hypothetical protein FLI20647	2.65 2.65	3.28 3.04
	430132 427792	AA204686 M63928	Hs.234149 Hs.180841	tumor necrosis factor receptor superfami	2.64	3.82
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	2.64	1.97,
	420991	AW504814	Hs.287379	Homo sapiens mRNA for FLJ00111 protein,	2.64	2.51
20	401566			NM_005159:Homo sapiens actin, alpha, car	263	3.74 2.13
	444119	R41231	Hs.184261	ESTs, Wealdy similar to T26686 hypotheti	2.63 2.61	2.95
	425231 417427	AA527161 M90391	Hs.82127	ESTs interleukin 16 (lymphocyte chemoattracta	2.61	1.90
	437669	AI358105	Hs.123164	ESTs, Weakly similar to match to ESTs AA	2.60	4.45
25	413856	D13639	Hs.75586	cyclin D2	2.60	5.71
	407928	NM_002262	Hs.41682	killer cell lectin-like receptor subfami	2.59	268
	443247	BE614387	Hs.333893	c-Myc target JPO1	2.58 2.58	2.77 9.28
	447131 443021	NM_004585 AA368546	Hs.17466 Hs.8904	retinoic acid receptor responder (tazaro lg superfamily protein	2.58	4.49
30	424779	AL046851	Hs.153053	CD37 antigen	2.58	3.88
	425235	AA353113	Hs.112497	Homo sapiens cONA: FLJ22743 fis, clone H	2.57	2.09
	424265	AF173901	Hs.144287	hairy/enhancer-of-split related with YRP	2.57	3.57
	426780	BE242284	Hs.172199	adenytate cyclase 7 sotute carrier family 37 (glycerol-3-pho	2.57 2.56	1.86 2.90
35	452721 442904	AJ269529 AW575008	Hs.301871 Hs.11355	thymopoletin	2.56	3.39
. 33	433646	AA603319	Hs.155195	ESTs	2.54	2.19
	417289	D86962	Hs.81875	growth factor receptor-bound protein 10	2.53	4.56
	422640	M37984	Hs.118845	troponin C, slow	2.53	5.38
40	448413	AI745379	Hs.42911	ESTs TC31	2.53 2.52	2.08 2.49
40	429536 446272	AA873016 BE268912	Hs.206097 Hs.14601	oncogene TC21 hematopoietic cell-specific Lyri substrat	2.52	3.46
	424378	W28020	Hs.167988	neural cell adhesion molecule 1	2.52	2.91
	410257	BE244044	Hs.61469	hypothetical protein	2.51	3.67
45	427609	AK000436	Hs.179791	hypothetical protein FLJ20429	2.51	3.11 2.30
45	424868	AI568170	Hs.96886 Hs.89499	ESTs arachidonate 5-lipoxygenase	2.51 2.50	264
	418945 420899	BE246762 NM_001629	Hs.100194	arachidonate 5-lipoxygenase-activating p	2.50	3.04
	413441	AJ929374	Hs.75367	Src-like-adapter	2.49	2.37
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.49	1.82
50	429493	AL134708	Hs.145998	ESTs	2.49 2.48	2.40 1.85
	419631 437175	AW188117 AW968078	Hs.87773	popeye protein 3 protein kinase, cAMP-dependent, catalyli	2.48	2.32
	421552	AF026692	Hs.105700		2.47	4.17
	420158	AI791905	Hs.95549	hypothetical protein	2.47	2.62
55	453987	AA323750	Hs.235026		2.47	2.49 2.57
	429640	U83508	Hs.2463 Hs.50115	angiopoletin 1 Homo sapiens mRNA; cDNA DKFZp761J1112 (I	2.47 2.46	2.42
	437330 426969	AL353944 Al936504	ns.30113	CDC-like kinase 1	2.46	2.41
	427674	NM_003528	Hs.2178	H2B histone family, member Q	2.46	2.17
60	405547	_		NM_018833":Homo sapiens transporter 2, A	2.46	2.84
	406678	U77534	11- 02070	gb:Human clone 1A11 immunoglobulin varia	2.45 2.45	2.89 3.40
	407013 428746	U35637 AW503820	Hs.83870 Hs.192861	gb:Human nebufin mRNA, partial cds Spi-B transcription factor (Spi-1/PU:1 r	2.43	6.25
	453953	AW408337	Hs.36972	CD7 antigen (p41)	2.39	4.01
65	427759	BE245578	Hs.2200	perforin 1 (pore forming protein)	2.39	4.56
	443071	AL080021	Hs.8986	complement component 1, q subcompone	2.39	3.31
	437211	AA382207	Hs.5509	ecotropic viral integration site 28 hypothetical protein MGC11034	2.38 2.37	3.15 3.68
	440596 452651	H13032 Al218918	Hs.103378 Hs.30209	KIAA0854 protein	2.36	4.08
70	421563				2.34	3.25
	421924		Hs.109606	coronin, actin-binding protein, 1A	2.33	3.38
	449092			alpha2,8-sialyttransferase	2.32	3.53
	425367		Hs.155975	protein tyrosine phosphatase, receptor t linker for activation of T cells	2.32 2.30	7.02 3.56
75	418117 425795		Hs.83496 Hs.159543		2.26	3.42
, ,	428111		Hs.2243	B lymphoid tyrosine kinase	2.25	3.69
	439981	AI348408	Hs.12467	ESTs, Weakly similar to T14742 hypotheti	2.25	4.05
	425722		Hs.97031	hypothetical protein MGC13047	2.25	3.44
80	436648		Hs.28607	ESTs hypothetical protein A-211C6.1	2.24 2.23	3.23 3.08
80	452250 441715		Hs.34265		2.23	3.30
	423397	NM_001B3		chemokine (C-C motif) receptor 7	2.22	3.25
	449626		Hs.30163		2.21	3.14

	412975	170956	Hs.75106	clusterin (complement lysis inhibitor, S	2.18	3.41 3.62
	418739	AA310984	Hs.88012	SHP2 interacting transmembrane adaptor	2.15 2.09	5.21
	418185 436420	AW958272 AA443966	Hs.347326 Hs.31595	intercellular adhesion molecule 2 (ICAM ESTs	2.07	3.81
5	418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	2.05	3.14
_	420626	AF043722	Hs.99491	RAS guanyl releasing protein 2 (calcium	2.01	4.42
	428289	M26301	Hs.2253	complement component 2	2.00	3.33
	429683	AF148213	Hs.211604	a disintegrin-like and metalloprotease (2.00 1.96	3.75 3.68
10	421445 450300	AA913059	Hs.104433 Hs.58210	Homo sapiens, clone IMAGE:4054868, mRNA ESTs, Highly similar to ITH4_HUMAN INTER	1.90 1.91	4.84
10	416445	AL041440 AL043004	Hs.79337	KIAA0135 protein	1.91	3.41
	409817	BE295464	Hs.56607	Williams-Beuren syndrome chromosome regi	1.87	3.53
	416967	BE616731	Hs.80645	interferon regulatory factor 1	1.86	3.55
1.5	437740	AA810265	Hs.122915	ESTs	1.85	3.79
15	437938	A1950087	LI- 4000	gb:wq05c02x1 NCI_CGAP_Kid12 Homo sapien	1.83 1.83	3.42 3.75
	425240 406972	AA306495 M32053	Hs.1869	phosphoglucomutase 1 gb:Human H19 RNA gene, complete cds.	1.80	4.03
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	1.78	3.53
	437470	AL390147	Hs.134742	hypothetical protein DKFZpS47D06S	1.78	3.39
20	416350	AF188625	Hs.189507	phospholipase A2, group IID .	1.78	5.48
	417852	AJ250562	Hs.82749	transmembrane 4 superfamily member 2	1.78	4.88
	414682	AL021154	Hs.76884	inhibitor of ONA binding 3, dominant neg	1.77 1.74	5.79 3.41
	444090 427278	S69115 AL031428	Hs.10306 Hs.174174	natural killer cell group 7 sequence KIAA0601 protein	1.74	3.80
25	418618	U66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dy	1.73	4.21
	420397	NM_007018	Hs.97437	centrosomal protein 1	1.73	3.21
	418678	NM_001327	Hs.167379	cancertestis antigen (NY-ESO-1)	1.73	3.77
	459245	BE242623	Hs.31939	manic fringe (Drosophila) homolog	1.72	3.12
30	425356	BE244879	Hs.155939	inositol potyphosphate-5-phosphatase, 14	1.71 1.70	3.55 7.70
30	423984 422355	AF163825 AW403724	Hs.136713 Hs.300697	pre-8 lymphocyte gene 3 coagulation factor VII (serum prothrombi	1.70	3.10
	451579	AW607731	Hs.26670	Human PAC clone RP3-515N1 from 22q11.2-q	1.68	4.19
	451287	AK002158	Hs.26194	likely homolog of mouse immunity-associa	1.68	5.76
25	416819	U77735	Hs.80205	pim-2 oncogene	1.67	3.17
35	409896	AW205479	Hs.279780	NY-REN-18 antigen	1.67	3.74 3.62
	447532 426666	AK000614 AW500131	Hs.18791	hypothetical protein FLJ20607	1.66 1.65	4.67
	412265	AA101325	Hs.171763 Hs.86154	CD22 antigen hypothetical protein FLJ12457	1.65	3.43
	416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial, pro	1.64	3.66
40	430449	AA352723	Hs.241471	RNB6	1.62	3.09
	424661	M29551	Hs. 151531	protein phosphatase 3 (formerly 28), cat	1.61	3.37
	453027	AI879341	Hs.539	ribosomal protein S29	1.61 1.60	11.60 3.28
	410068 440446	AI633888 NM_013385	Hs.58435 Hs.7189	FYN-binding protein (FYB-120/130) pteckstrin homology, Sec7 and coiled/coi	1.59	3.14
45	453657	W23237	Hs.296162	AD037 protein	1.59	3.12
	418102	R58958	Hs.26608	hypothetical protein MGC15880	1.58	3.55
	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	1.58	3.07
	406791	A1220684	Hs.347939	hemoglobin, alpha 2	1.55 1.53	5.06 3.59
50	421703 421859	AI936513 AA356620	Hs.1416 Hs.108947	Fc fragment of IgE, low affinity II, rec KIAA0050 gene product	1.52	3.41
50	416783	AA206186	Hs.79889	monocyte to macrophage differentiation-a	1.52	3.28
	456086	AL161999	Hs.77324	eukaryotic translation termination facto	1.47	3.34
	425783	AJ026740	Hs. 1948	ribosomal protein S21	1.46	4.95
55	407682	AL035858	Hs.3807	FXYD domain-containing ion transport reg	1.46	3.48 3.25
33	409169 435624	F00991 AF218942	Hs.50889 Hs.24889	(clone PWHLC2-24) myosin light chain 2 formin 2	1.45 1.45	3.11
	413969	X14034	Hs.75648	phospholipase C, gamma 2 (phosphatidylin	1.45	3.33
	426530	U24578	Hs.278625		1.44	4.27
CO	425928	\$55736	Hs.238852		1,44	3.65
60	418219	AA731836	Hs.137319		1.43	4.01
	429071	AW794126	Hs.195453		1,41 1,41	4.23 3.29
	418473 423766	AA243335 AA303799	Hs.309943 Hs.300141		1.40	3.22
	430150	L05148	Hs.234569		1.39	3.29
65	416370	N90470	Hs.203697		1.36	3.08
	406758	AA552326	Hs.77039	ATP synthase, H transporting, mitochondr	1.32	3.29
	448610	NM_006157		nel (chicken)-like 1	1.31	3.85 3.10
	444674 407694	8E562200 U77594	Hs.244 Hs.37682	amino-terminal enhancer of split retinoic acid receptor responder (tazaro	1.30 1.30	3.10
70	427349	AA360154	Hs.177415		1.28	3.59
. •	419032	W81330	Hs.99877	ESTs, Highly similar to JAK3B [H.sapiens	1.28	3.21
	436553	AW407157	Hs.8997	immunoglobulin lambda locus	1.27	4.00
	415138	C18356	Hs.295944		1.24	3.25
75	406623	X69392 AB014558	Un C000	ribosomal protein L26	1.24 1,21	3.31 3.33
, ,	437895 421143	AB014556 AB024536	Hs.5898 Hs.102171	KIAA0668 protein immunoglobulin superfamily containing le	1.18	3.35
	-21170			The state of the s		

TABLE 53B:

80 Pkey: Unique Eas probeset identifier number Gene cluster number Genbank accession numbers

Pkey CAT Number Accession

	441623	3362_1	BC022413 BE395396 BF754175 AA506621 BE706665 BE706678 AA723159 BE153169 BE706729 BE706558 BE153312 BE706706 AW371853 AW371849 BE153241 BC017410 A1337912 A090244 AW090300 BE219837 A1623661 BE501576 BE501734 A1742232 A0233964 AA58424 AA975373 A1288904 A1384583 AA890325 N32562 A1358102 AW241694 A038448 A1672071 A018389 AA576391 AA977874 AW189392 W37448 AA612894
5			A1277548 K89551 A1699774 H89365 AA315805 AW579186 BC014584 BC014581 AW780125 A1672414 BE328145 AW600919 BF031306 AW172758 BE708322 AA345675 BE875779 H28241 N25318 BF540913 BG179688 BF110202 AA528775 W37573 BE041644 AW365504 BM129522 BM129822 A1122760 BE718200 AW887496 AA149420 BE706307 BE539395 BE748765 A1373653 R75904 BF979185 BF691393 BG495595 B1094458 BE706702 BG4955595 BF248373 BG494590
10	416373	3442_1	AKUSSB82 AW755252 AL596757 BF827376 BF827373 BF827375 BF827369 BF826900 F01252 BC022888 BI850312 AA195845 BF825671 BF574821 Z21686 F32854 AA211780 F21569 A1288453 A1803678 AA180309 A1074627 AA192950 AA661688 F36698 F32290 F28773 F22692 AA424993 AW340328 AA192247 BF672229 BF575143 BF673106 BF693623
	433470	6624_1	X75684 AL573167 A445461 A453743 A1983655 A1564544 AA977180 A1694111 A1591358 AW071625 A1678712 A1720393 A1927769 BE439796 A1963432 AA292956 AW192593 A1865838 A1656905 A424384 A1161312 A191 1921 A159781 181494359 A194088 A149258 AW262737 BE044033 AW008570 AW629505 B1494958 AA088439 A4706057 BF222820 BF93608 BE501957 AA504359 BE044134 AW872531 AW015724 BE349186 AA043217 BF919784 A179878 A A6179777 A447013 BF646195 AW779725 AA90330 AA147228 A4404570 A1075878 W38161 A1972739
15			AW673152 AA723200 C06123 BF057147 AA627686 AA157944 A1990245 AA662517 T32487 A1800106 A1333170 A1859160 W45410 A1990827 AW275048 AA182540 AA78338 A1298935 AW085158 AW471421 AW103470 AW300456 AW191997 A1825466 AA962397 AA136658 A1251817 AW339104 AA724739 AA41100 AA191349 AA757735 AA037696 A1769516 AW772283 AA010631 A162846 A061065 H80983 R79933 A195693 A1245632 A1349390 AA148284 A1789502 AA487893 A1621320 AW194772 C06365 AA953880 BE858936 A1918523 A1872678 A1927217 A1453453 A1189366 AW338678 A1261359 A1500576 BF477735 A1032569 A1972899 A1985583 Z28771 A363829 A1693030 AA603586 BE773488 AW339301
20			BE773489 BE773492 BE773495 AIGS0338 BE773499 AT745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773495 AIGS0338 BE773499 AT745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773473 BE773473 BE773473 BE773473 BE773473 BE773473 BE773473 BE773473 BE773473 BE773473 BE773473 BE773473 BE773473 BE773473 BE773473 BE773473 BE773473 BE773473 BE773479 BE773473 BE773473 BE773473 BE773473 BE773473 BE773473 BE811346 BE811349 AIGS03740 AIGS0374 AIGS0374 BE773473 BE
25			BF843900 AW80G193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757738 BE926037 A377596 C06111 AW088968 BE811404 BE811472 AI855912 AI925607 AI871950 AI933510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BID44896 A1744233 AW984527 C15704 BF84388 A1248307 BE773483 AI567995 W60075 BF941183 A1738844 BE811458 BE773481 AI25230 AA948565 BE706942 BE156367 C15026 AW742958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BC482896 AA182734 AA877242
30			AW372926 H27252 R33114 BF851859 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906859 BI750327 BI550847 BI55084 BC010166 ALS50134 ALS5096 AL548700 AL55073 AL547376 AL55286 AL540634 AU1158652 BG741786 BB68522 AU135666 BI552770 BI259210 BI256520 BI255559 BC485098 BI258228 BC498501 BM044512 AU133984 AL556585 BE745111 BI222633 AU133917 BC288151 BI250715 BIS50550 BC50073 BI551761 BC707601 BI318593 BC503783 BC721129 BC541578 BE206566 BC571098 BI25221313 BC407474 BC478075 BC507605 BC507678 AU137540 BC478078 AU807678 AU807
35			AW551691 BM048974 BM043805 BG142185 AA315188 A446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA391631 AA376800 D56120 AA343532 AA308536 F00242 AA376086 AA316988 AA343799 BI870221 BE910282 BG538748 AW990564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 AF030234 BC017465 BG008526 AW505550 BM460141 N47324 AA361037 AA321632 N45606 AV752798 AV657116 AA296632 AU137857 AW467027
40 45	409245	3199_2	AT-0.00234 B017465 B600855 AVY95559 BWR01611 A7524 AAS3107 AA252605 AT 9505 AV75659 B1259830 AVY960845 AT42080 A1624350 H58206 AA478518 AW439897 AW393555 AW393523 A1559753 A1808727 E66856 H01374 B1257369 B1259830 AW960845 BM466252 AW956813 BE768647 AV658853 BM055248 BF372070 BF372055 BF372061 AA347852 AA905863 BG505078 AV654024 BF093291 AW021929 H22550 AA459715 BC496341 BE697763 B1254209 BC499543 H42946 B1059780 B1086741 H87989 H87599 BF691752 BE768511 BG940948 W737155 BF372041 BE883796 BF372082 BF367329 BF909744 AW966003 AV714014 B1492868 B1495144 AA921845 A1693426 A1652147 A435449 N47325 A1434429 AA573137 A183429 A1629862 A1332526 BF513937 A1189561 A1221962 A1378034 AW118897 AW7665247 AW340077 N41605 AA478519 AA463875 A1858260 AA463379 A1292305 BE045947 AA971089 A1125820 BG940947 A1080245 AA884954 A1125702 A1382934
43			AAS31835 AJSS6531 AW439905 AJ027833 AJ399648 AJ014533 AAS47851 AA738261 N67374 N69081 AJ768667 AA948472 A815214 AA253133 AJ186725 AA889214 AJ222635 BJ495143 N29605 N48812 AA769041 AJ492769 D56771 AA095911 BE222062 D56772 AW372265 BM054985 D12455 BG534562 AW003511 H87486 H42880 AW190293 BF594697 BF377611 H22043 BJ255749 BJ492848 H16217 H21980 H22651 H68179 H87354 H44052 H23165 M44128
50	417141	9517_1	AJ391712 UZ2662 NM_005693 AW166878 BF339795 AJ970974 AIS21157 AJ356082 AW339789 AI288682 BF477594 BF477593 A1703008 A1290961 AD49684 AW770753 AI208561 A1699406 F33996 AA630563 AJ885346 AJ927058 AA533982 AW204589 AI206938 AW599068 AI263769 AA991550 A192006 AL558946 AL524337 AL516239 AL580848 AL580658 AI719135 AW026500 AI698217 AJ872977 AJ670883 AJ654870 AA493407 AA548525 AJ016420 AA843563 W15576 H61726 AA913245 BF438146 AL524338 BJ762380 AU136488 BJ759892 AV655930 T78977 BJ524075 BE538944
55	425231 419531 426969	235504_1 2743_1 12113_1	AAS27161 BC2111784 AAS27065 AAS05489 AW512550 BCD22323 AF204171 NM_022361 BM264431 BE670789 AW188117 AI025298 AA861832 H84897 AI382294 AA662874 AW993380 BE813742 H84368 A1188074 N20482 H84369 M59287 AI938504 AI694705 AI679216 AI679235 BF110184 AW518110 AI679811 AW054981 BE465531 BE327409 AW339105 BI714787 AI871568
60		12113_1	AW129115 AU145080 AI223299 AW129986 AA780771 BG654629 AU144657 BF437422 AI478374 AA492513 AU157562 AI826962 AU145528 AI951093 AW513819 AA042856 AA725690 AA733176 AI028702 AI251890 AI811729 AW9975208 AW339589 A147868 AU157862 AA623327 BF476670 BE464796 AW510511 AA399098 AA398210 AI291998 AI160296 AU158075 N34811 BE326407 AI270539 AA4693702 AI270284 AI139504 BF437009 AI354626 AI936336 AA287250 AA491855 BF445818 AA688026 AA284510 AW151564 AA412072 AA769721 H89332 BF445769 BF989466 BF989472 AA631105 AI129915 W96362 AA515277 AA541513 L29222 AV758119 D82109 AL040956 BE244413 AV645640 BE246321 BE246314
65			D82116 AL036176 AA331779 AU100105 BE243857 AU076865 AW972327 AA497087 AI587039 AW072798 A117455 AU156788 AA0444U1 AA046086 RE244986 AI634466 RE242946 RE242946 AI634466 RE242946 AI634466 RE242946 RE242946 AI634466 RE242946 RE242948 AI634466 RE242946 RE242948 AI634466 RE242946 RE242946 RE242948 AI634466 RE242946 RE242948 RE244948 AI634464 RE24294 RE242948 AI634464 RE24294 R
65	406678	0_0	AA373395 BE710347 AL564154 AI708332 AA729530 N9Z729 AI573015 T29655 H89333 H85847 AI886473 AW189980 H02905 AI811986 AU157753 W86829 AA020844 AU158204 AA057356 AA283466 AA405504 AA017027 W94754 AA226498 W72391 H66461 C00442 H01925 BI912232 U77534 U77537
70	449092 436648	_	AK056270 AV706896 AK92935 AK81140 AW162481 AW087114 AW157019 AK689795 AW251085 AW266911 BF438207 AW134945 BE041668 BF111425 U91641 NM_013305 BF968902 U55966 AU130750 BE174853 AI929731 AW161524 R43753 BE779688 AJ002788 AL118666 AJ381600 BE672862 AW500520 BF223709 AW593740 AA262174 AA810597 AA810595 F09382 BF976590 AW968002
			AA262288 BF931698 AW968014 R18656 BAM59356 AW794189 BF954184 242558 BF891641 BF963380 Z45874 F05187 X93079 BF742651 BF742649 R51324 080031 BI457883 F06613 Z43128 F12243 BF950830 H19040 BF950829 F06439 R14947 F06702 R51037 R52173 R14953 R12174 R13610 H10426 R11851 T65264 R18737
75	437938	66997_1	U71456 AA482911 W78802 AW856538 BF737212 N36809 N35320 AA282915 AW505512 AI653832 W87891 AI961530 T85904 H59397 R97278 W01059 AI820532 T82391 AI820501 T63226 R66056 R67840 AW9611011 AA337499 W37181 AA180009 AW205862 AA988777 AA856975 BF172457 BG751124 A1741346 AJ950344 AI689062 AI872193 AW102898 AW1173586 AJ763273 AI890387 AW1503049 AJ76588 AA488892 AJ356394 AI539642 AA642789 AJ950087 BF589902 N70208 AA283144 AA488964 H60052 R97040 BF886630 AW967677 AW971573 AW967671 AJ308119 AA251875 AA908598 AJ819225 AJ564269 AA908741 AA29373 AA969759 AW276905 AA044209 H83488 T92487
80	405623	0_0	X69392 T24055
	TABLE Pkey:	53C:	Unique number corresponding to an Eos probeset

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Indicates DNA strand from which exons were predicted. Indicates nucleotide positions of predicted exons. Ref:

Nt_position:

Strand 1054740 Plus

405545 401566 405547 B469090 1054740

Nt_position 118677-118807,119091-119296,121626-12182 96277-96420,96979-97160 124361-124520,124914-125050 Minus Plus

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TABLE 54A: ABOUT 161 GENES UPREGULATED IN PRIMARY MELANOMAS FROM TUMORS THAT LATER METASTASIZED RELATIVE TO PRIMARY MELANOMAS THAT DID NOT METASTASIZE LATER

Table 54A fisis about 161 genes upregulated in primary metanomas from tumors that later metastasized relative to primary metanomas that did not metastasize later. These genes were selected from 59680 probesets on the Ecos/Affymetrix Hud3 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (Af), a normalized vature reflecting the relative level of mRNA expression.

Pkcy: Unique Ecos probeset identifier number

ExAcor: Exemplar Accession number, Genbank accession number 15

UnigenelD: Unigene Title: R1: 20

Unigene number

R2:

Unique gene title

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25	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	7.15	3.41
	413916	N49813	Hs.75615	epolipoprotein C-II	5.93	6.55
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	5.64	2.98
20	415668	AW957684	Hs.306814	hypothetical protein FLJ21889	5.03	4.56
30	440274	R24595	Hs.7122	scrapie responsive protein 1	4.98	4.83
	417542	J04129	Hs.82269	progestagen-associated endometrial prote	4.96	7.07
	427882	AA640987	Hs.193767	ESTs	4.68	4.68
	452744	AJ267652	Hs.246107	Homo sapiens mRNA; cONA DKFZp434E082 (fr	4.29	3.06
	407907	A1752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio	3.94	3.86
35	424410	W79027	Hs.271762	ESTs -	3.67	3.19
	429083	Y09397	Hs.227817	BCL2-related protein A1	3.46	2.49
	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	3.31	3.06
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.27	2.12
	440099	AL080058	Hs.6909	DKFZP564G202 protein	3.22	2.69
40	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	3.20	1.85
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.18	4.61
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	3.13	2.11
	430643	AW970065	Hs.287425	MEGF10 protein	3.10	3.31
	412262	W26406		seven in absentia (Drosophita) homolog 1	3.06	3.94
45	438328	AJ492261	Hs.32450	ESTs	3.05	3.09
	409760	AA302840		gb:EST10534 Adipose tissue, white I Homo	3.01	2.65
	453912	AL121031		SWI/SNF related, matrix associated, acti	2.94	1.86
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	2.91	3.70
	407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	2.88	2.53
50	453935	AI633770	Hs.42572	ESTs	2.88	2.00
	452689	F33868	Hs.284176	transferrin	2.84	6.47
	449550	AA353125	Hs.184721	ESTs	2.83	4.74
	409417	AA156247	Hs.104879	serine (or cysteine) proteinase inhibito	2.82	2.43
	438898	AI819863	Hs.106243	ESTs	2.81	2.08
55	430191	A1149880	Hs.188809	ESTs	2.80	2.69
-	408418	AW963897	Hs.44743	KIAA1435 protein	2.79	1.75
	450157	AW961576	Hs.60178	ESTs	2.77	3.40
	420380	AA640891	Hs.102406	ESTs	2.77	4.28
	443172	AW662964	Hs.199061	p300/CBP-associated factor	2.75	2.88
60	456629	AW891965		histone deacetylase 3	2.72	2.24
	407857	AI928445	Hs.92254	synaptotagmin-like 2	2.72	1.93
	421097	AJ280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	2.68	2.59
	436280	AI690734		Homo sapiens cDNA: FLJ22562 fis, clone H	2.67	2.79
	407550	Y10515		gb:H.sapiens mRNA for CD58 T7 protein.	2.65	1.98
65	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	2.64	1.76
~~	427899	AA829286	Hs.332053	serum amyloid A1	2.59	3.01
	442793	AI01779B		ESTs, Weakly similar to TI47_HUMAN CARGO	2.58	1.60
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	2.57	1.91
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.57	2.13
70	458247	R14439	Hs.209194	ESTs	2.56	2.61
. •	451668	Z43948	Hs.326444	cartilage acidic protein 1	2.52	2.74
	433980	AA137152	Hs.285049	phosphoserine aminotransferase	2.51	1.88
	412719	AW016610	Hs.816	ESTS	2.50	1.68
	441789	052059	Hs.7972	KIAA0871 protein	2.50	3.11
75	405885	002000	114	Target Exon	2.50	3.15
,,,	453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	2.48	3.33
	417821	BE245149	Hs.82643	protein tyrosine kinase 9	2.48	1.66
	450202			ESTs, Weakly similar to B49647 GTP-bindi	2.47	2.79
	436825			ESTs	2.47	2.55
80	424762		Hs.183684	eukaryotic translation initiation factor	2.42	2.28
00	432426			ESTs	2.42	1.76
	409095			ESTs, Moderately similar to S72481 proba	2.41	2.41
	403752		113,230030	NM_002753*:Homo sapiens mitogen-activate	2.41	2.87
	403732			outpetts manager detrate		

	404400					
	404489 411690	AA669253		Target Exon	2.39	1.97
	439195	H89360		RNA, U2 small nuclear gb:yw28d08.s1 Morton Fetal Cochlea Horno	2.37 2.37	2.54 2.27
_	453582	AW854339	Hs.33476	hypothetical protein FLJ11937	2.36	2.81
5	438461	AW075485	Hs.286049	phosphoserine aminotransferase	2.35	2.91
	432878	BE386490	Hs.279663	Pirin	2.35	2.28
	416647 428666	BE297139	Hs.79411	replication protein A2 (32kD)	2.33	1.97
	413645	AL080190 AA130992	Hs.189242	Homo saplens mRNA; cDNA DKFZp434A202 (fr gb:zo15e02.s1 Stratagene colon (937204)	2.32 2.31	2.92
10	421282	AA286914	Hs.40782	ESTs	231	2.63 1.85
	434418	AF134707	Hs.278679	a disintegrin and metalloproteinase doma	231	2.21
	413204	BE071603		gb:QV3-BT0510-161299-032-f03 BT0510 Homo	2.31	1.49
	449720	AA311152	Hs.288708	hypothetical protein FLJ21562	2.30	1.78
15	451838	AW005866	Hs.193969	ESTs	2.28	2.05
13	410943	AW968322	Hs.11156	low molecular mass ubiquinone-binding pr	2.28	2.39
	459711 429489	BE386801 AF008203	Hs.21858 Hs.204039	trinucleotide repeat containing 3 aristaless-like homeobox 3	2.27 2.26	2.39 1.97
	429493	AL134708	Hs.145998	ESTs	2.26	2.77
••	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	2.26	1.78
20	441989	AA306207	Hs.286241	protein kinase, cAMP-dependent, regulato	2.26	1.84
	419352	A1675008	Hs.199493	ESTs	2.25	1.47
	427393	AB029018	Hs.177635	KIAA1095 protein	2.25	1.83
	418522 433468	AA605038 AA832055	Hs.7149 Hs.172843	Homo sapiens cDNA: FLJ21950 fis, clone H	2.24 2.24	2.42
25	452782	AA028166	Hs.17733	ESTs, Wealdy similar to ALU1_HUMAN ALU S ESTs	2.24	1.76 2.34
	443910	AW051711	Hs.132440	ESTs	2.24	1.79
	408832	AW085690	Hs.63428	ESTs, Wealthy similar to 2195_HUMAN ZINC	2.22	1.52
	407283	T51008		gb:yb55e08.s1 Stratagene ovary (937217)	2.22	1.31
30	437376	AA749400	Hs.257890	ESTs	2.22	2.44
20	450712 421362	AI732130 AK000050	Hs.270496	ESTs, Wealdy similar to ALUB_HUMAN !!!!	2.22	1.62
	445183	AB007877	Hs.103853 Hs.12385	hypothetical protein FLJ20043 KIAA0417 gene product	2.22 2.20	2.36
	438501	Z44110	Hs.86149	phosphoinosital 3-phosphate-binding prot	2.20	1.84 1.76
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	2.19	1.59
35	414900	AW452420	Hs.248678	ESTs	2.18	1.89
	427704	AW971063	Hs.292882	ESTs	2.17	1.86
	404942			splicing factor, arginine/serine-rich 9	2.17	1.86
	448019 459254	AW947164 AA694386	Hs.195641 Hs.290914	ESTs, Moderately similar to 138022 hypot	2.17	1.64
40	418965	A1002238	Hs.11482	ESTs splicing factor, arginine/serine-rich 11	2.16	1.61
	443357	AW016773	113.11402	low molecular mass ubiquinone-binding pr	2.16 2.16	1.79 2.32
	412432	AA126311	Hs.9879	ESTs	2.15	2.73
	449567	AJ990790	Hs.188614	ESTs	2.08	2.85
45	433179	AW362945	Hs.162459	ESTs	2.07	4.77
45	408243	Y00787	Hs.624	interleukin 8	2.05	3.12
	435294 449656	T84084 AA002008	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	1.97	2.89
	412649	NM_002206	Hs.188633 Hs.74369	ESTs integrin, alpha 7	1.94 1.93	3.60 2.76
	445162	AB011131	Hs.12376	piccolo (presynaptic cytomatrix protein)	1.93	2.66
50	419356	AI656166	Hs.7331	hypothetical protein FLJ22316	1.92	3.39
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hydrocephalus	1.89	3.10
	414694	NM_015362	Hs.76907	HSPC002 protein	1.88	4.25
	415825 409105	Y18024	Hs.78877	inositol 1,4,5-bisphosphate 3-kinase 8	1.87	2.66
55	444784	AW467539 D12485	Hs.255877 Hs.11951	ESTs ectonucleotide pyrophosphatase/phosphodi	1.87 1.85	2.96 2.80
	404149	0.2400	113.11331	C6002509*:gij5031885[reqNP_005568.1] ii	1.84	2.93
	406387			Tamet Exon	1.82	2.96
	420871	AA702972	Hs.65300	ESTs	1.76	3.12
60	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	1.75	3.12
00	418751 412347	BE389014	11- 72040	phosphoinositide-3-kinase, regulatory su	1.70	3.20
	413211	AW970026 AW967107	Hs.73818 Hs.109274	ubiquinol-cytochrome c reductase hinge p hypothetical protein MGC4365	1.67 1.66	3.65 2.89
	459317	BRCA1b	113.103214	Eos Control	1.61	7.34
	425525	AA358883	Hs.23871	ESTs	1.59	2.67
65	436823	AW749865	Hs.117077	ESTs, Weakly similar to 138022 hypotheti	1.56	2.76
	433669	AL047879	Hs.194251	ESTs, Weakly similar to ALU2_HUMAN ALU S	1.55	2.76
	424389 426672	AA339786	11- 474774	lymphocyte-specific protein 1	1.53	2.95
	415977	AW270555 AL037622	Hs.171774 Hs.78935	hypothetical protein methionine aminopeptidase; elF-2-associa	1.51 1.47	3.39
70	404780	ALGO OLL	113.10333	Target Exon	1.47	2.65 2.77
	436476	AA326108	Hs.33829	bHLH protein DEC2	1.41	3.04
	428284	AA535762	Hs.183435	NM_004545:Homo sapiens NADH dehydrogenas	1.38	2.94
	448571	AA486794	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [1.37	2.80
75	428156	BE269388	Hs.182698	mitochondrial ribosomal protein L20	1.36	3.29
13	447752 447455	M73700 H38335	Hs.105938 Hs.6750	lactotransferrin	1.35	2.70
	453281	W46280	Hs.55940	Homo sapiens mRNA for FLJ00058 protein, ESTs, Weakly similar to A25704 synapsin	1.35 1.34	3.03 2.69
	413142	M81740	Hs.75212	omithine decarboxylase 1	1.33	2.96
00	407194	AA621644		gb:af54a01.s1 Soares_lotal_fetus_Nb2HF8_	1.32	2.70
80	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	1.26	3.27
	406797	AJ432224	LA TERRE	ribosomal protein L6	1.26	2.72
	406711 414608	N25514 BE396215	Hs.77385 Hs.76572	myosin, light polypeptide 6, afkali, smo	1.25	7.10
	414000	DE-130K 13	113.10312	ATP synthase, H transporting, mitochondr	1.24	2.72



	401846			NM_000988*:Homo sapiens ribosomal protei	1.24	2.82	
	432982	AA531058	Hs.182248	truncated calcium binding protein	1.23	3.10	
	428578	BE391797	Hs.343588	ribosomal protein S12	1.23	2.74	
	400199			Eos Control	1.21	3.58	
5	400079			Eos Control	1.20	2.99	
-	412623	R28898	Hs.74170	metaflothionein 1E (functional)	1.19	263	
	406713	U02629	Hs.77385	myosin, light polypeptide 6, atkali, smo	1.19	4.15	
	406712	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.18	4.75 ·	
	442492	AA528489	Hs.234518	ribosomal protein L23	1,17	274	
10	431526	Y10129	Hs.258742	myosin-binding protein C, cardiac	1.17	3.15	
	436398	H87136	Hs.5174	ribosomal protein S17	1.16	3.22	
	432205	AI806583	Hs.125291	ESTs .	1.15	2.76	
	406859	AI581134	Hs.181357	laminin receptor 1 (67kD, ribosomal prot	1.09	2.66	
	401254	71301134	15.10155	Target Exon	1.00	3.08	
15	405752			Target Exon	1.00	2.87	
13	445772	AI733941	Hs.145493	ESTs, Weakly similar to ALU7_HUMAN ALU S	1.00	2.70	
	452916	AA642831	Hs.31016	putative DNA binding protein	1.00	2.62	
	451411	AA017492	Hs.135655	EST	1.00	2.64	
	415658	BE501921	Hs.270471	ESTs	1.00	2.82	
20					1.00	3.30	
20	448610	NM_006157	Hs.21602	nel (chicken)-like 1	1.00	•••	
	TADIFE						
	TABLE 548:						
	Piter: Unique Eos probeset identifier number						
25	CAT number: Gene cluster number 5 Accession: Genbank accession numbers						
23	Accession	i. Gei	IDANK BODESSION IIU	nipers			
	Dienu	CAT Numbe	r Accession				
	Pkey		AMDESSUII	1250 ALCO 134 ATTACTA AIRN3300 AAG17325 AAG236	63 RE895068 A	U304442 AJ167464 AJ284188 AA054272 AA829262 AJ351910	
	412262	4362_1	TOOODO A 19000	20 11200CC A1111001C DEAACC27 DEGA207 REGA2840	1698102 AA25	8553 AV718529 AV719917 BF724133 BI438668 AI804000	
30			DC340403 AI03	2204 DCC4C117 AA227064 AA446520 AA870147 AA281	770 AW13687	2 AAR07907 AI435989 AI339626 AI383274 AA418512 BE771804	
30	BE349103 A012294 BE645117 AA227954 AA446520 AA879147 AA281770 AW136872 AA807907 AI435989 AI339626 AI383274 AA418512 BE77 I8D- BF894509 AA455093 AI379061 A1150855 BF769906 R17298 AU138740 BF808607 BE674533 AV700132 AA227789 AA253099 AW975199 AAS35418						
	T74315 F12666 AA022923 T89028 AA258606 W26406 BE838620 AV700706 AA101321 R41382 H14479 AA253044 R54810 R42784 R44804 R41						
		005100 4	174313 F12000	016 T92950 AU184997 AA077551	MI W AN 1010	111100	
	409760	865166_1	PA302040 193	UID 132330 AU 104337 PANUT 331 CCOAN DUNCESSE AMINSSOSS DINCSONA DINCSONAD AASARS	es Algoesou A	A041551 AW043754 A1086702 AW008105 AA974849 AW614893	
35	453912	32562_3	DM4/2224 BIS	00043 Pi300133 WARRING DESJERVS VIVERSSIJ NJSE.	25 8 8 8 1 3 2 3 3 7 1	BG460936 AW388482 AW388420 BF374777 W01360 N94710	
22				10330 WAS05305 WIDORSS 1 DL 150043 WAG223 15 4422	E3 101003321 1	00-00300 /111000-102 /111000-102 01 01 1111	
	400000	207 22	H87967	CO 4740 DE 000073 DICCEO DE 177633 AMBRICO AMB	5343 AI246162	7 T07082 AW805679 W96278 AA135796 W32615 AW995418	
	456629	207_22	AVV001000 DE	004749 BC000072 K13333 BE177023 A17003320 A175 nonnna Alamonecka Alamberrae Alamberrae Alamberrae	NEDA757 W87	409 AW604738 AW385757 AW580796 AW801247 BE003239	
			AWSU1688 BE	UU3837 AWBU 1021 AW383721 AW383742 AW383714 A	003000 AM2C	791 AW604759 AW866589 AW604758 N44337 Al378548	
40			BE003183 AA8	347112 AW580975 AW604760 AW385727 BE 164590 BE	UUJUJU AWJ01	AN AIMPOCCOOD AIMPOADES AIMERDAA AADAA TO TOGGO	
			AW890438 AA	077172 AI288683 AA229639 AAU91945 AVV945454 AAU	03023 FALUES	04 AW861938 AW894816 AW580841 AA094372 T06399	
			AW\$85686 BE244085 BE005035 AW\$61913 AA551773 AW\$58460 AW370926 AW754352 AW\$89695 AW38408 AI907428 BE067491 AW861939 AA248197 AW381373 AW177325 AW806879 AA935217 BE067498 BE083742 BE067470 AW894935 BE082529 AI248811 BE179917 BE002200				
			AA248197 AW	381373 AW177325 AW806879 AA935217 BE067498 BE	083742 BE067	4/0 AW894935 BE082529 AIZ48811 BE179917 BE002200	
			AW607506 AW392899 AW894560 AW381360 AI904206 AW863533 C00609 AW381372 BE082530 AW898120 BE075323 AW392799 AW601420 AI695314 BE083790 AW858568 AW945550 BE177153 AW970506 BE350419 AI906919 AW360794 AI906917 AW885979 AW794240 AW945566				
45			A1695314 BE0	83790 AW858568 AW945550 BE177153 AW970506 BE	50419 AJ9069	19 AW380794 A1906917 AW885979 AW794240 AW943300	
			AICARCA3 AICA	1960A AWAAGEA AWEA1421 AW380793 RE066524 RE0	83901 AW3698	M7 AW381871 AW935435 AW664582 AW817775 AW636449	
			BE180466 AW	BE180466 AW858501 BE180464 AJ371163 AA778231 AJ174991 BE011720 AW877776 AW877800 AW877795 T19900 AW856355 AW898099			
			DE011715 DE	BE011715 BE167842 BE011718 BE011724 AW363639 AW878658 AW878662 AW894887 BE082356 AW389211 AW804286 AW610312 AI904717			
			AW610318 AW996999 AW610296 AW901923 AW880003 AI762171 AW062S82 AW368713 AW062593 AW176663 AW842064 AW842089 AW842095 AI243049 AW902074 AW062592 AW176664 AW751692 BE087703 AI907439 BE009686 BE172115 BE077030 AW608556 AW835577 AI999628				
50			AIDADAG AMA	202074 AW062502 AW176664 AW751692 RF087703 AI	107439 RF009£	28 BE 172115 BE 07/030 AW 608556 AW 8355/7 AI909020	
			BE077020 AW176241 RE077552 RE160370 RE160288 AW835656 AW606765 AW606770 AW835678 AW606728 AW606728 AW606728 AW606728				
			AMIENEZER AV	AW606768 AW999517 AW844165 BE171738 AW751683 AW610493 BE177484 BE177487 AA090510 AW844117 BE173367 AW999878 A1124870 BE163472 AW841823 AW379762 AW893297 A1290296 BE089132 AA610287 AW176676 AW607622 BE172639 AW893232 AA329629 BE089008			
			RE163472 AV	MA1R23 AW379762 AW893297 AI290296 BE089132 AA	610287 AW176	676 AW607622 BE172639 AW893232 AA329629 BEU09U0	
			RE178350 RE	178214 RE063291 AW820236 AW999653 BE089486 BE	173126 BE 171	775 BE 185787 AA55828U AI 17484U AWSSS 112 BE 2103S1	
			RE172734 RE	178021 RE 172738 RE 173324 AW603494 AL036722 R38	192 R60905 H	53721 H41052 AL037917 R37795 AW998972 AA767189	
55			AMMARTT NO	DERO AA768300 AA767764 AIDR7R88 H44202 RF22279	7 N90597 W81.	396 N90615 AI935353 BE501168 F10945 AW118215 AI970480	
			AI627641 AW	236081 AA574090 AI627652 AI681913 AI759983 N6959	N69276 BE46	57722 AW392780 BE172467 H92861 AI524921 F02989 Z39328	
			E02705 E0141	IA TRRETR ALDISIES HR7220 AW374781			
	436280	36296_1	AV036316 AI3	2012/R RE671206 AAR60/36 AA7307R7 AAR3/4507 D79	104 D79806 AV	v961628 AI017068 BE044373 AA322458 AA987927 AA385869	
			BI492783 AW	021853 R79299 N73208 AI016622 N24609 AW192569 A	A707819 AI69	0734 R79189 AI535900 AW589301 AI128434 BE638011 BE837891	
60	•		BF894555 H9	5408			
•••	442793	417820_2	RG741247 RG	2741022 AI017798 AI953594 AW445065 AI245087			
	411690	53926_1	AKN27001 RE	514593 RE768430 RI037830 RE175161 RG000114 RG8	97171 AA7453	91 AA669569 AA669253 BI049453 BE304449 BG010136	
			BG830874 RF	091358 BF762561 T56173 BC003629 BF091330 BE697	323 BF091340	BE843330 AA744150 AA745471 W26276 BI037837	
	439195	21979_1	AF086037 H8				
65	413645	1234345_1		V969537 AA503835			
•••	413204	1494523_1		071613 BE071603 BE071587 BE071607 BE071615 BE	71636		
	443357			3654500 AI052778 BG057892 AW016773 AI452937 AW			
	455797		4 DEA01033 DE	2001074 DE001071 /\			
	418751		BE600141 BE	150358 A1937311 A11151256 AW341542 AW274231 AV	/341609 AW45	0447 AA843698 AW188066 AW007171 AW007027 AI075008	
70	410/31	21330_1	ALESONEL AA	C02002 AW151R42 AA6221R1 AI273454 AIBB5661 AA2	15946 AA6778 9	39 AW473512 AW298620 AA872899 AU94216 AU25188 AA256998	
			ALGEOGRA ALE	200102 A1280A03 AINANZAN RE16ZRA1 AW1513ZA RE16	754 BF036108	AA299181 N23237 T62967 W96060 AA574412 AW606697	
			MOCUCO DEL	303 R09158 R59113 T48473 T59023 AA122066 AW606	43 R38386 R0	6567	
	424389	1059_4	DC100750 A	MOC 4118 M/7700A AA 330977 AWRAS121 AWRAS129 RG	181820 BF716	719 Al125483 Al161017 W73951 Al250771 AA912611 AA339786	
	424303	1033_4	DC02020C0	838282 BE716636 AA777158 W94063 BE716628 BE71	6625 RFR3837	1 RE371044 RE716631 RE716402	
75	406797	0_0	DE030400 B	/276890 A1499346 AA937014 AA653573 A1318525 A124	219 AA96169	A1270640	
13	400/3/	0_0	MANAGERA WA	THE ESCOTOR OF THE PARTY PARTY DESCRIPTION OF THE PARTY O			
	TABLE	640					
	Pkey:		briano anantre esca	esponding to an Eos probeset			
	FREY.	Ų	wadne imilita coul	copping to an Ena binocact	.an	"Dunbon, et al "colory to the subjection entitled "The DNA	
		•	CONTRACTOR SALVAGE	The 7 died numbers in this sections we Contract Identifier			
ያሰ	Ref:	S	Sequence source. 1	The 7 digit numbers in this column are Genbank Identifier	(GI) numbers. 195	Districting, et al. 16163 to the publication chance the order	
80	Ref.	s	equence of human	chromosome 22" Dunham, et al. (1999) Nature 402:489-	(GI) numbers. 495.	Duniani, et al. 1663 to the patheonor choice the orth	
80		s la	equence of human ndicates DNA stran	The 7 digit numbers in this column are Genbank trentifier chromosome 22" Dunham, et al. (1999) <u>Nature</u> 402:489- d from which exons were predicted. positions of predicted exons.	(GI) numbers. 495.	Dullian, et al. telds a dia pubication chiece the 5101	

	Pkey	Ref	Strand	N1_position
	405885	7677703	Minus	42574-42998
	403752	7678857	Plus	33704-33828
_	404489	8113772	Plus	98183-98480
5	404942	7382153	Plus	92095-92252
	404149	7534008	Plus	121831-121951,124044-124150
	406387	9256180	Plus	116229-116371,117512-117651
	404780	9887810	Minus	175708-175871
	401846	7712190	Minus	82775-82823,82912-83022
10	401254	9796309	Plus	152209-152383
	405752	9212305	Plus	91392-91528
10				

TABLE 55A: ABOUT 201 GENES UPREGULATED IN PRIMARY MELANOMAS FROM TUMORS THAT DID NOT METASTASIZE RELATIVE TO PRIMARY MELANOMAS THAT LATER METASTASIZED 15

LATER METASTASIZEU
Table 55A fists about 201 genes upregulated in primary melanomas from tumors that did not metastasize relative to primary melanomas that metastasized later. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative lavel of mRNA expression.

Pkay:
Unique Eos probeset identifier number
ExAcon:
Exemplar Accession number, Genbank accession number
Unique Dr. Unique Eos probeset identifier mumber

Exemplar Accession number, Genbank accession number

20

UnigeneID: Unigene Tide: R1: R2:

Unique number
Unique of the state of Als for primary melanomas that did not metastasize divided by the 90th percentile of Als from primary melanomas that metastasized later
90th percentile of Als for primary melanomas that did not metastasize divided by the 90th percentile of Als from primary melanomas that metastasized later,
where the 15th percentile of normal fissue Als was subtracted from both the numerator and denominator

25

23		wites	i die Tour percent	DE CE HOLLING 03508 PGS WES SOURCES HOLL GOD! DO HOLL GOD		~~
	Pkey	ExAcon	UnigeneID	Unigene Title	R1 8.08	R2 5.48
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	5.18	5.46 8.18
20	404854			Target Exon	4.89	4.95
30	406636	L12064		gb:Homo sapiens (clone WR4.12VL) anti-th	4.83	4.86
	433435	BE545277	Hs.340959	Ts translation elongation factor, mitoch	4.71	4.70
	408471	NM_012317	Hs.45231	leucine zipper, down-regulated in cancer	4.71	3.85
	433658	L03678	Hs.156110 Hs.74602	immunoglobulin kappa constant aquaporin 1 (channel-torning integral pr	3.98	4.01
35	412802 415801	U41518 R24219	Hs.278443	Fc fragment of IgG, low affinity IIb, re	3.92	3.35
33	400417	X72475	HS.270443	Target	3.83	2.78
	419870	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.67	2.29
	409190	AU076536	Hs.50984	sarcoma amplified sequence	3.62	3.68
	408692	AL040127	Hs.34074	dipeptidylpeptidase VI	3.61	3.89
40	423619	T48591	Hs.249159	adrenergic, alpha-2A-, receptor	3.56	3.61
	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	3.55	2.85
	445745	AB007924	Hs.13245	KIAA0455 gene product	3.38	2.55
	406663	U24683		immunoglobulin heavy constant mu	3.34	6.16
	414522	AW518944	Hs.76325	Immunoglobulin J chain	3.32	2.75
45	419235	AW470411	Hs.288433	neurotrimin ·	3.32	2.74
	441598	A1733219	Hs.58262	ESTs	3.31	3.71
	402294			Target Exon	3.24	2.35
	402737			Target Exon	3.22	2.87
50	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	3.20	3.04 2.81
50	410268	AA3161B1	Hs.61635	six transmembrane epithelial antigen of	3.18 3.17	4.62
	427335	AA448542	Hs.251677	G antigen 7B	3.17	2.34
	404995			ENSP00000251890":Monocytic leukemia zinc	3.13 3.12	2.21
	430540	AW245422		Homo sapiens cDNA: FLJ22105 fis, clone H	3.12	1.93
55	430015	AW768399	H- 200222	ESTs ESTs	3.09	2.87
23	414340	AI022656	Hs.296272	Eos Control	3.08	3.16
	400072 422567	AF111178	Hs.118407	glypican 6	3.06	2.73
	401284	APTITITO	HS.110407	Target Exon	3.04	2.56
	455839	BE145814		gb;MR0-HT0208-101299-202-a04 HT0208 Homo	3.02	2.76
60	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	3.00	3.15
00	437258	AL041243	Hs.174104	ESTs	2.99	2.44
	445612	N94126	Hs.12969	hypothetical protein .	2.98	2.40
	417777	AI823763	Hs.7055	ESTs, Wealdy similar to 178885 serine/th	2.97	2.13
	437723	AJ672731	Hs.13256	ESTs	2.95	2.46
65	439668	AI091277	Hs.302634	frizzled (Orosophila) homolog 8	2.95	2.77
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	2.94	2.68
	424761	AA534528	Hs.152944	loss of heterozygosity, 11, chromosomal	2.92	3.81
	405757			Target Exon	2.92	3.00
70	406621	X57809	Hs.8997	immunoglobutin tambda locus	2.92	6.71
70	409060	AI815867	Hs.50130	necdin (mouse) homolog	2.86	2.16
	431712	R26584	Hs.267993	hypothetical protein FLJ10143	2.82	2.50 2.48
	413441	AJ929374	Hs.75367	Src-like-adapter	2.82 2.82	1.13
	452651	AJ218918	Hs.30209	KIAA0854 protein	2.02 2.78	2.77
75	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	2.77	1.92
75	439778	AL109729	Hs.99364	putative transmembrane protein	2.75	2.89
	434293 406642	NM_004445 AJ245210	Hs.3796	EphB6 gb:Homo sapiens mRNA for immunoglobulin	2.70	2.03
	406638	M13861		gb:Human T-cell receptor active beta-cha	2.69	2.67
	432331	W37862	Hs.274368	MSTP032 protein	2.68	3.08
80	408989	AW361666	Hs.49500	KIAA0746 protein	2.68	2.58
00	401731	A11301000	13.43.00V	NM_017990*:Homo sapiens hypothetical pro	2.68	2.53
	401979			C17000767:gi[11990770]emb[CAC19651.1] (A	2.68	3.42
	415539	AI733881	Hs.72472	BMP-R1B	2.68	2.51
				550		

					0.07	2 42
	425032		Hs.154276	BTB and CNC homology 1, basic leucine zi	2.67 2.66	2.13 3.25
	406837 422550	R70292 BE297626	Hs.156110 Hs.296049	immunoglobulin kappa constant microfibrillar-associated protein 4	2.66	2.74
	425100	AF051850	Hs.154567	supervillin	2.65	2.80
5	452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	2.65	2.63
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	2.64	1.84 2.63
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	2.63 2.62	2.00
	425580 450680	L11144 AF131784	Hs.1907 Hs.25318	galanin Homo sapiens clone 25194 mRNA sequence	261	1.80
10	412482	AJ499930	Hs.334885	mitochondrial GTP binding protein	2.61	1.82
	433470	AW960564		transmembrane 4 superfamily member 1	2.60	2.44
	419138	U48508	Hs.89631	ryanodine receptor 1 (skeletal)	2.60	2.47
	401112			NM_024997":Homo sapiens hypothetical pro	2.60 2.59	2.58 2.32
15	411802 407856	AA733204 AA045281	Hs.266175	nuclear transcription factor Y, gamma phosphoprotein associated with GEMs	2.59	1.88
13	425209	AL049761	Hs.155140	casein kinase 2, alpha 1 polypeptide	2.58	2.81
	417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	2.56	2.10
	442560	AA365042	Hs.325531	ESTs, Wealtly similar to 2004399A chromos	2.55	3.97
20	408491	AI088063	Hs.7882	ESTs	· 2.54 2.54	2.74 2.02
20	420223	N27807	Hs.143844	ribosomal protein L4	2.54	2.59
	444467 436729	AI150368 BE621807	15.143044	transmembrane 4 superfamily member 1	2.53	2.29
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	2.53	1.80
	453507	AF083217	Hs.33085	WD repeat domain 3	2.52	1.99
25	420315	NM_006299	Hs.96448	zinc finger protein 193	2.52 2.50	2.50 2.35
	443060 453500	D78874 AJ478427	Hs.8944 Hs.43125	procollagen C-endopeptidase enhancer 2 esophageal cancer related gene 4 protein	2.50	2.44
	402692	M410421	PIS.43123	Target Exon	2.50	1.73
	427792	M63928	Hs.180841	tumor necrosis factor receptor superfami	2.50	4.55
30	440065	W03476	Hs.266331	hypothetical protein MGC4595	2.49	2.95
	420568	F09247	Hs.247735	protocadherin alpha 10	2.49 2.49	3.55 2.52
	444115	AW954585	Hs.271920	ESTs, Weakly similar to Z195_HUMAN ZINC NM_018937*:Homo sapiens protocadherin be	2.48	2.67
	404049 417694	R09486	Hs.193118	ESTs	2.48	2.09
35	420600	BE011657	Hs.165695	ESTs, Weakly similar to unnamed protein	2.48	2.00
	429922	Z97630	Hs.226117	H1 histone family, member 0	2.47	2.01
	404752			NM_024778:Homo sapiens hypothetical prot	2.47 2.47	3.07 2.46
	421429	NM_014922 AJ227874	Hs.104305 Hs.99244	death effector filament-forming Ced-4-fi ESTs	2.46	1.88
40	436378 429852	ABQ10445	Hs.225948	small inducible cytokine subfamily A (Cy	2.44	2.98
	431190	AL134172	Hs.120852	ESTs	2.44	2.48
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	2.44	2.96
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	2.44 2.43	3.16 3.33
45	445547 443030	D85181 R68048	Hs.273 Hs.9238	galactosylceramidase (Krabbe disease) hypothetical protein FLJ23516	2.43	2.07
43	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	2.43	3.36
	406782	AA430373	12.00121	gb:zw20f11.s1 Soares ovary tumor NbHOT H	2.40	3.38
	407250	L09095		gb:Horno sapiens mRNA fragment.	2.38	3.78
50	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	2.36 2.34	3.56 2.84
30	431365 414555	AA504080 N98569	Hs.191958 Hs.76422	immunoglobulin superfamily receptor tran phospholipase A2, group IIA (platelets,	2.33	3.21
	436485	X59135	Hs.156110	immunoglobulin kappa constant	2.31	2.94
	403632			Target Exon	2.27	2.80
	434232	AW297064	Hs.131862	ESTs	2.24	2.98 2.81
55	428114	AI821548	Hs.98363	ESTs, Wealdy similar to I38022 hypotheti	2.23 2.19	2.81
	403294 429249	X81479	Hs.2375	Target Exon egf-like module containing, mucin-like,	2.16	3.13
	403295	70.410		Target Exon	2.15	2.95
	427817	AA503373	Hs.186678	ESTs	2.13	2.80
60	425154	NM_001851		collagen, type IX, alpha 1	2.08 _. 2.04	3.28 3.50
	443176 401770	AI696081	Hs.223770	ESTs C17001739":gi 2327052 gb AAC48759.1 (U9	2.04	5.39
	407124	R08160		gb:yf18a07.s1 Soares fetal liver spleen	2.03	2.95
	456060		Hs.45184	Homo sapiens cDNA FLJ12284 fis, clone MA	2.03	2.97
65	413053	AW963263	Hs.65377	ESTs, Moderately similar to KIAA1399 pro	2.01 2.01	3.42 3.05
	426653		Hs.171695	dual specificity phosphatase 1	2.01	3.58
	410677 401673		Hs.65424	tetranectin (plasminogen-binding protein C16001416*:gi 12743112 ref XP_010131.2	1.99	4.99
	420983		Hs.100764	catheosin G	1.95	5.47
70	413624		Hs.75445	SPARC-like 1 (mast9, hevin)	1.94	4.58
	433554	AW957666	Hs.8108	disabled (Drosophila) homolog 1	1.93	2.82
	405121		11- 040400	mitogen-activated protein kinase 8 inter	1.92 1.92	2.82 2.80
	436456 450852		Hs.248122 Hs.7740	G protein-coupled receptor 24 oxysterol binding protein-like 1	1.91	5.08
75	432902		113.7740	histone deacetylase 3	1.90	2.84
	422100		Hs.111554	ADP-ribosylation factor-like 7	1.89	3.04
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	1.87	2.85
	424398		Hs.146393	homocysteine-inducible, endoplasmic reti	1.85 1.85	3,71 3.38
80	416714 433465		Hs.79630 Hs.3314	CD79A antigen (immunoglobufin-associated selenoprotein P, plasma, 1	. 1.85	3.57
00	447990		Hs.20144	small inducible cytokine subfamily A (Cy	1.82	6.17
	421563	NM_00643	3 Hs.105806	granutysin	1.80	3.50
	453804		Hs.35276	KIAA0852 protein	1.78	2.87



	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	1.78	3.54	
	437866	AA156781		metallothionein 1E (functional)	1.77	2.97	
	427751	AF000152		conserved gene amplified in osteosarcoma	1.75	6.89	
_	400442			DKFZP586G1722 protein	1.74	3.60	
5	456898	NM_001928	Hs.155597	D component of complement (adipsin)	1.74	3.45	
	414477	U41635	Hs.76228	amplified in osteosarcoma	1.71	4.99 2.86	
	432870	AW974124		gb:EST386227 MAGE resequences, MAGM Homo	1.68 1.68	3.09	
	456642	AW451623	Hs.109752	putative c-Myc-responsive	1.66	2.83	
10	456694	AW016382	Hs.105642 Hs.241471	Homo sapiens cDNA: FLJ23271 fis, clone H RNB6	1.65	2.84	
IU	430449	AA352723	MS.2414/1	v-myc avian myelocytomatosis viral relat	1.65	2.88	
	401029 402742			NM_002508:Homo sapiens nidogen (enactin)	1.64	3.37	
	402559			Rho GTPase activating protein 1	1.63	3.07	
	418271	NM_000919	Hs.83920	peptidylglycine alpha-amidating monooxyg	1.62	3.11	
15	406851	AA609784	1.0.000.0	major histocompatibility complex, class	1.62	2.86	
	450912	AW939251	Hs.25647	v-los FBJ murine osteosarcoma viral onco	1.60	3.94	
	447029	AL137281	Hs.17110	Homo sapiens mRNA; cDNA DKFZp434C2016 (I	1.60	3.75	
	417739	Z43995		gb:HSC1QB121 normalized infant brain cDN	1.59	2.96	
	452950	AA428123	Hs.302766	tyrosine 3-monooxygenase/tryptophan 5-mo	1.58	2.95	
20	427461	AA531527	Hs.332040	hypothetical protein MGC13010	1.58	4.11	
	444182	AW160432	Hs.296460	craniofacial development protein 1	1.57	2.98	
	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	1.57	3.88	
	452887	AJ702223	Hs.107253	hypothetical protein DKFZp761F241	1.56	2.88	
06	416819	U77735	Hs.80205	pim-2 oncogene	1.56	3.59	
25	414583	AA362907	Hs.76494	profine arginine-rich end leucine-rich r	1.56	4.38	
	426104	AI204418	Hs.190080	ESTs	1.55	3.47 4.28	
	441591	AF055992	Hs.183	Duffy blood group	1.52 1.49	2.87	
	446406	AI553681		Arg/Abi-interacting protein ArgBP2	1.49	2.88	
20	427343	AJ880044	Hs.176977	protein kinase C binding protein 2	1.47	4.82	
30	415550	L13720	Hs.78501	growth arrest-specific 6	1.46	3.48	
	411961	AJ478432	Hs.72956	hypermethylated in cancer 1 ENSP00000246202*:DJ63M2.2 (similar to AC	1.42	3.19	
	406213			NM_003105*:Homo sapiens sortiin-related	1.41	2.97	
	400847 404542			NM_021965*:Homo sapiens phosphoglucomuta	1.40	3.02	
35	452650	AW270150	Hs.254516	ESTs	1.40	2.86	
"	432894	AW167668	Hs.279772	brain specific protein	1.37	5.52	
	404030	ATT 107 000	113.277772	NM_015669*:Homo sapiens protocadherin be	1.37	3.03	
	422033	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	1.35	3.15	
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	1.34	3.09	
40	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	1.32	3.29	
	415198	AW009480	Hs.943	natural killer cell transcript 4	1.32	2.89	
	406908	Z25437		gb:H.sapiens protein-tyrosine kinase gen	1.31	2.89	
	423959	AA333025		gb:EST37122 Embryo, 8 week I Homo sapien	1.31	2.88	
	408135	AA317248	Hs.42957	methyltransferase-like 1	1.29	3.81	
45	427523	8E242779	Hs.179526	upregulated by 1,25-dihydroxyvilamin D-3	1.29	3.25	
	415512	Y16270	Hs.78482	paralemmin	1.29	2.85	
	413531	AL036958	Hs.75416	DAZ associated protein 2	1.28	3.06	
	419608	ALD37237	Hs.91586	transmembrane 9 superfamily member 1	1.27	2.80	
50	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	1.26 1.25	2.90 3.41	
50	422934	BE244189	Hs.122492	hypothetical protein	1.25	3.63	
	450935	BE514743	11- 174054	tumor suppressor deleted in oral cancer-	1.24	2.93	
	416630	H69392	Hs.174051	small nuclear ribonucleoprotein 70kD pol dermatopontin	1.22	2.81	
	416950	AL049798	Hs.80552	gb:EST374092 MAGE resequences, MAGG Horno	1,21	3.02	
55	412558 419593	AW962019 W73092	Hs.58282	ESTs	1.19	2.84	
33	403470	1113032	113.30202	Target Exon	1.14	2.82	
	402230			Foenesh predicted: CYTOCHROME P450 4F5 (1.12	2.96	
	400559			Target Exon	1.00	2.90	
	412695	AW984439		gb:PM3-HN0011-220300-002-c05 HN0011 Homo	1.00	2.84	
60	427072	H38046	Hs.293981	ESTs	1.00	2.89	
	430439	AL133561		DKFZP434B061 protein	1.00	3.09	
	418183	NM_00177	2 Hs.83731	CD33 antigen (gp67)	1.00	2.93	
15	TABLE						
65	Pkey:	Ur	ique Eos probese	et identifier number			
	CAT nu		ene cluster numbe				
	Accessi	on: G	enbank accession	numbers			
	~ .	CATALLER					
70	Pkey 406636		er Accession	083 L12065 L12075 L12066 L12085 L12072 L12082 L12081	1 12062 (12080		
70	430540		DC017171 D	C012195 NM_007126 AF100752 AL137377 Z70768 BM474	865 RG754806 AU124376	BG757203 BG7	64420 BG775028 BG824418
	430340	713_2	DIMMERSO A	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	15998 RM048875 RF88107	0 RF313689 BE	B79144 BM305834 AWZ45647
			A1770171 RE	C106861 RERS6807 AA463876 A1375927 AA648810 AA9481	93 AA490916 AJ459893 AI	145B188 AI24040	08 VI 181843 VI I 3 I 173 VA VPR333
			AIRESIDE AV	W337084 AWN3615N RE4665Q1 RE6745QQ AIRIR43R AA777	7197 Al651927 AW151143	BI198825 BGB1	19083 RW428/P4 RE302201
75			00777716	HANATON DECONOCS DECONOTOS RE731007 RE390023 RC87	45384 RE996406 RE988931) RM475542 AW	V246215 BE501897 BE903610
			DE561530 B	ESSASST REGASTRO RETSOUT RICOTOM RG761305 RE262	7642 8F391848 BF382475	BG008258 BI54	17991 B1459099 BE391391 BE259420
			DC208100 A	W245422 AI423847 AI914618 H80534 RF301004 AI 53179	1 AI435581 BF793112 AL5	77303 AA37326	55 BE /46965 BF /4 <i>3</i> 630 BE8/9290
			VISEOVOS BI	MATRICOR AIGROPEA AWAY 2450 F20201 AW 151405 AW 5175	72 AA773468 BG259694 B	3E391163 BG62	1529 A1421728 BG767231 BM462953
			DC3405343	MC2CAR AA113434 RE785A31 RINA10R1 RCR373R5 RG2531	68 BG759470 BF369329 F	1F981332 BE259	9418 BE785738 BI091658 N72512
80			W58737 WR	15690 RG958989 AI205206 H19721 W17051 W77958 BI262	010 AAB44319 W74143 W	72214 N85194 E	3E734033 BG164099 AA931069
			F13645 R41	394 AK025758 BG180977 BE349455 AA812018 AA740241	AI027722 AI150356 AA881	6395 AW977627	7 BE220225 AA884082 AW518114
			AI243844 A	A809493 AA481029 AA825718 A1347866 A1431670 AA8144	36 AJ251 109 R07704 AA76	55606 AA724593	3 AIS18399 AI537550 AA491103

PCT/US02/29560

5	430015	713_2	AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489581 AW971893 AW612086 BE077936 BI850809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591 BC017171 BC012195 NM, 007126 AF100752 AL137377 Z70788 BM474865 BG754806 AU124376 BG757203 BG764420 BG715028 BG824418 BM045810 AU120387 BG770238 BG6686740 BG913323 B1759980 BG395998 BM048875 BE881070 BE313589 BE879144 BM309834 AW245847 A1770171 BF196861 BE566897 AA468376 AU375977 AA548810 AA948193 AA49016 Al459893 A458188 AV24068 A191843 A1131029 AW768399 AJ353196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 B1198825 BG819083 BM458764 BE903367
			DC722745 DM042200 DE000262 DE00026 DE731007 RF390023 RC875384 RF996406 RF98850 BM47554Z AWZ46Z15 BE5U1897 BE5U3010
10			BESS1530 BESS0537 BES00382 BE732947 BIZ77204 BG761305 BE262642 BE331848 BE382475 BG008288 BIS47931 BHS9099 BE391391 BE259420 BE28109 AW245422 AM23847 AN314518 HB0534 BE301004 AL531791 AM35581 BF733112 AL577301 AA373265 BE745955 BF743830 BE879296 AM216724 BM35430 BE879296 AM216728 BM35485 BM362853 BM36285 BM36
			RG340524 WS2648 AA113434 BE785431 BID41981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 WS6732 WS6590 BG958989 AI205206 H19721 W17051 W77558 BI262010 AA84319 W76143 W77214 N8219 BG754039 BG164099 AA831069 F13545 R41394 AK025758 BG168097 BG349455 AA812018 AA740241 AI027722 A1150356 AA886395 AW977627 BC270225 AA88022 AW518114 AI243844 AA809493 AA481023 AA826718 AI347866 A4431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491 103
15	455839	1518842_1	AW003188 R07703 AA989120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 BE007760 BC746251 BE962912 BM454584 AL134894 BF104082 H80591 BE145823 BE145830 BE145846 BE145814 BE145905 BE145833 BE145834 BE145883 BE145889
	406642	0_0	A1245210 A1245212 A1245211 A1245213
20	406638 433470	0_0 6624_1	M13861 X75684 AL573167 A445461 A1453743 A1983655 A1564644 AA977180 A1694111 A1591358 AW071625 A1678712 A1720339 A1927769 BE433796
			ANGGAJZ AA292956 AW192593 AIBSSB38 AIGS9905 AI424384 A1161312 AI911921 AI597801 BIM94959 AI240988 AI49255A AW262737 BE044033 AW008570 AW623956 BIM94958 AA088439 AA706057 BF222920 BF533008 BE501957 AA524526 BE044131 AW5572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE64195 AW757257 AA900390 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF0657147 AA657656 AA157944 AB90245 AA662517 T32487 AI800106 AI333170 AIB59180 W45410 AI999887
25			AW7/5048 AA18260 AA478328 A1288335 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 A1251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 A1769516 AW772283 AA010631 AI692846 AU651065 H00983 R79933 A1950693 A1245632 AJ349390 AA148284 A1788502 AA897893 A1621320 AW194272 C0865 AA953883 BE689836 A198523 A1872628 A1927217 A14533453 A1189366 AW338678 A1261359 A1500576 BF477735 A1032569 A1972899 A189583 Z28771 AJ353829 A1693030 AA603368 BE773488 AW333301 BE773489 BE773462 BE773495 A1650338 BE773499 A1745717 BE811470 BE811470 BE811418 BE811418 BE811410 BE811398
30			BE/13489 BE/1340 BE/13593 AGOSDAS BE/13494 BE/13495 AGOSDAS BERT3417 BE/13417 BE/13417 BE/13418 BE/1340 BE/134
			DEDATORN AMERICA AASO2922 AASA2494 ALSSESON ALSSESON REFORMS REBITION BEF773498 BE811401 BE773494 BE811437 BE811437 BE811437 BE811401 BE773494 BE811401 BE77348 BE811401 BE77348 BE811401 BE77348 BE811401 BE77348 BE811401 BE77348 BE811401 BE77348 BE811401 BE77348 BE811401 BE77348 BE811401 BE77348 BE811401 BE77348 BE811401 BE77348 BE811401 BE77348 BE811401 BE7734 BE81140 BE7734 BE81140 BE7734 BE81140 BE7734 BE81140 BE7734 BE81140 BE7734 BE81140 BE7734 BE81140 BE7754 BE81140 BE
35			BEB11399 BF997171 BF757734 BE926037 AJ377595 C06111 AW088968 BEB11404 BE811472 AI855912 AI925607 AI871950 AI093510 BE905927 BE811435 AAI91387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AJ567995
•			W60075 BF941183 A1738844 BE811458 BE773481 A1262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197359 BE905184 AA722206 A1344043 A1248977 A1234860 BE621867 BE156290 AA454099 AA037722 BFR43897 AW806183 AA043216 BG482896 AA182734 AA877242
			AM27700C M277C3 030114 DEBEIRER DE156314 AA100477 T91762 AA035067 AAR37376 T10930 RF906587 B1/5502/ BUSU0/31 BUSU0444
40			BC010166 AL550134 AL550396 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255559 BC485098 BI259228 BG49501 BM044512 AU133984 AL555588 BE745111 BI222633 AU13377 BC28B151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721123 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429895 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW881735 BG528230 BI250895
			AMECICO: DIMAROTA RIMARRIS RC1421RS AA3151RR AMAR615 COR300 BG497644 AA088544 AUS 15987 BG528631 BED19182 AVV239183
45			AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BIB70221 BE910282 BGS38748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525
	41 1802	609_6	BF345917 AL549635 BI040919 AA733204 AA232382 T34425 T32000 BF906697 Z42382 BI544863 AL548378 AW816536 AW816719 BE152340
50			BF375392 AW816716 BE152336 BF375367
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55			AW573152 AA723200 C06123 BF057147 AA527686 AA157944 A1990245 AA662517 T32487 A1800106 A1333170 A1859160 W45410 A1990827 AW275048 AA182640 AA478328 A1298935 AW085188 AW471421 AW103470 AW300456 AW191997 A1822466 AA962397 AA136588 A1251817 AW375048 AA182640 AA478328 A1298935 A157735 AA037696 A1769516 AW772283 AA010631 A1692846 A1061055 H80983 R79933 A1950693 A1245632 A1349390 AA148284 A1798502 AA487893 A1521320 AW194272 C06365 AA953883 BE858936 A1918523 A1872628 A1927217 A1453453
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65			BF843900 AW86493 AA502832 AA64949 AL568520 AL547860 BE705937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811390 BE811393 AA502832 AA64949 AL568520 AL547860 BE705937 BE811390 BF973498 BE811401 BE7373484 BE811437 BE811380 BE811393 BF981717 BF757734 BE926037 AI377596 CO6111 AW088968 BE811404 BE811472 AI865512 A1925607 AI871950 A1093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW88452 C17594 BF84383 AI248307 BE773483 AI567995 W60075 BF941183 A1738944 BE811453 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206
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70			AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL550366 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL651379 BI259821 BG74768 BI868522 AU135866 BI552770 BI259821 BI255529 BG485098 BI258228 BG488501 BM044812 AU133985 BG55686 BE745111 BI222633 AU133917 BG288151 BI250715 BI550550 BG500773 BI551761 BG707501 BI818593 BF691383 BG721129 BG541578 BE906566 BG751098 BI224135 BG400746 BGA78065
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			AND 1436 ANT 351917 ANT 351926 ANT 2717 ANT 351926 ANT 2717 ANT 351927 AND 35



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	423959	887999_1	BE273069 /	NA333025 BC002850 BC016704 NIM_005851 AF089814 AK001498 AL537879 BG754157 A1129659 A1261895 BG397540 BF663515 AW517226
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40	412695	1243394_1	AW962019 AW984433	BE389091 AW984393 AW984439 AW984451 AW984367 AW984371 AW984349 AW984356 AW984444 AW984443 AW984449
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	412695 430439 TABLE 5 Pkey: Ref: Strand:	1243394_1 6750_2 5C: Uni Sec seq Ind	AW962019 AW984433 AL133561 que number co quence source quence of huma icates DNA stri	BE389091 AW984393 AW984439 AW984451 AW984367 AW984371 AW984349 AW984356 AW984444 AW984443 AW984449 AL117481 AL122069 AW439292 Al968826 AL041090 wresponding to an Eos probeset The 7 digit numbers in this conumn are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
45	412695 430439 TABLE 5 Pkey: Ref: Strand: NL positi	1243394_1 6750_2 5C: Uni Sec seq Ind	AW962019 AW984433 AL133561 que number co quence source. quence of huma icates DNA stra icates mucleotic	BE389091 AW984393 AW984439 AW984451 AW984367 AW984371 AW984349 AW984356 AW984444 AW984443 AW984449 AL117481 AL122069 AW439292 Al968826 AL041090 Interponding to an Eos probeset The 7 digit numbers in this codumn are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Interpolation which exons were predicted. In positions of predicted exons.
45	412695 430439 TABLE 5 Pkey: Ref: Strand: NL positi	1243394_1 6750_2 5C: Uni Sec seq Indi on: Indi	AW952019 AW984433 AL 133561 que number co quence source, quence of huma cates DNA str icates nucleotic Strand	BE389091 AWS84333 AWS84439 AWS84451 AWS84367 AWS84371 AWS84349 AWS84356 AWS84444 AWS84443 AWS84449 AL117481 AL122069 AW439292 Al968826 AL041090 Tresponding to an Eos probeset The 7 digit numbers in this codumn are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA and from which exons were predicted. The positions of predicted exons. Nt_position
45	412695 430439 TABLE 5 Pkey: Ref: Strand: Ni_positi Pkey 404854	1243394_1 6750_2 SC: Uni Sec seq Indi on: Indi	AW952019 AW984433 AL 133561 que number co quence source, uence of huma cates DNA str icates nucleotic Strand Plus	BE389091 AW984393 AW984439 AW984451 AW984367 AW984371 AW984349 AW984356 AW984444 AW984443 AW984449 AL117481 AL122669 AW439292 Al968826 AL041090 Tresponding to an Eos probeset The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA and from which exons were predicted. The DNA are from which exons were predicted. It positions of predicted exons. NIL position 14260-14537
45	412695 430439 TABLE 5 Pkey: Ref: Strand: Ni_positi Pkey 404854 402294	1243394_1 6750_2 5C: Uni Sec seq Indi on: Indi Ref 7143420 2282012	AW952019 AW884433 AL133561 que number co quence source. quence of hums icates DNA stra icates nucleotic Strand Plus Minus	BE389091 AWS84333 AWS84439 AWS84451 AWS84367 AWS84371 AWS84349 AWS84356 AWS84444 AWS84443 AWS84449 AL117481 AL122069 AW439292 Al968826 AL041090 Interponding to an Eos probeset The 7 digit numbers in this codumn are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Interpolation of predicted exons. NIL_positions of predicted exons. NIL_positions of predicted exons.
45	412695 430439 TABLE 5 Pkey: Ref: Strand: Ni_positi Pkey 404854 402294 402737	1243394_1 6750_2 5C: Uni Sec sec Indi on: Indi Ref 7143420 2282012 9212184	AW952019 AW984433 AL 133561 que number co quence of huma cates DNA str icates nucleotic Strand Plus Minus Minus	BE389091 AW984393 AW984439 AW984451 AW984367 AW984371 AW984349 AW984356 AW984444 AW984443 AW984449 AL117481 AL122069 AW439292 Al968826 AL041090 Tresponding to an Eos probeset The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Ounham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al. (1999) Nature 402:489-495. and from which exons were predicted. the positions of predicted exons. Nt_position 14260-14537 2575-3000 13358-13552
45	412695 430439 TABLE 5 Pkey: Ref: Strand: Ni_positi Pkey 404854 402294	1243394_1 6750_2 5C: Uni Sec seq Indi on: Indi Ref 7143420 2282012	AW952019 AW884433 AL133561 que number co quence source. quence of hums icates DNA stra icates nucleotic Strand Plus Minus	BE389091 AWS84333 AWS84439 AWS84451 AWS84367 AWS84371 AWS84349 AWS84356 AWS84444 AWS84443 AWS84449 AL117481 AL122069 AW439292 Al968826 AL041090 Interponding to an Eos probeset The 7 digit numbers in this codumn are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Interpolation of predicted exons. NIL_positions of predicted exons. NIL_positions of predicted exons.
45	412695 430439 TABLE 5 Pkey: Ref: Strand: NL positi 40294 402737 404995 401284 405757	1243394_1 6750_2 5C: Unit Sector Sector India on: Indi Ref 7143420 2282012 9212184 6006247 9800819 3334694	AW982019 AW984433 AL 133561 / que number co quence source. quence of hum cartes DNA stra cates nucleotic Strand Plus Minus Minus Minus Minus Minus Minus	BE389091 AW984393 AW984439 AW984451 AW984367 AW984371 AW984349 AW984356 AW984444 AW984443 AW984449 AL117481 AL122069 AW439292 Al968826 AL041090 Tresponding to an Eos probeset The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Ounham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al. (1999) Nature 402:489-495. and from which exons were predicted. the positions of predicted exons. Nt_position 14260-14537 2575-3000 13358-13352 154015-154123 101307-101421 66825-70456
45 50 55	412695 430439 TABLE 5 Pkey: Ref: Strand: NL_position Pkey 404854 402294 402737 404995 401284 405757 401731	1243394_1 6750_2 5C: Uni Sec seq Indi on: Indi Ref 7143420 2282012 9212184 6006247 9800819 3334694 9690317	AW952019 AW984433 AL133561 i que number co quence source. quence of hum cates DNA sir- cicates nucleotic Strand Plus Minus Minus Minus Minus Minus Minus Plus Plus Plus Plus Plus	BE389091 AW984393 AW984439 AW984451 AW984367 AW984371 AW984349 AW984356 AW984444 AW984443 AW984449 AL117481 AL122069 AW439292 Al968826 AL041090 rresponding to an Eos probeset The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al. (1999) Nature 402-489-495. Indiffrom which exons were predicted. In Epositions of predicted exons. NIL position 14260-14537 2575-3000 13358-13552 154015-154123 101307-101421 66825-70466 43830-43963,44787-44935,45698-45810,4741
45	412695 430439 TABLE 5 Pkey: Ref: . Strand: NL_positi Pkey 404854 402294 402737 404995 401284 405757 401731 401979	1243394_1 6750_2 SC: Uni Sec seq Ind on: Ind Ref 7143420 2282012 9212184 6006247 9800819 3334694 9690317 2628778	AW852019 AW884433 AL133561 / que number co quence source. uence of huma cates DNA stri cates mucleotic Strand Plus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus	BE389091 AW984393 AW984439 AW984451 AW984367 AW984371 AW984349 AW984356 AW984444 AW984443 AW984449 AL117481 AL122069 AW439292 Al968826 AL041090 responding to an Eos probeset The 7 digit numbers in this coturns are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al. (1999) Nature 402:489-495. and from which exons were predicted. fe positions of predicted exons. Nt_position 14260-14537 2575-3000 13388-13552 154015-154123 101307-101421 66825-70465 43830-43963,44787-44935,45698-45810,4741 75693-75851,76977-77112
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45 50 55 60 65 70	412695 430439 TABLE 5 Pkey: Ref: NLpositi 1040454 402237 404995 401284 405757 401731 401673 401731 401731 402692 40403 404752 403295 401770 40	1243394_1 6750_2 SC: Uni Sec seq Indi on: Indi Ref 7143420 2282012 9212184 6006247 9800819 3334694 9690317 2828778 9966198 8468956 3688074 7109522 8572864 8096528 9958312 7689903 8102330 9887672 9112700 9884675 9212200 98847672 9117523 9212200 98847672 9188605 9796810 97671252	AW982019 AW984433 AL 133561 / que number co quence source, quence source, quence of hums Africates nucleotic Strand Plus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	BE399091 AW984393 AW984439 AW984451 AW984367 AW984371 AW984349 AW984356 AW984444 AW984443 AW984449 AL117481 AL122069 AW439292 Al968826 AL041090 responding to an Eos probeset The 7 digit numbers in this codumn are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA in chromosome 27 Dunham, et al. (1999) Nature 402-489-495. Indications of predicted exons. NL_position 1426-14537 275-3000 1338-13552 154015-154123 101307-101421 66825-70466 43830-43963,44787-44935,45698-45810,4741 75693-75851,76977-77112 60628-61041 1124606-125387 75755-78155 120168-110326 35197-35358 41565-41881 22386-22708 183424-183576 122587-122705,122765-123047 33816-36004,36587-36684 59962-59974 41999-42172 24487-23613 33333-33715 52921-26612,34539-35161 44643-44835 102999-103145
45 50 55 60 65 70	412695 430439 TABLE 5 Pkey: Ref: Strand: NL position 404854 402237 40495 401237 401979 401173 405757 401731 405757 401731 405757 401731 40592 404049 404752 403294 404752 403294 404752 404049 404752 404049 404752 404049 404752 404049 404752 404049 404752 404049 404752 404049 404752 404049 404752 404049 404752 404049 404752 404049 404752 404049 404752 404049 404752 404049 404752 404049 404752 404049 404752 404049	1243394_1 6750_2 5C: Uni Sec Seq Indi on: Indi Ref 7143420 2282012 9212184 6006247 980819 3334694 9690317 2828778 9956198 8468956 3888074 7109522 8572864 8096495 8996528 9958312 7689903 8102330 9887672 8117523 9887672 8117523 9887672 8117523 9887672 8117523 9887672 8117523 9798810 9798810 9798810 9798810 7671252 999973	AW982019 AW984433 AL 133561 / que number co quence source. quence of hum cates DNA stri cates nucleolic Strand Plus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Plus Minus Minus Plus Minus Plus Minus Plus Minus Plus Minus Plus Minus Plus Minus Plus Minus Plus Minus Plus Minus Plus Minus Plus Minus Plus Plus Minus Plus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	BE389091 AW984393 AW984451 AW984367 AW984371 AW984349 AW984356 AW984444 AW984443 AW984449 AL117481 AL122069 AW439292 Al958826 AL041090 rresponding to an Eos probeset The 7 digit numbers in this coturns are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al. (1999) Nature 402-489-495. and from which exons were predicted. Ie positions of predicted exons. NI_position 14260-14537 2575-3000 1338-13552 154015-154123 101307-101421 66825-70466 43830-43963, 44787-44935, 45698-45810,4741 75693-75851,76977-77112 66026-81041 124606-125337 75765-78155 120168-120326 35197-35358 41565-41881 22365-22708 833424-183576 122587-122705, 122765-123047 35815-36004, 35587-36684 59362-59574 41999-42172 23487-23613 33539-33715 25921-26612,34539-35161 44643-44835 102999-103145 149362-151749 8376-8552
45 50 55 60 65 70	412695 430439 TABLE 5 Pkey: Ref: NLpositi 1040454 402237 404995 401284 405757 401731 401673 401731 401731 402692 40403 404752 403295 401770 40	1243394_1 6750_2 5C: Unit Sec Sec Indi on: Indi Ref 7143420 2282012 9212184 6006247 9800819 3334694 9690317 2828778 9666198 8466956 3888074 7109522 8572864 8096496 8096528 9958312 7689903 8102330 9887672 8117523 9212200 9864273 7342019 9188605 9929739 9966312	AW982019 AW984433 AL 133561 / que number co quence source, quence source, quence of hums Africates nucleotic Strand Plus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	BE399091 AW984393 AW984439 AW984451 AW984367 AW984371 AW984349 AW984356 AW984444 AW984443 AW984449 AL117481 AL122069 AW439292 Al968826 AL041090 responding to an Eos probeset The 7 digit numbers in this codumn are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA in chromosome 27 Dunham, et al. (1999) Nature 402-489-495. Indications of predicted exons. NL_position 1426-14537 275-3000 1338-13552 154015-154123 101307-101421 66825-70466 43830-43963,44787-44935,45698-45810,4741 75693-75851,76977-77112 60628-61041 1124606-125387 75755-78155 120168-110326 35197-35358 41565-41881 22386-22708 183424-183576 122587-122705,122765-123047 33816-36004,36587-36684 59962-59974 41999-42172 24487-23613 33333-33715 52921-26612,34539-35161 44643-44835 102999-103145

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TABLE 56A: ABOUT 277 GENES UPREGULATED IN MELANOMA METASTASES RELATIVE TO BENIGN NEVI
Table 56A lists about 277 genes upregulated in melanoma metastases relative to benign nevi. Genes were selected from 59680 probesels on the Eos/Affymetrix Hu03 Genechip
array. Gene expression data for each probesel obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA
expression.

Unique Eos probesel identifier number Exemplar Accession number, Genbank accession number Unigene number expression.
Pkey:
ExAcon:
UnigeneID:
Unigene Title:
R1: 5

Unique gene tills

Tith percentile of melanoma metastasis Als divided by the maximum of benign nevi Als

Tith percentile of melanoma metastasis Als divided by the maximum of benign nevi Als, where the 15th percentile of normal tissue Als was subtracted from both
the numerator and denominator 10 R2:

	Pkey	ExAcon	UnigenelD	Unigene Title	R1 13.73	R2 17.18
15	422424	A1186431	Hs.296638 Hs.313	prostate differentiation factor secreted phosphoprotein 1 (osteopontin,	11,57	13.25
13	446619 407846	AU076643 AA426202	Hs.40403	Obp/p300-interacting transactivator, wit	9.35	8.75
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	8.63	6.22
	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	8.21	8.65
	424321	W74048	Hs.1765	tymphocyte-specific protein tymsine kin	7.13	5.04
20	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	6.79	7.12
	417693	AW959741	Hs.40368	adaptor-related protein complex 1, sigma	6.55	5.94 3.45
	429500	X78565	Hs.289114	hexabraction (tenascin C, cytotactin)	6.43 6.43	5.44
	414812	X72755	Hs.77367 Hs.23889	monokine induced by gamma interferon ESTs, Wealdy similar to ALU7_HUMAN ALU S	6.31	6.08
25	451736 418870	AW080356 AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	6.20	6.04
23	428291	AA534009	Hs.183487	interferon stimulated gene (20kD)	6.03	4.72
	417308	H50720	Hs.81892	KIAA0101 gene product	6.01	7.07
	448569	BE382657	Hs.21486	signal transducer and activator of trans	5.99	8.88
	439310	AF086120	Hs.102793	ESTs	5.95	6.63
30	452838	U65011	Hs.30743	preferentially expressed antigen in mela	5.95 6.70	3.77
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	5.76 5.76	6.37 3.14
	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	5.65	5.01
	409274 442739	NM_003930 NM_007274	Hs.52644 Hs.8679	SKAP55 homologue cytosolic acyl coenzyme A thioester hydr	5.58	3.50
35	442711	AF151073	Hs.8645	hypothetical protein	5.45	5.84
	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	5.42	5.75
	412918	BE563957		activated RNA polymerase II transcriptio	5.35	4.94
	428125	AA393071	Hs.182579	leucine aminopeptidase	5.33	5.34
40	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	5.33	4.98
40	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	5.30 5.16	6.25 5.33
	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	5.05	8.77
	426600 415444	NM_003378 BE247295	Hs.171014 Hs.78452	VGF nerve growth factor inducible solute carrier family 20 (phosphate tran	5.03	5.17
	436701	AW959032	ris.10432	ESTs, Moderately similar to 178885 serin	5.03	4.17
45	406648	AA563730	Hs.277477	major histocompatibility complex, class	4.99	5.08
	410850	AW362867	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	4.98	4.71
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CO18 (p95), ly	4.98	4.08
	432469	AL080084		CGI-100 protein	4.97	4.70
50	404854			Target Exon	4.85	4.07 4.90
50	415701	NM_003878	Hs.78619	gamma-ghrtamyl hydrolase (conjugase, fol	4.82 4.81	3.45
	425397 408958	J04088 T99607	Hs.156346 Hs.49346	topoisomerase (DNA) It alpha (170kD) signal recognition particle 54kD	4.78	2.34
	453949	AU077146	Hs.36927	heat shock 105kD	4.78	6.32
	458079	A1796870	Hs.54277	DNA segment on chromosome X (unique) 992	4.77	6.57
55	440245	AK001913	Hs.7100	hypothetical protein	4.74	3.83
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	4.74	5.53
	417834	BE172058	Hs.82689	tumor rejection antigen (gp96) 1	4.73	4.35 4.60
	451003	AF058696	Hs.25812	Nijmegen breakage syndrome 1 (nibrin)	4.67 4.62	3.50
60	424571 434203	BE379766 BE262677	Hs.283558	polymerase (RNA) II (DNA directed) polyp hypothetical protein PRO1855	4.61	5.67
00	452268	NM_003512		H2A histone family, member L	4.60	3.79
	421311	N71848	Hs.283609	hypothetical protein PRO2032	4.60	3.58
	410491	AA465131	Hs.64001	Horno sapiens clone 25218 mRNA sequence	4.60	4.68
	425706	AW406678	Hs.122559	hypothetical protein FLJ22570	4.59	3.83
65	450293	N36754	Hs.171118	hypothetical protein FLJ00026	4.57	5.40
	406836	AW514501	Hs.156110		4.57 4.53	6.33 4.77
	413441	AI929374	Hs.75367	Src-like-adapter Homo sapiens mRNA; cDNA DKFZp434I0812 (f	4.48	4.89
	431129 418506	AL137751 AA084248	Hs.263671 Hs.85339	G protein-coupled receptor 39	4.47	4,17
70	411060	NM_006074			4.47	4.33
, 0	417501	AL041219	Hs.82222	sema domain, immunoglobulin domain (lg),	4.45	3.32
	437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1	4.43	4.43
	448883	BE614989	Hs.7503	hypothetical protein FLJ14153	4.42	3.91
	417274	N92036	Hs.81848	RAD21 (S. pombe) homolog	4.41	4.09
75	419285	D31887	Hs.89858	KIAA0062 protein	4.40 4.38	3.56 3.00
	418321	D63477	Hs.84087	KIAA0143 protein	4.38 4.37	4.26
	430154	AW583058	Hs.234726 1 Hs.184339		4.36	4.90
	428450 428297		Hs.184533 Hs.183583		4.36	3.57
80	447232		Hs.327	interleukin 10 receptor, alpha	4.36	4.07
- •	409598			mitochondrial ribosomal protein S28	4.35	3.29
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	4.34	5.80
	407047	X65965		gb:H.sapiens SOD-2 gene for manganese su	4.33	3.51
				564		

						. ~
	443991			potassium intermediate/small conductance plutaredoxin (thioltransferase)	4.33 4.32	4.23 2.68
	452322 420991	BE566343 AW504814		Homo sapiens mRNA for FLJ00111 protein,	4.32	4.54
	449722	BE280074		cyclin B1	4.31	3.73
5	408380	AF123050		diubiquitin	4.30	5.74
	427127	AW802282		pyruvate dehydrogenase phosphatase	4.28 4.28	4.80 3.59
	417933 432828	X02308 AB042326		thymidylate synthetase chondroitin 4-suffotransferase	4.25	4.15
	450306	AL080080		thioredoxin domain-containing	4.24	3.15
10	440266	AA088809	Hs.19525	hypothetical protein FLJ22794	4.23	4.12
	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	4.22 4.20	4.64 4.62
	427337 408989	Z46223 AW361666	Hs.176663 Hs.49500	Fc fragment of IgG, low affinity IIIb, r KIAA0746 protein	4.20	4.92
	449626	AA774247	Hs.301637	zinc finger protein 258	4.19	3.17
15	422846	BE513934	Hs.1583	neutrophil cytosolic factor 1 (47kD, chr	4.18	8.91
	415726	T89844	Hs.78712	aminolevulinate, della-, synthase 1	4.16 4.16	4.21 1.89
	444207 416980	AI565004 AA381133	Hs.80684	cathepsin D (lysosomal aspartyl protease high-mobility group (nonhistone chromoso	4.14	3.30
	438718	AL040058	Hs.6375	uncharacterized hypothalamus protein HTO	4.14	3.04
20	437802	A1475995	Hs.122910	ESTs	4.12	5.13
	446392	AF142419	Hs.15020	homolog of mouse quaking QKI (KH domain	4.12	3.87 4.96
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor integrin, alpha L (antigen CD11A (p180).	4.11 4.11	6.37
	427247 414359	AW504221 M62194	Hs.174103 Hs.75929	cacherin 11, type 2, OB-cacherin (osteob	4.10	4.16
25	450071	AA018283	Hs.24359	Homo sapiens cDNA FLJ11174 fis, clone PL	4.10	2.35
	452882	AW972990	Hs.196270	fotate transporter/carrier	4.10	4.50 6.07
	414522	AW518944	Hs.76325	Immunoglobulin J chain ubiquitin specific protease 18	4.09 4.09	5.03
	407756 405506	AA116021	Hs.38260	Target Exon	4.08	3.71
30	417497	AW402482	Hs.82212	CD53 antigen	4.07	B.61
	413715	AW851121	Hs.75497	Homo sapiens cDNA: FLJ22139 fis, clone H	4.06	4.05
	421508	NM_004833	Hs.105115	absent in metanoma 2 tymohocyte adaptor protein	4.05 4.02	4.61 4.56
	445701 443071	AF055581 AL080021	Hs.13131 Hs.8986	complement component 1, q subcomponent,	4.00	8.91
35	417615	BE548641	Hs.82314	hypoxanthine phosphoribosyltransferase 1	3.99	4.15
	444371	BE540274	Hs.239	forkhead box M1	3.86	4.58
	450515	AW304226	Hs.15159	biphenyl hydrolase-like (serine hydrolas	3.85 3.81	4.26 4.06
	446506 410668	AI123118 BE379794	Hs.159651	chemokine-like factor, alternatively spl hypothetical protein	3.80	6.84
40	443710	AI928136	Hs.9691	Homo sapiens cDNA: FLJ23249 fis, clone C	3.77	4.46
	406837	R70292	Hs.156110	immunoglobulin kappa constant	3.77	6.44
	419381	AB023420	Hs.90093	heat shock 70kD protein 4	3.76 3.76	4.00 4.67
	402474 454080	AI199711	Hs.576	NM_004079:Homo sapiens cathepsin S (CTSS tucosidase, alpha-L- 1, tissue	3.74	6.22
45	409264	NM_014937	Hs.52463	KIAA0966 protein	3.69	4.36
	428398	A1249368	Hs.98558	ESTs	3.68	5.18
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac	3.67 3.65	4.12 4.45
	414829 437239	AA321568 AW503395	Hs.77436 Hs.5541	pleckstrin ATPase, Ca transporting, ubiquitous	3.63	4.84
50	433867	AK000596	Hs.3618	hippocalcin-like 1	3.59	4.49
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	3.54	5.31
	418310	AA814100	Hs.86693	ESTs	3.49 3.48	4.57 4.33
	406868 438746	AA505445 AI885815	Hs.300697 Hs.184727	immunoglobulin heavy constant gamma 3 (G Human metanoma-associated antigen p97 (m	3.47	6.87
55	427527	AI809057	Hs.153261	immunoglobulin heavy constant mu	3.44	10.42
	442485	BE092285	Hs.29724	hypothetical protein FLJ13187	3.41	4.60
	432606	NM_002104		granzyme K (serine protease, granzyme 3;	3.40 3.40	4.50 4.22
	435080 436810	AI831760 AA353044	Hs.155111 Hs.5321	hypothetical protein FLJ 14428 ARP3 (actin-related protein 3, yeast) ho	3.40	5.03
60	422545	X02761	Hs.287820		3.39	7.32
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	3.36	4.47
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	3.34 3.34	5.02 4.24
	416975 448410	NM_004131 AK000227	Hs.1051 Hs.21126	granzyme B (granzyme 2, cytotoxic T-lymp hypothetical protein FLJ20220	3.33	4.29
65	432642		Hs.3069	heat shock 70kD protein 9B (mortatin-2)	3.32	4.48
	425234		Hs.165909		3.24	4.64
	443623		Hs.9641	complement component 1, q subcomponent.	3.23 3.23	13.58 4.20
	426490 443958		1 Hs.170087 Hs.10029	aryl hydrocarbon receptor catheosin C	3.16	5.05
70	407862		Hs.337988		3.15	4.04
	412577	Z22968	Hs.74076	CD163 antigen	3.14	5.32
	414050			coatomer protein complex, subunit beta 2	3.13	4.65
	442904		Hs.11355 Hs.106260	thymopoietin) sorting nexin 10	3.13 3.12	4.34 4.99
75	421633 413936		Hs. 29768		3.11	5.47
	428797		Hs.193700	Homo sapiens mRNA; cDNA DKFZp58610324 (f	3.10	4.30
	408515	AI289507	Hs.29988		3.10	4.03
	409442		Hs.16924	8 cytochrome c membrane-spanning 4-domains, subfamily A	3.07 3.04	4.00 4.38
80	456373 430413		Hs.89751 Hs.24139		3.04	5.53
	418526				3.03	4.97
	452139	AA099969	Hs.16331	Homo sapiens cDNA: FLJ21482 fis, clone C	3.01	4.87
	430478		9 Hs.24153	5 apolipoprotein L, 3	2.98	4.44

	439237	AW408158		ESTs, Wealdy similar to A47582 B-cell gr	2.95 2.93	7.45 8.49
	406782 450455	AA430373 AL117424		gb:zw20111.s1 Soares ovary tumor NbHOT H chloride intracefular channel 4	2.90	5.08
_	422530	AW972300		bone marrow stromal cell antigen 2	2.87	7.07
5	429490	AI971131	Hs.23889	ESTs, Wealthy similar to ALU7_HUMAN ALU S	2.87	4.29
	410231 419956	AA314163 AL137939	Hs.61153 Hs.40096	proteasome (prosome, macropain) 26S subu cadherin 19, type 2	2.82 2.80	5.53 4.26
	416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membr	2.79	5.55
	421712	AK000140	Hs.107139	hypothetical protein	2.79	6.29
10	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	2.78	4.74
	448517	AA082750	Hs.42194	hypothetical protein FLJ22649 similar to	. 2.78 2.77	4.69 5.18
	427792 446272	M63928 BE268912	Hs.180841 Hs.14601	tumor necrosis factor receptor superfami hematopoietic cell-specific Lyn substrat	2.75	4.90
	422173	BE385828	Hs.250619	phorbolin-like protein MDS019 (CEM15)	2.75	4.33
15	446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	2.72	4.19
	429402	AF116571	Hs.201671	SRY (sex determining region Y)-box 13	2.72 2.71	5.15 4.82
	421360 425762	AA297012 BE244076	Hs.103839 Hs.159578	erythrocyte membrane protein band 4.1-li AT-hook transcription factor AKNA	2.71	4.61
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	2.69	4.45
20	409202	AA236881	Hs.51043	hexosaminidase B (beta polypeptide)	2.68	4.89
	426124	A126B389	Hs.250697	phosphatidylinositol glycan, class F	2.68	4.25 5.00
	422672 417389	X12784 BE260964	Hs.119129 Hs.82045	collagen, type IV, atpha 1 midkine (neurite growth-promoting factor	2.67 2.65	9.54
	445784	AI253155	Hs.145065	ESTs	2.65	4.11
25	410341	AW499985	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	2.64	4.50
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	2.63 2.62	4.17 5.80
	424687 410016	J05070 AA297977	Hs.151738 Hs.57907	matrix metalloproteinase 9 (gelatinase 8 small inducible cytokine subfamily A (Cy	261	5.57
	424779	AL046851	Hs.153053	CD37 antigen	2.60	5.72
30	420224	M84371	Hs.96023	CD19 antigen	2.60	4.02
	421924	BE514514	Hs.109606	coronin, actin-binding protein, 1A	2.57	4.83 4.50
	426143 421563	BE379838 NM_006433	Hs.105806	proteasome (prosome, macropain) subunit, granufysin	2.56 2.56	5.35
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	2.55	4.32
35	428169	AI928984	Hs.182793	galgi phosphoprotein 2	2.54	5.78
	417022	NM_014737	Hs.80905	Ras association (RalGOS/AF-6) domain fam	2.54	4.09
	414646 429800	AA353776 AA333375	Hs.901 Hs.223014	CD48 antigen (B-cett membrane protein) antizyme inhibitor	2.53 2.50	4.41 5.68
	407241	M34516	NS.223014	gb:Human omega light chain protein 14.1	2.50	4.69
40	421739	AB004550	Hs.107526	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	2.45	4.35
	412819	T25829	Hs.24048	FK506 binding protein precursor	2.45	4.66
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	2.44 2.41	4.91 4.80
	434883 420340	AW381538 NM_000734	Hs.19807 Hs.97087	hypothetical protein MGC12959 CD3Z antigen, zeta polypeptide (TiT3 com	2.41	4.00
45	449296	AL137257	Hs.23458	Homo sapiens cDNA: FLJ23015 fis, clone L	2.41	4.77
	417370	T28651	Hs.82030	tryptophanyl-IRNA synthetase	2.41	4.04
	400223	ALIOTZOGE	11- 20027	Eos Control	2.39 2.38	5.47 7.67
	431629 414622	AU077025 A1752666	Hs.265827 Hs.76669	interferon, alpha-inducible protein (clo nicotinamide N-methyltransferase	2.38	5.32
50	415149	X12451	Hs.78056	cathepsin L	2.37	8.07
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.37	5.23
	454390	AB020713	Hs.56966	KIAA0906 protein	2.35 2.31	4.57 5.48
	427407 449029	8E268649 N28989	Hs.177766 Hs.22891	ADP-ribosyltransferase (NAD; poly (ADP-r solute carrier family 7 (cationic amino	2.24	4.08
55	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	2.23	4.02
	423397	NM_001838		chemokine (C-C motif) receptor 7	2.23	4.90
	416232	AW502678	Hs.79090	exportin 1 (CRM1, yeast, homolog)	2.18 2.17	4.97 4.13
	436692 420842	AW243158 AI083668	Hs.5297 Hs.50601	DKFZP564A2416 protein hypothetical protein MGC10986	2.14	5.14
60	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	2.13	4.43
	429642	X68264	Hs.211579		2.11	5.42
	416448	L13210	Hs.79339	tectin, galactoside-binding, soluble, 3	2.10 2.10	6.36 4.06
	416714 409220	AF283770 BE243323	Hs.79630 Hs.51233	CD79A antigen (immunoglobulin-associated tumor necrosis factor receptor superfami	2.09	4.67
65	414045	NM_002951		ribophorin II	2.07	4.32
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	2.07	4.24
	441211	AW946155	Hs.7750	hypothetical protein AL133206	2.06 2.05	4.64 4.33
	434692 452363	H06586 A1582743	Hs.94 Hs.94953	DnaJ (Hsp40) homolog, subfamily A, membe Homo sapiens, Similar to complement comp	2.04	13.36
70	438393		Hs.50740	Homo sapiens cDNA: FLJ22272 fis, clone H	2.03	4.52
	413313			glycyl-IRNA synthetase	2.02	4.11
	452700		Hs.288940		2.00	4.04
	406621	X57809	Hs.8997	immunoglobulin tambda locus	1.99 1.98	4.35 4.52
75	424415 429451		5 Hs.146580 Hs.202833		1.95	5.60
, ,	416967		Hs.80645	interferon regulatory factor 1	1.95	5.38
	414945	BE076358	Hs.77667	lymphocyte antigen 6 comptex, locus E	1.93	4.69
	418917		Hs.1217	adenosine deaminase	1.91	4.32
80	445411		Hs.12646 1 Hs.75627	hypothetical protein FLJ22693 CD14 antigen	1.91 1.90	4.48 6.03
60	413945 429119		1 Hs./562/ Hs.19643		1.90	4.08
	413317		Hs.75283	sorting nexin 1	1.89	4.06
	427239			ubiquitin carrier protein	1.67	5.98

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					0		
	450440	AB024334	Hs.25001	tyrosine 3-monocxygenase/tryptophan 5-mo	1.87	6.33	
	413142	M81740	Hs.75212	omithine decarboxylase 1	1.85 1.84	4.21 5.07	
	447131 430040	NM_004585 AW503115	Hs.17466 Hs.227823	retinoic acid receptor responder (lazaro pMS protein	1.83	5.57	
5	416819	U77735	Hs.80205	pim-2 oncogene	1.83	4.12	
_	425356	BE244879	Hs.155939	inositol polyphosphata-5-phosphatase, 14	1.82	5.71	
	414570	Y00285	Hs.76473	insulin-like growth factor 2 receptor	1.81	4.73	
	443639	BE269042	Hs.9661	proteasome (prosome, macropain) subunit,	1.80 1.78	4.71 5.16	
10	418707 425367	U97502 BE271188	Hs.87497 Hs.155975	butyrophilin, subfamily 3, member A2 protein tyrosine phosphatase, receptor t	1.78	7.00	
10	409154	U72882	Hs.50842	interferon-induced protein 35	1.74	5.10	
	444954	AW247076	Hs.12163	eukaryotic translation initiation factor	1.71	5.15	
	424825	AF207069	Hs.153357	procollagen-lysine, 2-oxoglutarate 5-dio	1.70	4.43	
15	428385	AF112213	Hs.184062	putative Rab5-interacting protein	1.69 1.67	4.06 5.68	
13	427378 413322	BE515037 AA380158	Hs.177556 Hs.75290	metanoma antigen, family 0, 1 ADP-ribosylation factor 4	1.67	4.56	
	442414	BE408758	Hs.8297	ribonuclease 6 precursor	1.65	4,40	
	410129	BE244074	Hs.58831	regulator of Fas-induced apoptosis	1.64	4.02	
	452472	AW957300	Hs.294142	ESTs, Wealty similar to C55663 digodend	1.63	4.49	
20	445143	BE245342	Hs.306079	sec61 homolog	1.62	4.73	
	413511	AJ627178	Hs.75412	erginine-rich, mutated in early stage to	1.60 1.60	4.19 4.61	
	415017 410361	F06434 BE391804	Hs.77805 Hs.62661	ATPase, H transporting, tysosomal (vacuo quanytate binding protein 1, interferon-	1.59	4.26	
	410068	AI633888	Hs.58435	FYN-binding protein (FYB-120/130)	1.56	4.10	
25	419489	AW411280	Hs.90693	replication initiation region protein (6	1.55	4.30	
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	1.55	6.54	
	414427	L19711	Hs.76111	dystroglycan 1 (dystrophin-associated gl	1.53 1.53	4.00 4.79	
	416971 426059	R34657 BE292842	Hs.80658 Hs.166120	uncoupling protein 2 (mitochondrial, pro interferon regulatory factor 7	1.51	4.12 .	
30	418879	AW162087	Hs.5437	Tax1 (human T-cell leukemia virus type I	1.50	4.93	
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	1.45	4.15	
	422481	AL050163	Hs.117339		1.45	4.03	
	432805	X94630	Hs.3107	CD97 antigen	1.43 1.43	4.11 4.08	
35	447150 421975	AI439011 AW961017	Hs.86386 Hs.6459	myeloid cell leukernia sequence 1 (BCL2-r hypothetical protein FLJ11856	1,41	4.36	
	427458	BE208364	Hs.29283	ESTs, Weakly similar to LICHU proteoglyca	1.41	4.10	
	412968	AW500508	Hs.75102	alanyl-tRNA synthetase	1.40	4.25	
	428511	AA019912	Hs.184693		1.38	4.91	
40	413825	BE299181	Hs.75564 Hs.178710	CD151 entigen	1.37 1.30	4.45 4.04	
70	427496 407143	D21260 C14076	Hs.332329		1.29	4.37	
	TABLE 5		na Fos nrobe	set identifier number			
45	CAT num		e cluster numb				
	Accessio	n: Gen	bank accessio	on numbers			
	n	CATAL					
	Pkey 412918	2764_3	Accession RE784583	AL519009 AV755430 AV756363 AV711927 8I53	23434 A1521453 AA846815 AW	024829 AW949702 B	G218926 AA626658 AI445621 AI452815
50	412310	2,00	AA946555	AA723580 AA612925 BG105326 BG532618 AV	/513994 AW602165 Al373448 /	AA907901 AW135104	BG186662 W69205 BG219754
-			BE774875	BG190378 AA483698 BE056066 BE066067 BE	066062 AW304207 BE939361 i	AW795569 BG210592	2 AW795644 BE939358 AW102886
				BG182971 H97042 O58090 BI046351 H81248 A		58287 D57835 AA93	5095 BF700910 BG215802 BG195459
	420704	20142 1	AW368467	' BG495535 BG533177 BI087962 BE541579 BF \210833 BM353155 AI473754 AI147901 AI80310	130753 YO AARA22GG AAA18G25 AIA7R	552 AIA00067 AI3603	04 A4418828 AW301673 RF218952
55	435701	28142_1	AI632804 I	BF433234 AA394157 BF378047 BE467036 AA3	19724 AW290940 AI222671 AI	347724 AW001711 A	028652 AA398130 AI470582 AI915936
-			AA908929	C75102 N36920 H50440 AI919034 AI004399 AI	383862 Al123606 AA648518 A	as16258 ai855321 n	22865 AAB48101 AI589792 AA758196
			AA214630	AI373911 AW194733 AA213447 AI290291 BF4	37165 AA757592 BF086904 A\	N959032 AW992466 1	BF446888 A1936337 BE938849
			AW149064	A1701629 N90021		3 DESASCES AMETINE	4 AMAZONONE AMAZONANA DIATENTA
60	432469	58644_1	BC016556	BC016365 NM_016040 AF151858 BI561037 AV AI824135 AI632346 AI129838 BM147664 AI29	NYOOB/J AWYD/4Y/ BEZ1940 2112 BE244667 AA261094 AW	2 BEU 1663U AW/ /U3 1503659 RM193866 RI	M194481 RF446862 AL 597435 BF000262
UU			AIR243R6	AI990100 AW087624 AA668793 AL080084 BI33	5866 BI820940 BG779242 BM	D69854 AA282620 AA	256771 AW964511 AA451623 HD0335
			AW370399	9 AW954201 BM145846 BG111760 AI750065 BG	3655794 AA564086 BG494071	BM069606 AI675331	BE302224 AI476466 AI625980
			BM144854	I A1184602 Al343932 AW136586 AW029464 AI7	08651 AA824243 BM145917 A	A662210 AA825708 /	A1335858 A1273704 AA662171 N48971
65			AA976614	Al344537 AA609603 Al873901 Al859995 AA83	3589 AA765811 AI150322 AI9	26816 BM148634 N98	862 AAD19347 AA897062 AA83110U
0.5			NPASSA R	E243185 AA282179 AA831098 AA112676 AI702 9 AA393405 BF115146 AA910851 AA013099 N2	/407 BG621752 BE006432 AA. XRR78 AA2R7713 RF34R72R Rf	333202 86674236 N4 3616446 AI 599953 AI	599952 RE381073 AW505056 AA094735
			H03613 A	A287714 H27168 R54718 BF792697 AV693603	AV685883 BG619956 BF5415	04 BF216789 AA3197	51 BM452652 BF335838 AA280397
			BG171509	9 BF571997 AA490239 AW388161 BE842126 BI	3165309 N71903 Al955397 Al:	536898 BE242040 FO	9718 AA772421 AA450218 M78543
=0				AA013098 H00297 AW576477 AW150918 AW		497 AJ285602 AA7450	055 AI281647 BF377670 T65207
70			BG53288	0 BG721680 AA285143 H27167 AW500235 BG4	94497 BF668899	E4E00 A14E4900 A190	0242 A122074E A1274E11 A13473RR
	424571	9758_1	RE3/9/60	5 AW152643 AIB03450 AI564343 AI092711 AI14 AI140529 AI366124 AA493912 AA406235 AA49	U323 AVI 132130 AIB2U/ 4U AI3 I3880 AIR57160 AWN33364 AIf	197977 ALLANDE AIRS	R0051 AA9R3529 AAR60507 N53469
			AAR43767	7 N81163 N70628 AA424577 AA983537 BF0030	04 AA626688 AA235977 AI057	152 AI095366 AI0953	356 AA458646 AW194479 AA150439
			Al375272	AW571777 Al359198 AA993793 BE614394 BE7	738239 AA127883 A1034344 T!	59504 D81608 AA908	704 AW051665 AA382785 AA307208
75			N24639 A	J370715 BE244980 AA548596 AW449675 AJ191	1008 BF223749 N70752 N2226	6 A1191012 AA02800	1 AI419106 BF215651 BF591548
		0475.0	BG94235	6 A1474968 BE858217 BF793358 AV756758 BG	483603 A1093724 BF693395 B	£14990 مەدەكەت مەدەمەمە مەدەمەم	DYDAY AABI 11/3 BG499/5/
	444207	9172_3	BE73942	5 AA514221 AA865491 A1828293 AA470456 A12 BG533994 AA513783 A1887309 AA528036 AW	10134 AA 103331 BE332464 A 073006 AW873038 ACOACOA	45051 WA 0188181	AWD84946 A1521413 AIRR95R3 8E932521
			AI581370	BE 180238 AW089750 AW771461 AW089714 A	1590949 A1819148 AA731056 I	BF815234 BF911506 /	AA235803 AA485373 AI735658
80			AW39313	I3 AW073080 A1707637 BF353320 BE843111 A	N819036 AW393135 BG69729	1 AV648670 AV65433	32 AV687530 BG566964 AI807430
			AI676072	AA837010 AI452482 AI625817 AW241750 BEO	48516 AI290928 AI580714 AA	485530 BE175687 AV	648513 AW130312 AI000556 AA632893
			BE67416	9 BF001208 AA948166 BE175650 AA524664 AA 0 Al565004 AW819026 BE843092 AV686437 AV	490345 AI244948 AA602956 A	A483492 AA918178	AW802049 BG675859 AV658871
			HCS7806	A AINNYUU AWKISUZN BE 843097 AVKAK437 A\	/// g1414 HG-6 169445 A191 164/	8 deui eura ue <i>pea</i> in	CODIZO I AUSOZUTA AAUAUUZT AYYTOSSIT



		4	4A903144 BF3 RE095761 RE9	(0112 BF876213 R82948 H26425 H82876 BE84 18083 BF984258 AV657996 A1749532 BE76861 11511 BE710793 BE180119 BG617338 H45942	4 8E857252 8E932516 BE768573 A T55897 AV657718 BG563497	W657993 AV65777	AV/52631 BE//49/4 15584/				
5		13638_2	BE 299605 AI58 N34543 AW603 H14620 H2847	9870 AA847598 A1470122 BF939896 A1304356 1578 AA526961 AA983631 N99134 AA626645 R 5 H26247 BF333581 AW842369 H06848 H0560	BE223045 BF435800 A1394207 A17 45023 AA902417 AW672925 AA449	7985 AA953982 AWI	5/54/1 AA010062 N80194				
	406782 426143	3806 1	AA430373 AA9 BC005265 BG1	76720 AW006027 BM352064 AW026316 AI635	822 AI880584 AI593769 AI092211 E	01492387 A1400449	AW166297 BF939910 AA232282				
10			AA465237 AL33	33893 AA494308 AA854899 A1436795 AW0692 16096 AA035579 A1087306 AA448162 AA12997	7 A1090903 A1080686 A1288939 N33	1004 A1801240 AWD	21546 AI370773 AI086064				
			AI582295 AI41 BG952443 AW RM47R404 RF	50053 A1870113 AA853181 AA858014 BG05556 7525 A1563975 A1933566 A1707743 A1290741 A 854221 AW854208 BE156348 BEB43056 AW85 126296 AA375499 AA248473	W073417 BE875418 BM264076 BG 8991 BE937569 BG878291 BG8764	876884 A1680535 A1 150 AW819099 A190	W854219 BE774535 AW854212 8570 AA449871 AU135228				
15	400223	236R 1	NM_005648 BI AL521812 BG7 BM019558 BM	_005648 BC013809 L34587 BF103775 BG702618 BG716553 BI567090 BG505863 BF983483 BG716195 BIB57891 BG501016 BM043599 21812 BG705730 B495545 BH95546 BF112248 BM023162 BM023123 AU75173 AW051799 BF058224 BI324885 BF436008 AA398446 BG822375 119558 BM023382 BG164174 N56909 B1457064 BM023464 AI207475 BM311415 BG758430 BG758807 AI934826 N90351 BG422026 BE910312 27778 AI081950 AI368890 BM009115 A1191829 BG759597 AI138728 AA399403 AI355589 AI336427 AA868702 AA333660 AA025127 BG027630							
20			AA962774 AA4 A1129091 AA4 AW135664 A12	331224 BG940967 BE791087 AA573315 W8168 61234 AA781198 AA759256 AA888954 AA9758 806607 AW263599 AA813219 AI684453 AA8786	IS AA393525 BG944103 A1339125 A 44 A1184099 AI018025 AA398363 A 526 AA772222 A1085496 A1630226 E	1149864 AA977655 1003331 A1193380 A	N90314 BE612839 BG491847 A626020 A1244476 A1601114				
	427239	20459_2	AL 532360 RET	530040 AA037091 AA019912 BI160457 H64512 /94750 AA582906 AW015067 AW271034 BG2710 /075181 AA464019 AW302733 AW075100 AW0	336 AW075177 AW071374 AL345569	AI307208 BE1389	53 8E049086 Al334881 11 Al340734 Al307478 Al251289				
25			AW302327 AV AI252926 AI25 AI802837 AI26	NOT311 AAAGAU ANTOJC 19 NOT2520 A1312145 AW073656 AW072513 AW0 12160 A1251662 A1251262 A1610913 A1270787 A 11264 AW073049 AW071311 A1340643 BE1389 19711 BE139228 AW470478 AW271039 AW302	71289 Al307559 AA876186 129587 . U270156 Al252075 AW073469 AW0 65 BE138502 AW073456 Al334733 .	AI307493 AI255068 72901 AW072496 A AI054335 BE139260	AI252868 AI252839 AWU74809 W071420 AI305762 AI254764) AI054302 AI054060 AI054057				
30	TABLE 560					•					
	Pkey: Ref:	Seque seque	ence source. Ti noe of human o	sponding to an Eos probeset ne 7 digit numbers in this column are Genbank to thromosome 22° Dunham, et al. (1999) <u>Nature</u> 40	lentifier (GI) numbers. *Dunham, et a 02:489-495.	al." refers to the publ	ication entitled "The DNA				
35	Strand: Ni_position			from which exons were predicted. positions of predicted exons.							
•	Pkey	Ref	Strand	NI_position							
	404854 405506	7143420 6466489	Plus Plus	14260-14537 80014-80401,80593-81125							
40	402474	7547175	Minus	53526-53628,55755-55920,57530-57757							
45	ToNe 574	lists about 304 g ne expression da	enes uncernitat	SULATED IN MELANOMA METASTASES RELA ed in melanoma metastases relative to normal s beset obtained from this analysis was expressed	kin. Genes were selected from 5968	O probesets on the li ed value reflecting t	Eos/Affymetrix Hu03 Genechip he relative level of mRNA				
	Pkey: ExAcon:	Uniqu		t identifier number number, Genbank accession number							
50	UnigenelC	t Unige	ne number	Hallos, Gendera Beessadi Hallaci							
30	Unigene T R1: R2:	90th 90th	percentile of me	elanoma metastasis Als divided by the 90th pero elanoma metastasis Als divided by the 90th pero and denominator	entile of normal skin Als entile of normal skin Als, where the 1	5th percentile of nor	mal tissue Als was subtracted from				
55	Pkey	ExAcon	UnigenelD	Unigene Title	RI	R2					
	422424 438549	AI186431 BE386801	Hs.296638 Hs.21858	prostate differentiation factor trinucleotide repeat containing 3	18.94 17.45	25.00 18.47					
	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecu	le 14.05	11.15					
60	452838	U65011	Hs.30743	preferentially expressed antigen in mela							
00	446619 426555	AU076643 NM_000372	Hs.313 Hs.2053	secreted phosphoprotein 1 (osteopontin tyrosinase (ocutocutaneous albinism IA)							
	439310	AF086120	Hs.102793		10.12						
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologou		10.16					
65	447210 414812	AF035269 X72755	Hs.17752 Hs.77367	phosphatidytserine-specific phosphotipa monokine induced by gamma interferon		11.69 10.97					
03	430377	NM_001922	Hs.301865			7.96					
	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	9.06	19.93					
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	8,66 8,65	5.87 6.62					
70	418310 433447	AAB14100 U29195	Hs.86693 Hs.3281	ESTs neuronal pentraxin II	8.27	4.68					
70	430280	AA361258	Hs.237868		8.01	6.37					
	430822	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydroge		6.10					
	456373	8E247706	Hs.89751	membrane-spanning 4-domains, subfar	many A 7.78 7.68	7.60 5.41					
75	415752 419628	BE314524 H67546	Hs.78776 Hs.49768	putative transmembrane protein ESTs	7.66	8.96					
, ,	417355	D13168	Hs.82002	endothelin receptor type B	7.56	4.59					
	424321	W74048	Hs.1765	tymphocyte-specific protein tyrosine kin		5.77					
	412228	AW503785	Hs.73792	complement component (3d/Epstein Ba	nt vi 7.43 7.35	4.93 7.98					
80	436485 414646	X59135 AA353776	Hs.156110 Hs.901	 immunoglobulin kappa constant CD48 antigen (8-cell membrane protein 		5.06					
	422241	Y00062	Hs.17012	protein tyrosine phosphatase, receptor	ť 6.83	5.20					
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	6.67 nle 6.67	3.77 15.22					
	417542	J04129	Hs.82269	· · · · · · · · · · · · · · · · · · ·	ole 0.07	13.22					

	428398	AI249368	Na DOCCO	Fot-	C 67	3.60
	408989	AW361666	Hs.98558 Hs.49500	ESTs KIAA0746 protein	6.57 6.48	4.93
	417022	NM_014737	Hs.80905	Ras association (Ra/GDS/AF-6) domain (am	6.38	3.65
_	449644	AW960707	Hs.148324	ESTs	6.35	5.84
5	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	6.30	7.18
	457211	AW972565	Hs.32399	ESTs, Wealthy similar to S\$1797 vasodilat	6.25	7.21
	420991	AW504814	Hs.287379	Homo sapiens mRNA for FLJ00111 protein,	6.25	5.36
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	6.18	6.01
10	432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	6.12	6.51
10	449078	AK001256	Hs.22975	KIAA1576 protein	6.05	8.55
	438856	A1469355	Hs.127310	ESTs	6.00	5.54
	43365B 424247	L03678 X14008	Hs.156110 Hs.234734	immunoglobulin kappa constant	5.92 5.89	7.18 4.07
	409417	AA156247	Hs.104879	lysozyme (renal amyloidosis) serine (or cysteine) proteinase inhibito	5.86	6.07
15	431574	AW572659	Hs.261373	hypothetical protein dJ434014.3	5.74	6.03
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.72	5.92
	440274	R24595	Hs.7122	scrapie responsive protein 1	5.69	3.22
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	5.69	5.17
20	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	5.68	3.35
20	436315	BE390513	Hs.27935	hypothetical protein MGC4837	5.67	4.56
	452973	H88409	Hs.40527	ESTs	5.63	5.50
	426559 406663	A8001914 U24583	Hs.170414	paired basic amino acid cleaving system	5.62	3.09
	416975	NM_004131	Hs.1051	immunoglobulin heavy constant mu granzyme B (granzyme 2, cytotoxic T-lymp	5.54 5.52	9.68 6.42
25	408380	AF123050	Hs.44532	diubiquitin	5.51	4.49
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	5.43	4.50
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	5.42	3.54
	446341	AL040763	Hs.310735	ESTs, Moderately similar to ALU7_HUMAN A	5.41	5.29
20	425234	AW152225	Hs. 165909	ESTs, Weakly similar to I38022 hypotheti	5.40	4.35
30	434203	BE262677	Hs.283558	hypothetical protein PRO1855	5.38	4.16
	420338	AA825595	Hs.88269	Homo sapiens, clone MGC:17339, mRNA, com	5.37	5.77
	430580 428804	AA806105	Hs.300697	immunoglobulin heavy constant gamma 3 (G	5.31	5.32
	447735	AK000713 AA775268	Hs.193736 Hs.6127	hypothetical protein FLJ20706 Homo sasiens cDNA: FLJ23020 fis, clone L	5.29 5.29	4.80
35	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	5.27	3.61 5.35
-	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	5.26	6.00
	412561	NM_002286	Hs.74011	lymphocyte-activation gene 3	5.26	5.04
	450293	N36754	Hs.171118	hypothetical protein FLJ00026	5.23	3.60
40	400750			Target Exon	5.18	3.62
40	417933	X02308	Hs.82962	thymidylate synthetase	5.14	3.33
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	5.12	5.36
	445784	AI253155	Hs. 146065	ESTs	5.12	4.06
	420602 421508	AF060877 NM_004833	Hs.99236 Hs.105115	regulator of G-protein signalling 20 absent in melanoma 2	5.06 5.03	7.68 5.59
45	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	4.96	6.25
	402474	73 130001	. G.ZZZGG	NM_004079:Homo sapiens cathepsin S (CTSS	4.95	5.13
	400417	X72475		Target	4.90	3.93
	420137	AA306478	Hs.95327	CO3D antigen, delta polypeptide (TiT3 co	4.88	6.81
50	409264	NM_014937	Hs.52463	KIAA0366 protein	4.88	3.18
50	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	4.87	4.20
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	4.85	5.86
	409142 425088	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	4.83	5.94
	405506	AA663372	Hs.169395	hypothetical protein FLJ 12015	4.82 4.74	5.19 4.09
55	409512	AW979187	Hs.293591	Target Exon melanoma differentiation associated prot	4.74	3.72
	430838	N46664	Hs.169395	hypothetical protein FLJ 12015	4.73	3.50
	439963	AW247529	Hs.6793	platelet-activating factor acetythydrola	4.72	3.66
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	4.71	5.16
60	447,217	BE465754	Hs.17778	neuropilin 2	4.70	4.52
60	422309	U79745	Hs.114924	solute carrier family 16 (monocarboxytic	4.69	3.51
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	4.68	3.69
	419956 429903	AL137939 AL134197	Hs.40096 Hs.93597	cadherin 19, type 2	4.68	5.83
	449217	AA278536	Hs.23262	cyclin-dependent kinase 5, regulatory su ribonuclease, RNase A family, k6	4.68 4.66	5.29 3.84
65	449722	BE280074	Hs.23960	cyclin B1	4.64	4.29
••	424006	AF054815	Hs.137548	CD84 antigen (teukocyte antigen)	4.62	4.54
	407845	AA426202	Hs.40403	Obp/p300-interacting transactivator, wit	4.62	6.78
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.59	5.81
70	406673	M34996	Hs.198253	major histocompatibility complex, class	4.57	5.60
70	431620	AA126109	Hs.264981	2-5-ofgoadenylate synthetase 2 (69-71	4.56	4.44
	441224	AU076964	Hs.7753	calumenin	4.56	3.75
	442739 444371	NM_007274 BE540274	Hs.8679	cytosofic acyl coenzyme A thioester hydr	4.56	3.22
	448719	AAD33627	Hs.239 Hs.21858	forkhead box M1 trinucleotide repeat containing 3	4.53 4.48	5.28 9.09
75	420301	AA767526	Hs.22030	paired box gene 5 (8-cell lineage specif	4.48 4.47	9.08 5.61
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	4.43	4.11
	428513	8E220806	Hs. 184697	Homo sapiens clone 23785 mRNA sequence	4.41	4.43
	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	4.39	3.99
00	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	4.38	5.50
80	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	4.37	3.25
	421633	AF121860	Hs.106260	sorting nexin 10	4.36	6.23
	414829 417166	AA321568 AA431323	Hs.77436	pleckstrin EST-	4.35	2.91
	411100	WW1100	Hs.42146	ESTs	4,35	4.08

	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	4.34 4.34	5.35 3.72
	419381	AB023420	Hs.90093	heat shock 70kD protein 4	4.32	4.18
	411305 425289	BE241596 AW139342	Hs.69547 Hs.155530	myefin basic protein interferon, gamma-inducible protein 16	4.28	2.44
5	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	4.27	4.48
	432642	BE297635	Hs.3069	heat shock 70kD protein 98 (mortalin-2)	4.25	2.69
	422282	AF019225	Hs.114309	apolipoprotein L	4.25	3.75
	433867	AK000596	Hs.3618	hippocatcin-like 1 - protein tyrosine phosphatase, receptor-l	4.23 4.20	5.13 2.15
10	415817 438619	U88967 AB032773	Hs.78867	TU12B1-TY protein	4.19	3.32
10	426317	AA312350	Hs.169294	transcription factor 7 (T-cell specific,	4.16	5.14
	420208	BE276055	Hs.95972	silver (mouse homolog) like	4.16	5.08
	416602	NM_006159	Hs.79389	Protein kinase C-binding protein NELL2	4.15	2.38
15	430770	AA765694	Hs.123296	ESTs ESTs, Wealdy similar to A56194 thromboxa	4.15 4.15	3.67 3.98
13	424541 427337	AW392551 Z46223	Hs.180559 Hs.176663	Fc fragment of IgG, low affinity IIIb, r	4.14	3.51
	456760	AW961251	Hs.127828	guanine nucleotide binding pretein (G pr	4.14	4.42
	406858	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	4.13	5.07
20	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.12	6.43
20	410016	AA297977	Hs.57907	small inducible cytokine subfamily A (Cy	4,11 4,11	8.73 4.48
	452698 444863	NM_001295 AW384082	Hs.301921 Hs.104879	chemotine (C-C motif) receptor 1 serine (or cysteine) proteinase inhibito	4.10	4.78
	435080	AJ831760	Hs.155111	hypothetical protein FLJ14428	4.07	2.76
	442711	AF151073	Hs.8645	hypothetical protein	4.06	3.49
25	423605	AF047826	Hs.129887	cadherin 19, type 2	4.06	2.42
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	4.05 4.02	3.26 7.60
	421712 422283	AK000140 AW411307	Hs.107139 Hs.114311	hypothetical protein CDC45 (cell division cycle 45, S.cerevis	4.00	3.87
	409415	AA579258	Hs.6083	Homo sapiens cDNA: FLJ21028 fis, clone C	4.00	5.87
30	412719	AW016610	Hs.816	ESTs	3.99	5.46
	437179	AA393508		serologically defined colon cancer antig	3.96	4.51
	420319	AW406289	Hs.96593	hypothetical protein	3.95 3.91	5.47 4.58
	438380 418064	T06430 BE387287	Hs.6194 Hs.83384	chondroitin sutfate proteoglycan BEHAB/b S100 calcium-binding protein, beta (neur	3.84	4.42
35	420286	AI796395	Hs.111377	ESTs	3.83	4.56
	410600	AW575742		ESTs, Moderately similar to \$65657 alpha	3.80	5.70
	410326	AI368909	Hs.47650	ESTs	3.76	4.86
	424779	AL046851	Hs.153053	CD37 antigen	3.70 3.69	8.72 6.38
40	452194 411027	AI694413 AF072099	Hs.67846	Ubiquitin-like protein FAT 10777 - diubiq leukocyte immunoglobulin-like receptor,	3.65	5.40
40	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.65	4.48
	424153	AA451737	Hs.141496	MAGE-like 2	3.64	5.82
	421666	AL035250	Hs.1408	endothelin 3	3.64	5.52
45	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	3.60 3.59	5.56 4.35
7.7	422173 421563	8E385828 NM_006433	Hs.250619 Hs.105806	phorbotin-like protein MDS019 (CEM15) granulysin	3.49	7.38
	453837	AL138387	Hs.256126	bacutoviral IAP repeat-containing 7 (fiv	3.49	6.13
	424326	NM_014479	Hs.145296	ADAM-like disintegrin protesse, decysin	3.48	4.23
50	427247	AW504221	Hs.174103	integrin, alpha L (antigen CD11A (p180),	3.47	5.38 4.59
20	408838 402829	A1669535	Hs.40369	ESTs C1002500:gij6754254 ref NP_034610.1 hea	3.45 3.42	5.01
	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	3.42	8.14
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	3.40	4.35
	429714	BE561801	Hs.2484	T-cell teukemia/lymphoma 1A	3.36	4.84
55	414324	Y14768	Hs.890	lymphotoxin beta (TNF superfamily, membe	3.35 3.35	4.45 4.28
	421958 428291	AA357185 AA534009	Hs.109918 Hs.183487	ras homotog gene family, member H interferon stimulated gene (20kD)	3.34	5.18
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.31	8.00
	451736	AW080356	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.29	4.50
60	412790	NM_014767	Hs.74583	KIAA0275 gene product	3.28	5.42
	404854			Target Exon	3.28 3.26	4.28 4.41
	400860 430413	AW842182	Hs.241392	Target Exon small inducible cytokine A5 (RANTES)	3,24	5.65
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	3.24	4.35
65	422846	BE513934	Hs.1583	neutrophil cytosolic factor 1 (47kD, chr	3.24	4.90
	440065	W03476	Hs.266331	hypothetical protein MGC4595	3.20	6.21
	440704	M69241	Hs.162	insulin-like growth factor binding prote ESTs	3.20 3.18	4.72 4.20
	411088 447513	BE247593 AW955776	Hs.145053 Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A	3.18	4.68
70	413190	AA151802	Hs. 40368	adaptor-related protein complex 1, sigma	3.15	4.27
	430017	AA263172	Hs.35	protein tyrosine phosphatase, non-recept	3.15	4.28
	406837	R70292	Hs.156110	immunoglobulin kappa constant	3.12	4.09 4.04
	409103 425706	AF251237 AW406678	Hs.112208 Hs.122559	XAGE-1 protein hypothetical protein FLJ22570	3.04 3.04	4.28
75	447656	NM_003726	Hs. 19126	src kinase-associated phosphoprotein of	3.03	4.30
	427792		Hs.180841	tumor necrosis factor receptor superfami	3.01	4.82
	402994			NM_002463*:Homo sapiens myxovirus (influ	2.99	5.74
	434276		Hs.93605	leucine zipper, putative tumor suppresso	2.97 2.96	5.07 4.15
80	449523 439237		Hs.54443 Hs.318893	chemokine (C-C motif) receptor 5 ESTs, Weakly similar to A47582 B-cell or	2.96 2.96	5.81
00	406621		Hs.8997	immunoglobulin lambda focus	2.93	7.88
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	2.91	13.22
	426322	J05068	Hs.2012	transcobatamin I (vitamin B12 binding pr	2.90	8.37

	440000	0554424	14- 00000	Nimale (Inc. 9	2.87	4.15
	448275 423397	BE514434	Hs.20830 Hs.1652	tinesin-like 2 chemokine (C-C motif) receptor 7	2.86	5.53
	406782	NM_001838 AA430373	ns.1032	gb:zw2011.s1 Soares ovary tumor NbHOT H	281	4.60
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	2.80	5.89
5	412819	T25829	Hs.24048	FK506 binding protein precursor	2.78	4.90
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	2.76	4.21
	428380	NM_004271	Hs.184018	MD-1, RP105-associated	2.76 2.76	5.15 4.30
	408209 416511	NM_004454 NM_006762	Hs.43697 Hs.79356	ets variant gene 5 (ets-related molecule Lysosomal-associated multispanning membr	2.75	4.13
10	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	2.74	5.05
10	428746	AW503820	Hs.192861	Spi-B transcription factor (Spi-1/PU.1 r	2.73	9.20
	453953	AW408337	Hs.36972	CD7 antigen (p41)	2.72	4.38
	407241	M34516		gb:Human ornega light chain protein 14.1	2.68	4.07
1.5	437669	AI358105	Hs.123164	ESTs. Weakly similar to match to ESTs AA	2.66 2.65	4.71 4.31
15	453779	N35187	Hs.43388 Hs.279651	28kD interferon responsive protein metanoma inhibitory activity	2.64	4.15
	432874 410129	W94322 BE244074	Hs.58831	regulator of Fas-induced apoptosis	2.62	7.36
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	2.62	4.43
	418739	AA310964	Hs.88012	SHP2 interacting transmembrane adaptor	2.61	5.42
20	424825	AF207069	Hs.153357	procollagen-lysine, 2-oxoglutarate 5-dio	2.60	9.69
	417370	T28651	Hs.82030	tryptophanyl-IRNA synthetase	2.60 2.59	5.17 4.01
	411358	R47479	Hs.94761	KIAA1691 protein	2.58	13.24
	425367 426470	8E271188 AA528794	Hs.155975 Hs.128644	protein tyrosine phosphatase, receptor t ESTs	2.54	4.52
25	425535	AB007937	Hs.158287	KIAA0468 gene product	2.52	11.31
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	2.50	7.80
	425722	AI659076	Hs.97031	hypothetical protein MGC13047	2.49	4.25
	438291	BE514605	Hs.289092	Homo sapiens cDNA: FLJ22380 fis, clone H	2.49 2.48	4.04 4.08
30	415426	AA180256	Hs.210473 Hs.94814	Homo sapiens cDNA FLJ14872 fis, clone PL	2.48	5.25
30	441859 416714	AW194364 AF283770	Hs.79630	ESTs, Wealdy similar to FIG1 MOUSE FIG-1 CD79A antigen (immunoglobulin-associated	2.48	4.88
	431186	NM_012249	Hs.250697	ras-like protein	2.46	6.04
	417389	BE260964	Hs.82045	midkine (neurita growth-promoting factor	2.45	5.34
25	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	2.43	6.57
35	428437	AV656017	Hs.184325	CGI-76 protein	2.42	4.96
•	427634	Al399745	Hs.18449	hypothetical protein MGC10820	. 2.39 · 2.38	8.46 5.90
	420842 428289	A1083668 M26301	Hs.50601 Hs.2253	hypothetical protein MGC10986 complement component 2	2.38	5.32
	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	2.37	6.99
40	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	2.34	9.69
	433671	AW138797	Hs.132906	19A24 protein	2.34	4.81
	432403	AA550815	Hs.124840	ESTs	2.34	4.99
	427759	BE245578	Hs.2200	perforin 1 (pore forming protein)	2.32 2.30	4.56 4.22
45	419870	AW403911 AA913059	Hs.266175 Hs.104433	phosphoprotein associated with GEMs Homo sapiens, clone IMAGE:4054868, mRNA	2.30	6.18
45	421445 401591	AN313033	rts.104433	Target Exon	2.29	7.01
	451708	Al306536	Hs.60975	ESTs	2.26	4.50
	452700	AJ859390	Hs.288940	five-span transmembrane protein M83	2.24	4.90
50	424618	L29472	Hs.1802	major histocompatibility complex, class	2.22	5.40
50	409208	Y00093	11- 040400	integrin, alpha X (antigen CD11C (p150),	2.21 2.19	4.74 4.61
	436456 419741	AW292677 NM_007019	Hs.248122 Hs.93002	G protein-coupled receptor 24 ubiquitin carrier protein E2-C	2.17	7.43
	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	2.16	5.58
	438555	A1222089	Hs.143878	Homo sapiens mRNA for FLJ00024 protein,	2.13	4.26
55	407260	L09095		gb:Homo sapiens mRNA fragment.	2.13	4.00
	448243	AW369771		integrin, beta 8	2.10	4.03
	437938	A1950087	14- 455440	gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapien	2.07 2.06	4.45 4.36
	425262 414945	D87119 BE076358	Hs.155418 Hs.77667	GS3955 protein lymphocyte antigen 6 complex, locus E	2.05	4.66
60	400261	0000	143.77007	Eos Control	2.04	4.22
	432468	AW402155	Hs.3003	CD3E antigen, epsilon polypeptide (TiT3	2.02	4.23
	416967	BE616731	Hs.80645	interferon regulatory factor 1	1.99	4.45
	420626	AF043722	Hs.99491	RAS guanyt releasing protein 2 (calcium	1.98	4.42 4.55
65	440672	AF083811	Hs.7345	MAD1 (mitotic arrest deficient, yeast, h	1.98 1.96	4.53 4.54
05	452923	BE276018	Hs.288940	five-span transmembrane protein M83 ESTs	1.95	4.23
	452244 427239		HS.1766/4	ubiquitin carrier protein	1.94	4.93
	418678		Hs.167379	cancer/testis antigen (NY-ESO-1)	1.94	5.28
	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	1.93	4.17
70	444090		Hs.10306	natural killer cell group 7 sequence	1.93	5.06
	404067		44-204	Target Exon	1.92 1.91	6.16 4.23
	426890 453597		Hs.41294 Hs.33713	ESTs myo-inositol 1-phosphate synthase A1	1.91	4.10
	401914		113.337 13	Target Exon	1.87	4.76
75	448499		Hs.77550	hypothetical protein MGC1780	1.87	5.17
	439627	BE621702	Hs.29076	hypothetical protein FLI21841	1.85	6.59
	425923			phosphomositide-3-kinase, catalytic, de	1.85	4.03
	416819		Hs.80205	pim-2 oncogene	1.84 1.84	4.57 6.40
80	425069 430378		Hs.298184	potassium voltage-gated channel, shaker- tumor necrosis factor receptor superfami	1.78	4.02
30	435968		Hs.2556 Hs.111577	integral membrane protein 3	1.76	5.26
	410423		Hs.63489	protein tyrosine phosphatase, non-recept	1.75	4.30
	434224		Hs.84	interteukin 2 receptor, gamma (severe co	1.74	4.91



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	413566	AW604451	Hs.285814	sprouty (Drosophita) homolog 4	1.71	6.00	
	430148	BE387620	Hs.234489	tactate dehydrogenase B	1.70	4.34 4.04	
	410068	AI633888	Hs.58435	FYN-binding protein (FYB-120/130)	1.69 1.66	5.95	
5	437696	Z83844	Hs.5790	hypothetical protein dJ37E16.5	1.64	6.26	
,	423984 426665	AF163825 AW500131	Hs.136713 Hs.171763	pre-8 lymphocyte gene 3 CD22 antigen	1.63	4.33	
	406908	Z25437	15.171703	gb:H.sapiens protein-tyrosine kinase gen	1.62	7.19	
	440087	W28969	Hs.7718	hypothetical protein FLJ22678	1.61	4.33	
	421859	AA356620	Hs.108947	KIAA0050 gene product	1.59	4.30	
10	415198	AW009480	Hs.943	natural killer cell transcript 4	1.56	4.12	
	406827	AA971409		gb:op92c04.s1 NCI_CGAP_Lu5 Homo sapiens	1.55	4.29	
	413969	X14034	Hs.75648	phosphotipase C, gamma 2 (phosphatidylin	1.53	4.63	
	456085	AL161999	Hs.77324	eukaryotic translation termination facto	1.52	4.11	
• •	433320	D60647	Hs.250879	ESTs, Highly similar to CTXN RAT CORTEXI	1.52	4.36	
15	406906	Z25424		gb:H.sapiens protein-serine/threonine ki	1.50	8.67 5.07	
	406885	028423		gb:Human mRNA for pre-mRNA splicing fact	1.49 1.48	4.50	
	443759	BE390832	Hs.134729	FXYD domain-containing ion transport reg	1.48	4.91	
	452423	AA991724	Hs.180535	hypothetical protein MGC10966	1.43	4.26	
20	448143 451524	AF039704 AK001456	Hs.20478 Hs.26516	ceroid-lipofuscinosis, neuronal 2, late hypothetical protein FLJ10604	1.43	4.74	
20	417287	AI831678	Hs.285714	KIAA1599 protein	1.41	4.01	
	432665	AW603880	113.2.031 14	ATPase, H transporting, lysosomal (vacuo	1.38	4.07	
	403043	A11003000		Target Exon	1.36	4.89	
	407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	1.32	4.57	
25	436553	AW407157	Hs.8997	immunoglobulin lambda locus	1.30	4.00	
	422934	BE244189	Hs.122492	hypothetical protein	1.30	4.37	
	442680	BE270707	Hs.8583	similar to APOBEC1	1.26	4.48	
20	TABLE 57					•	
30	Pkey:		ique Eos probeset	identifier number			
	CAT num		ne cluster number				
	Accession	n: Ge	enbank accession n	umbers			
	Okan	CAT Alumb	er Accession				
35	Pkey 438619	35124_1	NIA MEETE A	B032773 A1765521 BF593742 A1497757 A1761233 AW46793	R RECOGGE A 1818496 N	24761 AL 043306 BF476138 BF593836 AA13278	17
55	430013	33124_1	AI1.47248 AID	36795 AA151317 T95298 AW083548 AA058371 N27951 AJ76	9860 AI784548 AW2055	06 AI800679 AI041733 AI459902 BE327641	
			AIR65829 A125	54736 AI302433 AI744176 AI241825 AA027842 AL524933 AL	524932 BF947764 BF34	0737 BF948700 BG996395 N53455 N21027	
			AI127616 N35	901 AA682443 AA678249 AA719371 AA132582 T15981 H99	958 N40717 AW959402	N267251 BF909329 AI142035 T95379 H29420	
			RS9632 H173	18 H17331 H29327 R40829 R43395 R59573 A1749561 R5659	39 H16755 Al694500 AAI	127907	
40	437179	12239_1	AKOSSTOS RC	019085 AA 187684 RG656226 RMD23227 AIB32311 AW26438	31 AA398371 BM021483	AI432433 AI375777 AI129580 AW262782	
	-	_	AA 134107 RM	0023515 AA977504 A1859222 AL348454 R69725 AA975268 BI	M021207 AL080074 AA1	29218 AW207842 N90581 AA771919 AW92259	
			AI028416 AI0	74114 BG656536 BE501677 AW193419 AA917040 W90430 A	u342984 al378957 alo3	6486 AW020068 BI491093 BF476021 R41226	
			R69631 F041	25 C02343 AA 115589 R56480 AI400988 R54266 R31422			
	410600	497855_1	BF347859 AV	V499616 AA191322 AW499617 AL601010 AW575742 AA7290	343 BE463447 AA086179	BE549623 AJ335824 AW408712 BM149172	
45	452194	90339_1		994700 Al912946 N73548 Al082035 AW271652 W24189 W24	4182 AI719718 AA02465	8 AW810120 AW015394 179755 AA988043	
			A1709339				
	406782	0_0	AA430373 AA	968771		ACCOC AMPROCOC AMPROCOCA A A 700042 DATA	4333
	409208	10117_2	AK074047 AI	144342 AWD14280 BM145128 N28267 AW206231 AA989041	M93197 AW594063 BG4	30290 A11230000 A1100 103 1 AA703043 BM14	4372
50			AA989341 AI	824838 AI953970 AI637671 AW196330 BG427526 BM148789	9 BF093044 BF001340	AA234175 AA043006 BE006303 BE327669	
50	448243	13061_2		M79726 BE622314 AL 134913 BE006305 BE006312 BE00625	90 MAU44302 MV7334330	/ / / / / / / / / / / / / / / / / / /	
	407020	66007 1	BE000317 BF	7326759 BF541959 12911 W78802 AW856538 BF737212 N36809 N35320 AA282	D15 AWS05512 AI65383	W87891 AI961530 TR5904 H59397 R97278	
	437938	66997_1	U/ 1450 AAA	0532 T82391 AI820501 T63226 R66056 R67840 AW961101	313 AVISOSS 12 AUSSON	0009 AW205862 AA988777 AA856975 BF 1724	57
			PG751124 AI	741346 AI950344 AI689062 AI872193 AW102898 AW173586	AI763273 AI890387 AW	150329 A1762688 AA488892 A1356394 A153964	2
55			AA642789 AI	950087 BF589902 N70208 AA283144 AA488964 H60052 R97	7040 BF886630 AW9676	77 AW971573 AW967671 AI308119 AA251875	
55			A AGGREGE AL	R19225 AI55A269 AA908741 AA293273 AA969759 AW27690	5 AAO44209 H83488 T92	487	
	400261	23110_1	8C006097 X	03066 NM_002120 M26040 AW469119 AW469127 AI299772	AW518149 AJ144456 AV	/628070 Al629032 Al358810 Al880433 Al44047	2
	100201	200	A1357070 A18	165365 AWD14799 AL767973 AW518041 AA909398 AW76860	16		
	427239	20459_2	A1 532360 RF	794750 AA582906 AID15067 AW271034 BG271636 AW0751	77 AW071374 AI345565	AI307208 BE138953 BE049086 AI334881	
60		_	AWN75006 A	W0751R1 AA464019 AW302733 AW075100 AW073433 AI80	2854 Al334909 Al802853	A1345036 A1348921 A1340734 A1307478 A1251	289
			AW302327 A	.W072520 Al312145 AW073656 AWD72513 AW071289 AJ307	559 AA876186 T29587 A	1307493 A1255068 A1252868 A1252839 AVVU748	צעצ
			A1252926 A12	252160 A1251662 A1251262 A1610913 A1270787 A1270156 A12	252075 AW073459 AW07	Z901 AWU72496 AWU7142U ALSUS762 ALZS476	4
			AI802837 AI	251264 AW073049 AW071311 Al340643 BE138965 BE13850	2 AW073456 A1334733 A	1054335 BE 139260 A1054302 A1054060 A10540	7022
15				289711 BE139228 AW470478 AW271039 AW302085 BE0418	172 A1254494 A12/1496 P	1252427 BF / 18//3 BF / 18045 AWU/4000 BE05	1022
65	406827	0_0	AA971409		**********	14000 42 4 400 4405 4 4 7 C00 72 AWE7 47 CD	
	432665	27095_3	BG165971 B	E143233 AL577712 Al400326 AA769318 AA427866 AW0887	14 AI150/55 AI9248/4 A	1180243 AA0U4133 AA70317 AA707670	
			AW341643 A	NW204520 AA235326 AID05076 BE826687 AW004816 AW007 NG90331 AI673409 AA627727 AI923685 AA931499 AI249783	41010CC2 44E49E22 AA	702005 AA022205 DI250508 AA262903 AW075	RAN .
				1030331 AID / 3403 AAD 2 / 1 / 2 / 1 / 3 / 3 / 4 / 4 / 6 / 6 / 6 / 6 / 6 / 6 / 6 / 6	AND TUGOS PARSHOUZE PAR	102033 AAG32333 BIE33300 AAE0E333 ATTOTO	~~
70			AA810885				
70	TABLE	57C-					
	Pkey:	1	Injure number con	responding to an Eos probeset			
	Ret.	ì	Sequence source.	The 7 digit numbers in this column are Genbank Identifier (GI)	numbers. "Dunham, et a	I." refers to the publication entitled "The DNA	
	TAGI.		sequence of human	chromosome 22' Dunham, et al. (1999) Nature 402:489-495.		•	
75	Strand:			nd from which exons were predicted.			
	Nt_posi			positions of predicted exons.			
	Pkey	Ref	Strand	Nt_position			
	400750	8119067	Plus	198991-199168, 199316-199548			
80	402474		Minus	53526-53628,55755-55920,57530-57757			
	405506		Ptus	80014-80401,80593-81125			
	402829		Plus	101532-101852,102006-102263			
	404854	7143420	Plus	14260-14537			

	400860	9757499	Minus	151830-152104,152649-152744
	402994	2996643	Minus	4727-4969
	401591	9966977	Minus	55410-55835
	404067	3282162	Plus	1415-2071
5	401914	9369520	Plus	62537-62945,63155-63308
_	403043	7768753	Minus	314423-316252

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TABLE SBA: ABOUT 183 GENES UPREGULATED IN MELANOMA METASTASES FROM PATIENTS WITH LIMITED DISEASE RELATIVE TO MELANOMA METASTASES FROM PATIENTS WITH PROGRESSIVE DISEASE

Table SBA fists about 183 genes upregulated in melanoma metastases from patients with limited disease relative to melanoma metastases from patients with progressive disease.

Genes were selected from 59580 probesets on the Eos/Aflymetrix Hu03 Genechlp array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey:

EVACOT:

Unique Eos probeset identifier number

Exacot:

Unique Proposition of Accession number, Genthank accession number

Unique Tide:

Unique gene of title

Unique gene gene title

R1:

90th percentile of Als for metastases from patients with limited disease divided by 90th percentile of Als for metastases from patients with progressive disease, where the 15th percentile of normal tissue Als was subtracted from both the numerator and denominator

15

	Pkey	ExAcon	UnigeneID	Unigene Title	R1	R2
	415668	AW957684	Hs.306814	hypothetical protein FLJ21889	12.74	12.92
	447414	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	7.66	5.88
25	412659	AW753865	Hs.74376	offactomedin related ER localized protei	7.23	5.76
	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	6.91	14.26
	414430	AJ346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	6.86	7.10
	436485	X59135	Hs.156110	immunoglobulin kappa constant	6.85	6.81
	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	6.73	11.21
30	430822	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	5.53	4.63
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	5.48	7.08
	423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp43480650 (f	5.27	5.94
	433658	L03678	Hs.156110	immunoglobulin kappa constant	4.78	3.07
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-fin	4.68	3.27
35	413916	N49813	Hs.75615	apolipoprotein C-II	4.62	4.82
	407825	NM_006152	Hs.40202	lymphoid-restricted membrane protein	4.55	3.12
	406648	AA563730	Hs.277477	major histocompatibility complex, class	4.31	4.15 3.44
	409060	AI815867	Hs.50130	necdin (mouse) homolog	4.23	3.19
40 .	401941			Target Exon	3.89 3.88	2.43
40	447471	AF039843	Hs.18676	sprouty (Orosophila) homolog 2	3.66	4.16
	419628	H67546	Hs.49768	ESTs	3.63	2.81
	414863	AW131473	Hs.106185	ral guarine nucleotide dissociation stim	3.47	3.06
	423416	NM_004920	Hs.128316	apoptosis-associated tyrosine kinase	3.47	3.43
45	400275	4114 002027	11- 400430	NM_006513":Homo sapiens seryl-IRNA synth	3.42	1.96
43	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase) ESTs; hypothetical protein for IMAGE:447	3.41	2.89
	442117	AW864964 AW862589	Hs.128899	gb:QV0-CT0387-180300-167-a07 CT0387 Homo	3.37	6.31
	411763 402007	AW002303		C18000503*:gi[8922165]ref]NP_060080.1] h	3.34	3.74
	424775	AB014540	Hs.153026	SWAP-70 protein	3.30	2.00
50	424036	AA770688	HS. 133020	H2A histone family, member L	3.30	3.16
50	453464	AI884911	Hs.32989	receptor (calcitorin) activity modifying	3.30	5.58
	401739	71004311	113.32303	NM_005622":Homo sapiens SA (rat hyperten	3.30	3.23
	440274	R24595	Hs.7122	scrapie responsive protein 1	3.27	2.47
	413398	D21262	Hs.75337	nucleolar and coiled-body phosphprotein	3.26	2.61
55	417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	3.26	2.58
-	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.14	4.04
	436965	Z11894	Hs.156110	gb:H.sapiens rearranged mRNA for immunog	3.13	2.38
	453857	AL080235	Hs.35861	OKFZPS86E1621 protein	3.13	2.47
	404405			Target Exon	3.11	4.69
60	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	3.11	2.10
	443247	BE614387	Hs.333893	c-Myc target JPO1	3.10	2.26
	400417	X72475		Target	3.08	2.32
	401512			NM_014080:Homo sapiens dual oxidase-like	3.07	2.87
	423242	AL039402	Hs.125783	DEME-6 protein	3.06	2.78
65	417501	AL041219	Hs.82222	sema domain, immunoglobulin domain (lg),	3.06	2.81
	451952	AL120173	Hs.301663	ESTs	3.05	2.65 4.24
	427419	NM_000200	Hs.177888	histatin 3	3.05 3.05	4.55
	406663	U24683		immunoglobulin heavy constant mu	3.03	1.90
70	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	3.02	1.71
70	451993	AA765776	Hs.122983	ESTs	3.02	311
	421097	AI280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	3.00	3.47
	430129	8E301708	Hs.233955	hypothetical protein FLJ20401	3.00	2.22
	427700	AA262294	Hs.180383	dual specificity phosphatase 6	2.98	3.43
75	400237	H26904	Un 76726	NM_001087*:Homo sapiens angio-associated	2.97	5.76
13	414063		Hs.75736	apolipoprotein D	2.94	2.38
	426153 414781	AF057169 D50917	Hs.182771 Hs.77293	vitelliform macular dystrophy (Best dise KIAA0127 gene product	2.94	2.88
	414781	AI478563	Hs.145519	FKSG87 protein	2.92	1.98
	404439	A410.003	15.173313	ENSP0000067222":Mitochondrial 28S ribos	2.92	2.57
80	421218	NM_000499	Hs.72912	cytochrome P450, subtamily I (aromatic c	2.90	2.47
30	420350	AW406896	Hs.88269	Homo sapiens, clone MGC:17339, mRNA, com	2.90	3.87
	424855	AW204725	Hs.25560	ESTs	2.89	2.61
	436700	A1693690	Hs.301406	hypothetical protein PP3501	2.88	3.63
				573		
				572		

					2.07	202
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	2.87	2.92 2.11
	427157	U51166	Hs.173824	thymine-DNA glycosylase	2.87	2.48
	402273			Target Exon	2.87	
•	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	2.83	3.09
5	430643	AW970065	Hs.287425	MEGF10 protein	2.83	3.04 2.12
	451979	F06972	Hs.27372	endothelial tyrosine kinase (Etk) (BMX),	2.82	2.88
	406642	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	281	
	407360	X13075		gb:Human 2a12 mRNA for kappa-immunoglobu	2.81	3.43
10	405441			Target Exon	2.80	3.15
10	450816	BE271927	Hs.87385	ESTs	2.80	2.48
	435675	AA694099	Hs.266820	ESTs	2.78	2.70
	426495	NM_001151	Hs.2043	solute carrier family 25 (mitochondrial	2.78	2.53
	441623	AA315805		desmoglein 2	2.78	2.27
	413336	A1569936	Hs.296178	hypothetical protein FLJ22637	2.76	3.18
15	408527	AL135018	Hs.33074	Homo sapiens, done IMAGE:3606519, mRNA,	2.76	1.92
	437740	AA810265	Hs.122915	ESTs	2.76	1.88
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	2.75	8.06
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	2.74	330
	428422	A1557280	Hs.184270	capping protein (actin filament) muscle	2.73 .	231
20	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	2.72	2.19
	401454			NM_014226":Homo sapiens renal tumor anti	2.72	1.99
	436825	AW341123	Hs.120275	ESTs	2.72	2.89
	407705	AB023139	Hs.37892	KIAA0922 protein	2.72	2.48
	416782	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	2.72	2.63
25	449151	AI632331	Hs.196038	ESTs	2.72	2.99
	433464	N92481		gb:zb12g02.s1 Soares_fetal_fung_NbHL19W	2.69	3.17
	401009			Target Exon	2.69	3.28
	427227	AF103803	Hs.283690	hypothetical protein	2.68	2.02
	405268			ENSP00000223174":KIAA0783 PROTEIN.	2.67	2.18
30	410295	AA741357		nidogen (enactin)	2.65	2.06
	435905	AW997484	Hs.5003	KIAA0456 protein	2.65	2.12
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	2.65	2.52
	457423	AK000642	Hs.265018	hypothetical protein FLJ20635	2.64	2.51
	448752	AA593867	Hs.300842	KIAA1608 protein	2.63	2.20
35	414931	AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZp761M0223 (f	2.63	1.83
	441283	AA927670	Hs.131704	ESTs	2.62	1.92
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	2.60	2.21
	421391	AW304350	Hs.191958	immunoglobulin superfamily receptor tran	2.60	3.06
	406678	U77534		gb:Human clone 1A11 immunoglobulin varia	2.54	3.06
40	430278	AI673074	Hs.116567	ESTs, Weakly similar to T22914 hypotheti	2.49	3.44
	425970	AK001500	Hs.165186	hypothetical protein FLJ13852	2.47	3.46
	407363	AF035032	Hs.8997	gb:Homo saplens clone MCA1L myosin-react	2.45	3.45
	408367	AK001178	Hs.44424	homolog of rat orphan transporter v7-3	2.44	3.52
	420103	AA382259	Hs.95197	aldehyde dehydrogenase 1 family, member	2.44	6.15
45	418635	L11329	Hs.1183	dual specificity phosphatase 2	2.42	3.92
	451558	NM_001089		ATP-binding cassette, sub-family A (ABC1	241	3.08
	430354	AA954810	Hs.239784	human homotog of Orosophila Scribble	2.36	3.99
	405701			ENSP0000004954°:Adseverin (Scinderin).	2.33	4.25
	433427	AI816449	Hs.171889	cholinephosphotransferase 1	2.30	3.30
50	401965			CGI-148 protein	2.29	3.45
•••	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	2.23	4.07
	428142	NM_001308		carboxypeptidase N, polypeptide 1, 50kD	2.19	3.17
	422103	AA984330	Hs.111676	protein kinase H11; small stress protein	2.18	4.18
	425746	NM_001701		bile acid Coenzyme A: amino acid N-acyll	2.12	3.48
55	404835			NM_018943*:Homo sapiens tubulin, alpha-l	2.09	5.72
•••	401127			Target Exon	2.09	4.38
	406161			Target Exon	2.08	3.22
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	2.08	3.03
	406632	AB006838		gb:Homo sapiens mRNA for HRV Fab N31-VH,	2.07	3.25
60	447940	D86982	Hs.20060	KIAA0229 protein	2.05	4.80
• • •	411773	NM_006799		protease, serine, 21 (testisln)	2.05	5.33
	413211	AW967107	Hs.109274	hypothetical protein MGC4365	2.02	4.74
	425722		Hs.97031	hypothetical protein MGC13047	2.01	3.76
	437044		Hs.69517	differentially expressed in Fanconi's an	1.96	5.27
65	436420		Hs.31595	ESTs	1.94	3.68
	414809		Hs.77356	transferrin receptor (o90, CD71)	1.92	3.88
	423420		Hs.128382	Homo sapiens mRNA; cDNA DKFZp70111224 (f	1.90	3.63
	427923			hypothetical protein PP3501	1.90	3.04
	406652			major histocompatibility complex, class	1.88	3.00
70	435624		Hs.24889	formin 2	1.88	3.54
	436552			HSPC028 protein	1.86	3.29
	408204		Hs.43666	protein tyrosine phosphatase type IVA, m	1.86	3.78
	402728		14.44000	C1002541*:gij4758590fref[NP_004249.1] im	1.86	3.14
	420932		Hs.11607	ESTs, Weakly similar to T21697 hypotheti	1.84	4.72
75	458559			ESTs	1.78	3.06
, ,	400278		1-3.203014	ENSP00000243264: Dolichyl-diphosphooligos	1.76	3.55
	425751		Hs.1940	crystallin, alpha B	1.76	5.31
	420737		Hs.99899	CD70: tumor necrosis factor (figand) s	1.74	3.00
	410006			eukaryotic translation initiation factor	1.74	3.79
80	454429		Hs.301406	hypothetical protein PP3501	1.73	3.57
00	426321			zinc finger protein 162	1.72	3.27
	402897		16.100011	NM_023068*:Homo sapiens sialoadhesin (SN	1.69	3.81
	423639		Hs.130411	KIAA1405 protein	1.67	3.31
	423035	, 4001020	19,130411	imarino prosess	7.01	0.0



	448848	AF131851	Hs.22241	hypothetical protein	1.65	4.27	
	414420	AA043424	Hs.76095	immediate early response 3	1.60	302	
	440747	AW297226	Hs.137840	ESTs, Moderately similar to SIX4_HUMAN H	1.56	3.28	
•	450635	AW403954	Hs.25237	mesenchymal stem cell protein DSCD75	1.55	3.73 3.26	
5	400252			NM_004651*:Homo sapiens ubiquitin specif	1.55 1.55	3.18	
	411825	AK000334	Un 200462	hypothetical protein FLJ20327 aconitase 2, mitochondrial	1.52	4.03	
	414328 400263	Z21666	Hs.300463	Eos Control	1.51	3.42	
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	1.50	3.19	
10	436673	AF201931	Hs.5268	hypothetical protein FLJ10479	1.49	3.33	
	404739		,	Target Exon	1.49	3.10	
	438344	8E387726	Hs.343411	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.46	3.42	
	421696	AF035306	Hs.106890	Homo sapiens clone 23771 mRNA sequence	1.44	3.15	
	425240	AA306495	Hs.1869	phosphoglucomutase 1	1.44	3.04	
15	412099	U64198	Hs.73165	interleukin 12 receptor, beta 2	1.43	3.71 3.07	
	434642	W25739		chromobox homolog 5 (Drosophila HP1 alph	1.42 1.42	3.87	
	404406	000043	11- 200000	Target Exon ESTs, Highly similar to CTXN RAT CORTEXI	1.41	3.80	
	433320 447697	D60647 W52125	Hs.250879	tubulin alpha 1	1.40	4.45	
20	415780	U75898	Hs.78846	heat shock 27kD protein 2	1.40	3.28	
20	447216	R75812	Hs.169248	p75NTR-associated cell death executor, o	1.39	3.77	
	401772			NM_014520:Homo sepiens MYB binding prote	1.39	3.67	
	413031	BE515051	Hs.75160	phosphofructokinase, muscle	1.38	3.31	
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	1.37	3.17	
25	428011	BE387514	Hs.181418	KIAA0152 gene product	1.37	3.05	
	445580	AF167572	Hs.12912	skb1 (S. pombe) homolog	1.35	3.11 3.05	
	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	1.34 1.34	3.09	
	438277	AL022326	Hs.6139	synaptogyrin 1 hypothetical protein DKFZp434N1923	1.32	123 .	
30	451481 421818	AA300228 AW992976	Hs.295866 Hs.50098	NM 002489:Homo sapiens NADH dehydrogenas	1.31	3.01	
50	412968	AW500508	Hs.75102	atanyl-IRNA synthetase	1.28	3.58	
	452378	AA025855	Hs.19597	KIAA1694 protein	1.25	3.08	
	447455	H38335	Hs.6750	Homo sapiens mRNA for FLJ00058 protein,	1.24	3.45	
	402212			KIAA0430 gene product	1.21	3.03	
35	428773	BE256238	Hs.193163	bridging Integrator 1	1.20	3.20	
	430067	U79458	Hs.231840	WW domain binding protein 2	1.18	3.03	
	418289	AW403103	Hs.83951	Hermansky-Pudlak syndrome	1.17	3.32 3.40	
	405752			Target Exon	1.00 1.00	3.00	
40	422836	AL037365	Hs.194093	AKAP-binding sperm protein ropporin	1.00	3.00	
40	TABLES	DD-					
40	TABLE 5		nua Fos ombesel				
40	Pkey:	Uni	que Eos probeset ne cluster number				
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	406632	0_0	ARMORRES AF	ROMERTY ARROSERSE ARROSERSA ARROSERSE
	400278	170_1	Y00281 NM	002950 RC010R09 RC0107995 RC675232 RM458552 AL555484 BG831516 BF035300 BG677277 BF852972 BE314901 BF850656
10			AI371816 AA	292474 AA375747 AA308414 BM454544 BI333370 BM049921 BI461428 BI465007 BIZZ3401 BE856245 AW821164 BF914775 BF914761
			A11125835 RI	1222678 R1091137 RF340536 RM462798 B1224452 BG707915 AL569160 AA443815 AW572867 AW353410 BF739268 BG010283
			RI013120 BE	R1RR45 RF76345R AA305165 A1630370 AA039826 R24906 H02046 T96891 BF981330 AW936510 AA478169 H04587 BG166574
			RISEQUAD RE	SG24R2 RES2GS2 AA16S0R9 A1579118 A1553699 REG44054 AW117440 A1520674 BF435417 AW245648 A952404 129534 AU153459
			AU152168 A	W591591 AU146918 AI393187 AA478013 AU148143 AI224471 AI640728 AIB71537 AW264752 N93787 AI189357 AV756134 AI471659
15			AU147466 A	A779206 AU149419 AU149104 AU159135 AA312221 AW445119 AW021912 A1799771 F04407 A1285530 A1914643 AW068751 AA513325
			AA164627 A	AG39285 AA569644 T96892 A1923594 BF439180 B1770936 BF032438 AU154884 AA682793 AW072992 AU158815 A1884444 AL048031
			AU1589ZZ A	U152546 AIG95187 AL048033 AI245650 AU148507 AW467451 BE536868 BF913001 BF062707 AL573082 AW067993 AA523354 I890705 AU159092 AI982693 AI817553 AA236729 AI687858 BG163767 AI524675 AIG78155 AA127100 AI762661 AU159718 A469720
			BE660121 A	W131696 R26868 A1199885 AW875614 AW938694 AW578974 B1763988 BC819168 BE874767 BC978292 BE162948 AL555483
20			AV403021 A	TISTIBS R20000 ATTSSCS RI492837 AI824440 BC996262 AA932887 AI380726 R79530 AA622108 AI262575 T56782 R27437 BE784153
20			AW/120549 A	ME75567 AIRS6759 RC987935
	400252	2656_2	HAARRO NIA	004551 BC000350 RM5R316 AUT 17940 BG759024 BG749694 BE799505 BG831537 AI816335 AA325352 AL547005 AW157038 AI859331
	TOLOC	2000_2	AURTETRS AT	1157788 ALDARSAD AW162880 AL1159233 AL143169 T03478 BE727648 AA764725 BE206603 AL369814 AI984369 AW157545 BE221480
			HOGOTE ALLI	ISONYS AINTAINS AIANAISIS REPAISNIS AATOARSAS AAPROBED AIATUS 95 AIRSONTTO BEET 1398 TOSS38 AABRIZAU BIB/7303 BEDAUSID
25			AL359434 HS	32868 D52599 D53609 D54715 T06015 BE222174 AI954706 D53218 D53787 R69889 W86896 AI497670 K70771 BF309414 BE020147
			BG910597 A	W964968 BEB36120 AL579715 H56512 D55956 BID44097 AL555239 BF220278 AA081991 AI819544 AW001573 AW131600 AI858764
				2034 BGB18979 BG024561 BE702779 BI458863 BI910399 BG707755 BF348284 H10055 BI086315 BE620574 H41088 BG119517 W23267
			W21941 AA	328817
30	411825	7891_1	AK000695 A	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
30			BE2/2330 A	1830568 AA159183 AA977141 BG231801 AA631733 AA973134 BF017337 AA474290 BISOCCOT AT BG231801 AA631733 AA973134 BF017337 AA474290 AI927759 BG951502 AW881353 BI765535
	400263	18977_1	711602 YS1	AGG NIA MAGGA MAGGA PRISSASSA RCRAMAR ALI122147 ALI123437 RG113591 RG752624 RE886804 B1868669 RG337216 AW623935
	400203	10311_1	RM016525 /	NISSAND AL SEZRES AIGNO178 REFARSSE AA371735 REG38841 RE727115 RC006547 RG757526 AL555664 RI261304 RG770095 RI033486
			RIS17580 R	GR76486 BIN11828 A1313235 RGR31724 RF869862 BG998348 BIN11834 BF888337 BF898627 BF092380 AW8U3215 FU1241 BF8U3719
35			RCR764R7	AWAGRSTS REGRARGS REGGRAAG AA248724 RES29202 BE756456 BE032392 BIS59287 BM016990 BE332369 BE933685 BE166758
			DMAS2AAS	A1037808 AWD36138 N2368A AWD660A1 A1337621 F33111 RF344301 RG105450 RG387343 RF569547 RF154671 RMUU/368 RF369383
			BE772007 F	RI 199487 RE761700 RI261519 RE944452 RE898506 A1038390 BMD44934 AW381142 BG743618 BE769206 BE893973 BID15047 BF866479
				3E769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503
40			BG674499 I	BG774174 BI015084
40	434642	15461_1	AF 147443 E	BM471094 AA948055 AA973157 AA284289 W25739 BI021926 BF898367 W02720 BF798341 BF378312 AA427766 BG955568 BF899591
	443003	MILLOR C	BF884215	AL528391 AA328484 W52125 AA321596 AA022458 AW971024 A1052029 A1761638 AA628498 BE619513 AA412069 A1027538 AW514954
	447697	MH497_6	BE1420211	1097362 A1499259 A1419408 AW469200 A1992152 A1142045 A1066572 A1275439 AA581877 A1347308 A1016726 A1127541 AW002064
			AISASTRE A	WASTRAD AIRESDO ALIOR OR AIRADRER AIROTRAN AIROSIGS AASTREES AIRESDE AIRESDO AIRESDO AIRESDO AASTREE AAASTREE
45			A1139667 F	20651 Al201510 AAR32171 RM464599 RM464574 Al972621 Al183887 AW131911 AW771584 BE619828 AA492Z18 AA025767 AA977354
			AA385481	NA5137 W73596 AI864400 AI200026 AI270963 F18139 W46301 H55825 AI039867 AI457570 AI928639 AI824685 AI083898 AW024570
				AW381097 AW582409 BE964181
50	TABLE 5			
30	Pkey:	Un	idne unuper co	rresponding to an Eos probeset The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Ounham, et al." refers to the publication entitled "The DNA"
	Ref:	56	quence source.	in chromosome 22" Dunham, et al. (1999) <u>Nature</u> 402:489-495.
	Strand:			and from which exons were predicted.
	Nt_positi			te positions of predicted exons.
55		-		
	Pkey	Ref	Strand	Nt_position
	401941	4982556	Plus	112022-112204
	402007	7381786	Plus	143964-144081
60	401739	2982169	Plus	132194-132404
60	404405	7272262	Plus	83251-83415 136399-136557
	401512 404439	7622346 7139680	Plus Plus	55316-55585
	402273	2979528	Plus	28990-29203,32299-32402,32474-32668
	405441	7408124	Plus	100952-101283
65	401454	9186923	Minus	114659-114832
	401009	8117391	Minus	83179-83304
	405268	4156151	Minus	24404-24521
	405701	4263751	Plus	93243-93364
70	401965		Minus	18239-18389,19921-20076
70	404835		Plus	85452-85584,88139-88287,90338-91018,9462
	401127		Minus	88327-88458,96150-96266
	406161		Ptus	16666-16836 3192-3569.4267-4728
	402728 402897		Plus Plus	5192-5509,4207-4728 61939-62241,64304-64615,65140-65391
75	404739		Ptus	42742-43671
. 5	404406		Minus	47543-47928
	401772		Plus	183917-184042
	402212	7689783	Minus	69382-69936
00	405752		Plus	91392-91528
80				

TABLE 59A: ABOUT 201 GENES UPREGULATED IN MELANOMA METASTASES FROM PATIENTS WITH PROGRESSIVE DISEASE RELATIVE TO MELANOMA METASTASES FROM PATIENTS WITH LIMITED DISEASE



Table 59A lists about 201 genes upregulated in melanoma metastases from patients with progressive disease relative to melanoma metastases from patients with limited disease.

Genes were selected from 59680 probesets on the Eos/Affymetrix Hur03 Genechlp array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mr0VA expression.

Pkey:

Unique Eos probeset identifier number

Exacon:

Uniquene CD:

Uniquene CD:

Uniquene Title:

Uniquene gene title

R1:

90th percentifie of Als for metastases from patients with progressive disease divided by the 90th percentifie of Als for metastases from patients with limited disease.

R2:

90th percentifie of Als for metastases from patients with progressive disease divided by the 90th percentifie of Als for metastases from patients with limited disease, where the 15th percentifie of normal tissue Als was subtracted from both the numerator and denominator

5

	Oka	ExAccr	DiseasiD	Unigene Title	RI	R2
	Pkey 422168	AAS86894	UnigenelD Hs.112408	S100 calcium-binding protein A7 (psorias	8.58	13.77
15	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	7.43	5.91
1.5	440099	AL080058	Hs.6909	DKFZP564G202 protein	7.07	4.56
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	6.91	3.51
	420859	AW468397	Hs.100000	S100 calcium-binding protein AB (calgran	6.90	6.44
	418067	Al127958	Hs.83393	cystatin E/M	6.62	10.34
20	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	6.47	13.26
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	6.25	3.41
	401780			NM_005557°:Homo sapiens keratin 16 (foca	6.10	4.24
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	5.97	6.60
26	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	5.89	3.57
25	412636	NM_004415		desmoplakin (DPI, DPII)	5.82	3.51
	417124	BE122762	Hs.25338	ESTs	5.16 5.03	3.16 3.57
	430686	NM_001942	Hs.2633	desmoglein 1	4.84	4.15
	421733	AL119671	Hs.1420 Hs.113019	fibroblast growth factor receptor 3 (ach fis485	4.79	4.59
30	422192 407366	AA305159 AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	4.33	2.37
50	407300 429493	AL134708	Hs.145998	ESTs	4.28	4.79
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	4.23	4.82
	409010	AI648675	143.100000	Homo sapiens, Similar to RIKEN cDNA 1700	4.23	3.69
	410748	BE383816	Hs.12532	chromosome 1 open reading frame 21	4.11	2.33
35	409760	AA302840	***************************************	gb:EST10534 Adipose tissue, white I Homo	4.06	3.65
-	424670	W61215	Hs.116651	epithelial V-like antigen 1	4.02	4.07
	417366	BE185289	Hs.1076	small proline-rich protein 18 (cornifin)	3.97	4.71
	418663	AK001100	Hs.41690	desmocollin 3	3.95	5.08
	402075			ENSP00000251056*:Plasma membrane calcium	3.93	5.85
40	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.90	3.19
	427809	M26380	Hs.180878	lipoprotein lipase	3.87	3.21
	413859	AW992356	Hs.8354	Homo sapiens pyruvate dehydrogenase kina	3.85	5.75
	431048	R50253	Hs.249129	cell death-inducing DFFA-like effector a	3.60	3.10
4.5	431369	BE184455	Hs.251754	secretory teukocyte protease inhibitor (3.79	3.36
45	421485	AA243499	Hs. 104800	hypothetical protein FLJ10134	3.67	3.35
	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	3.65	4.14
	418686	Z36830	Hs.87268	annexin AB	3.65 3.64	3.62 3.18
	448429	D17408	Hs.21223	catponin 1, basic, smooth muscle	3.60	4.10
50	422963	M79141	Hs. 13234	ESTs	3.58	3.97
20	428874 401785	W32133	Hs.194366	transthyretin (prealbumin, arryloidosis t NM_002275":Homo sapiens keratin 15 (KRT1	3.58	5.05
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	3.56	1.92
	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	3.54	5.62
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	3.53	4.70
55	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.52	8.33
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	3.51	2.32
	454229	AW957744	Hs.278469 .	lacrimal proline rich protein	3.50	3.12
	401781			Target Exon	3.45	3.57
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	3.45	5.07
60	431567	N51357	Hs.260855	Homo sapiens cDNA: FLJ21410 fis, clone C	3.44	5.03
	419648	T73661	Hs.91877	thyroid hormone responsive SPOT14 (rat)	3.42	7.72
	414798	AI286323	Hs.97411	hypothetical protein MGC12335	3.41	2.65 5.03
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	3.41	2.86
65	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	3.32 3.28	3.18
0.5	410883	D43767	Hs.66742 Hs.83213	CCL17 chemokine (TARC) (SCYA17)	3.26	3.10
	418026	BE379727 AI791809	Hs.32949	fatty acid binding protein 4, adipocyte defensin, beta 1	3.24	3.64
	453309 420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.21	3.64
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	3.19	4.37
70	413163	Y00815	Hs.75216	protein tyrosine phosphatase, receptor t	3.16	5.48
, 0	452101	T60298	Hs.10844	Homo sapiens cDNA FLJ14476 fis, clone MA	3.15	3.60
	412633	AF001691	Hs.74304	periplakin	3.15	3.98
	407839	AA045144	Hs.161566	ESTs	3.15	4.11
	427318	AF186081	Hs.175783	zinc transporter	3.11	3.58
75	427899	AA829286	Hs.332053	serum armyloid A1	3.10	3.53
	421948	L42583	Hs.334309	keratin 6A	3.08	2.75
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	3.05	2.99
	410001	AB041036	Hs.57771	kallikrein 11	3.04	3.02
0.0	413435	X51405	Hs.75360	carboxypeptidase E	3.00	2.40
80	428500		Hs.184641	fatty acid desaturase 2	2.98 2.97	5.22 2.05
	410099		1 15 5753	KIAA0036 gene product	2.97	3.45
	437679 413835		Hs.5753 Hs.249163	inositol(myo)-1(or 4)-monophosphatase 2 fatty acid hydroxylase	2.53	4.78
	41,035	MILITIE	H2742103		2.50	7.70
				577		

	440000	** ***	11. 13010	Mar. 21.		
	446068 450680	AL049801 AF131784	Hs.13649 Hs.25318	Novel human gene mapping to chomosome 13	2.89	2.93
	428398	AI249368	Hs.98558	Homo sapiens clone 25194 mRNA sequence ESTs	2.88 2.88	3.14 2.05
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	2.86	2.12
5	427919	AA173942	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	2.84	2.98
	412676	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con	2.83	2.82
	428695	A1355647	Hs.189999	purinergic receptor (family A group 5)	2.83	2.37
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	2.82	273
10	428471	X57348	Hs.184510	stratifin	2.79	3.31
10	416305	AU076628	Hs.79187	coxsackie virus and adenovirus receptor	2.79	3.72
	433147	AF091434	Hs.43080	platelet derived growth factor C	2.77	1.70
	412326 425787	R07566	Hs.73817	small inducible cytokine A3 (homologous	2.76	2.18
	450172	AA363867 NM_005864	Hs.155029 Hs.24587	ESTs signal transduction protein (SH3 contain	2.75 2.75	2.42 2.36
15	421773	W69233	Hs.112457	ESTs	273	5.59
	408536	AW381532	Hs.135188	ESTs	2.73	5.17
	437143	AW204056	Hs.8917	ESTs	2.72	1.84
	452862	AW378065	Hs.8687	ADAMTS2 (a disintegrin-like and metalio	2.70	1.82
~~	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	2.69	4.62
20	410325	AB023154	Hs.62264	KIAA0937 protein	2.69	2.32
	447164	AF026941	Hs.17518	vipirin; similar to inflammatory respon	2.69	3.74
	444984	H15474	Hs.132898	fatty acid desaturase 1	2.67	2.36
	434727	H43374	Hs.7890	Homo sapiens mRNA for KIAA1671 protein,	2.65	1.78
25	420876 426105	AA918425	Hs.177744	ESTs	2.64 2.64	7.26
23	419517	AJ678765 AF052107	Hs.21812 Hs.90797	ESTs Homo sapiens clone 23620 mRNA sequence	2.64	2.51 2.66
	409509	AL036923	Hs.322710	ESTs	2.62	209
	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne	2.62	268
	432503	AA551196	Hs.188952	ESTs	2.62	4.64
30	409341	AI963376	Hs.12532	chromosome 1 open reading frame 21	2.62	1.74
	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	2.62	2.90
	456247	R09746		gb:yf27d10.r1 Soares fetal liver spleen	2.61	3.43
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.60	3.84
35	439706	AW872527	Hs.59761	ESTs, Wealty similar to DAP1_HUMAN DEATH	2.58	3.49
22	440659	AF134160	Hs.7327	claudin 1	2.57	3.97
	459710 430937	AI701596 X53463	Hs.121592 Hs.2704	ESTs	2.57 2.56	3.59
	433882	U90441	Hs.3622	glutathione peroxidase 2 (gastrointestin procollagen-proline, 2-oxoglutarate 4-di	· 2.51	3.35 3.75
	427666	AJ791495	Hs.180142	calmodulin-like skin protein (CLSP)	2.51	3.02
40	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	2.47	3.53
•	449550	AA353125	Hs.184721	ESTs	2.43	4.22
	424675	NM_005512	Hs. 151641	glycoprotein A repetitions predominant	2.40	6.22
	442000	H38671	Hs.8071	KIAA0735 gene product; synaptic vesicle	2.38	3.14
4.0	427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	2.35	3.59
45	420039	NM_004605	Hs.94581	sulfotransferase family, cytosofic, 28,	2.36	2.91
	412477	AA150864		microsomal glutathione S-transferase 1	2.34	4.15
	450693	AW450461	Hs.203965	ESTS	2.32	3.93
	406433 423017	AW178761	Hs.227948	Target Exon	2.29 2.24	3.20 4.40
50	422158	L10343	Hs.112341	serine (or cysteine) proteinase inhibito protease inhibitor 3, skin-derived (SKAL	2.23	4.87
- 0	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	2.23	4.22
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	2.22	5.71
	442503	AF147078	Hs.150853	p53-responsive gene 5	2.21	4.86
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	2.19	3.90
55	442572	AJ001922	Hs.135121	hypothetical protein FLJ22415	2.16	2.87
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	2.13	3.27
	414521	D28124	Hs.76307	neuroblastoma, suppression of tumorigeni	2.09	5.28
	428899 41,7079	AA744610 U65590	Hs.194431 Hs.81134	palladin	2.08 2.06	3.76 3.09
60	439496	BE616501	Hs.32343	Interleukin 1 receptor antagonis1 Homo sapiens, Similar to RIKEN cDNA 1110	2.05	2.88
-	450423	AA486735	Hs.31869	sialoadhesin	2.02	3.04
	444105	AW189097		ESTs	2.01	3.05
	430410	AF099144	Hs.347933	tryptase beta 1	2.01	3.71
	409453	AI885516	Hs.95612	ESTs	2.01	4.34
65	429655	U48959	Hs.211582	myosin, light polypeptide kinase	2.00	5.28
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	1.99	3.59
	447990	BE048821	Hs.20144	small inducible cytokine subfamily A (Cy	1,92	4.16
	451541	BE279383	Hs. 26557	plakophilin 3	1.89	3.90
70	425206 410197	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	1.89	3.29
70	401760	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy Target Exon	1.84 1.84	3.04 3.32
	427579	AA366143	Hs.179669	hypothetical protein FLJ20637	1.83	4.69
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hydrocephalus	1.83	2.96
	452208	AA024792	Hs.31895	hypothetical protein MGC4093	1.82	3.70
75	420074	AA253425	Hs.190074	ESTs	1.81	2.90
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	1.79	3.65
	427540	R12014	Hs.20976	ESTs	1.77	2.92
	429259	AA420450	Hs.292911	Plakophilin	1.76	3.65
QΛ	422106	D84239	Hs.111732	Fc fragment of tgG binding protein	1.75	4.06
80	453556	AA425414 AF037335	Hs.33287	nuclear factor I/B	1,74	3.07
	436895 406851	AA609784	Hs.5338	carbonic anhydrase XII major histocompatibility complex, class	1.73 1.73	3.22
	444726	NM_006147		interferon regulatory factor 6	1.73	3.96 3.65
	44.50	000.47				J.00

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	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	1.71	4.13	
	446051	BE048061	Hs.37054	ephrin-A3	1.68	3.61	
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	1.67	3.00 3.11	
•	450835	BE262773	Hs.25584	hypothetical protein FLJ10767	1.66 1.66	3.23	
5	432004	BE018302	Hs.2894 Hs.195432	placental growth factor, vascular endoth atdehyde dehydrogenase 2 family (mitocho	1.64	3.29	
	431179 415213	AJ338644 NM_002933	Hs.78224	ribonuclease, RNase A family, 1 (pancrea	1.57	3.94	
	423184	NM_004428	Hs.1624	eptrin-A1	1.56	2.88	
	414694	NM_015362	Hs.76907	HSPC002 protein	1.56	2.92	
10	458746	AI380797	Hs.158992	ESTs	1.56	2.92	
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.55	3.75	
	438367	N79688	Hs.204354	ras homolog gene family, member 8	1.54 1.53	4.56 3.99	
	403903	MANAGE	Hs.21299	C5001632":gi]10645308 gb AAG21430.1 AC00 ESTs, Wealdy similar to AF151840 1 CGI-8	1.52	3.16	
15	445656 443604	W22050 C03577	Hs.9615	myosin regulatory light chain 2, smooth	1.50	4.25	
13	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.50	3.35	
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.49	3.21	
	418226	AA424202	Hs.83834	cytochrome b-5	1.49	3.90	
20	454194	BE141599		gb:OV2-HT0083-071299-018-h01 HT0083 Homo	1.48 1.46	2.9(; 3.26	
20	434879	M34572	Hs.159263	collagen, type VI, alpha 2 KIAA0246 protein	1,46	4.00	
	418400 409178	BE243026 BE393948	Hs.301989 Hs.50915	kalikrein 5	1.45	2.94	
	433662	W07162	Hs.150826	RAB25 RAB25, member RAS oncogena family	1.44	3.18	
	429002	AW248439	Hs.2340	junction plakoglobin	1.43	3.07	
25	422087	X58968	Hs.111301	matrix metalloproteinase 2 (gelatinase A	1.40	4.61	
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.38 1.37	3.11 4.32	
	417483	BE549343	Hs.82208	acyl-Coenzyme A dehydrogenase, very long Homo sapiens mRNA; cDNA DKFZp434F0217 (f	1.37	2.99	
	427929	BE613835	Hs.181159 Hs.155048	Lutheran blood group (Auberger b antigen	1.36	3.17 .	
30	4251B4 407143	BE278288 C14076	Hs.332329	EST	1.36	2.99	
50	416950	AL049798	Hs.80552	dermatopontin	1.35	3.39	
	406799	AA908548		gb:og83g12.s1 NCI_CGAP_Ov8 Horno sapiens	1.34	3.17	
	442599	AF078037	Hs.324051	RelA-associated inhibitor	1.33	3.30 2.89	
25	413659	BE155647		gb:PM2-HT0353-130100-002-e09*HT0353 Homo	1.32 1.30	3.50	
35	454478	AW805749		superoxide dismutase 2, mitochondrial Target Exon	1.29	3.57	
	404467 452516	AA058630	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE	1.28	3.00	
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	1.27	3.05	
	422354	U20982	Hs.1516	insufin-tike growth factor-binding prote	1.24	2.86	
40	406711	N25514	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.24	3.29	
	450796	NM_001988		envoplakin	1.23 1.23	3.21 3.65	
	431526	Y10129	Hs.258742	myosin-binding protein C, cardiac hypothetical protein FLJ20509	1.23	2.90	
	452791 406742	AA227581 AI468091	Hs.30634 Hs.279860	tumor protein, translationally-controlle	1.19	3.47	
45	406712	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.18	2.91	
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	1.10	3.50	
	413048	M93221	Hs.75182	mannose receptor, C type 1	1.00	2.99	
	453165	S74727	Hs.32042	aspartoacytase (aminoacytase 2, Canavan	1.00	2.91	
50	TARIE (ron.					
50	TABLE S		ique Eos probeset id	lantifier number			,
	Pkey: CAT nur		na chaster number	Charles Harrison			•
	Accessi		nbank accession nu	mbers			
55	Pkey	CAT Number	er Accession	04415 AF139065 BG681115 BG740377 BI712964 BG000656	A A 120470 D142	9224 1127409 13	C021630 RE167165 AW370827 AW370813
	412635	1438_1	M77830 NM_00	14415 AF 139065 BG6811115 BG740377 B1712964 BG000636 1365 BG740734 BG680618 BG739778 B1765807 BM353403 E	MAT20470 BI45	77784 AW20578	19 AW951576 AW848592 BE182164
			DE 1403CC DE0.	40187 DIAGAAAS RIAGAAAA RE35A9R3 RE72A095 RE72A069 I	BE 715154 BEOB	2584 BE0825/0	PREADMINI WWW. PROPERTY OF THE
			DE712649 AM	1702C2 DE 160422 RIO39775 AWRR6475 RM462504 RE9317.	34 HF 149764 AP	L340/// BF3811	103 B/021131 MU 121200 MW304033
60	•		DE0033E3 DC3	22480 BER10000 RE281184 RE715956 R58704 AAR52212 A	XW366566 BIO9	1358 BF087707	RERIANS REPIAND WATLLIST DENIMOL
••			DEB400E0 DEB	10049 RI036306 RC000973 RI040954 RF919911 A11140155	A1951766 A1434	518 AW804674	RF 125303 RF 031003 RF 353050 RL 143502
			AW995615 BE8	314264 BI039782 AU140407 BE144243 BE709863 BF98564	2 BE001923 BF	53351U AW205	128 BG430319 BE 102100 MW303173
			AW847688 BE	818280 AW177933 BF873679 AW178000 BE082526 BF4766 847678 BF804153 AW365157 BE813930 BE002030 AW365	163 DE1010334 B	7392270 BEVO	14920 RER39562 RE184933 RE842254
65			DECOMAN DEC	21048 DC000880 DC368818 RF184924 RF159646 RF71453	7 BF 184948 BG	986845 AA1311	128 AAU33031 WJ3400 CU47 IJ DEVJU124
O)							
			DECOCODA AMA	0.40274 AM2776702 AM248780 AM2480076 "W361417 RF92"	7725 RFN94211	AW997139 BF 8	8654/4 RE18518/ RE130021 BE/13003
			DEA02017 DEG	1311BN DE7631NG DENNGGG1 RC959933 RFN94833 RFN9474	R RF0945B3 AV	/3/7699 AW6U/	(\$38 PE095313 WAA31 (100 PL34340)
70			Al 190590 Al 55	4403 A1392926 AU158477 B1467252 AU159919 A1760816 B 39975 AA946936 AA644381 BM314884 AA702424 A1417612	F082516 AI4391	U1 AA451923 A	2 A1270345 A1627383 AA552300 A1911702
			AJ142882 AAU	39975 AA946936 AA644381 BM314884 AA702424 A417612 A46078 W95070 AA149191 AA026864 A1830049 AW780435	2 AVV 190000 A12	20373 AGO477	146R588 AIB60584 AI025932 AA026047
			4 4 70 2 2 2 2 4 4 5	CC04E4 AAK4EEM NIMIOONRS AAQ18OR1 T77861 AIQ777N7 /	41205263 RF082	491 AW021347	N 9120R030 RE333005 WYOODOO D 15005
			A AGCCEGG AA	2024AA WHADDO WADDIEG AWISAADD AAADDOOL TRYIRI HAA	MOS AIGTOM 34 R	F037513 AI494	Uby AIZ/WZ/ AIDJOD/O AA I ZOJOV
75			00001436.00	70C070 D30004 DC680060 DC676647 RF764409 AA026654	AV745530 RI76	2796 HG28/39	U WAAAARAA REAAAAAA
			A14/200140 DE	007000 DE002222 AMBTOAST AIST 1075 RE0577RS AV7213	วก ムเกววกรว พว	9754 CO3378 N	184/67 AA131U// NSU146 BE/14230
			AICOCOCO AICC		1F067737 RG31	94RB AA24/685	S AW/YEESES AW IUSSEI EFECTIVS
			A140C0070 0C	939707 BE185750 BE714064 BE713903 BE713868 BE7137 905927 BF992780 AW853812 BG954443 B1770853 BG6794	KA BIJUSAHKA R	-/1.9330 AW.93	15 15 1 BU3535463 DEUU3212 DF 3 1 J 3 J 1
80			D1000403 DE0	^^** ncozooc Auroliolo DEOSEELE DCE77019 DC7/10	70 AANZKARN RI	- 705444 KG677	/ 15/ BEUU9U9U 8G0013/0 BE/ 14431
80			DO0C4400 DO		50 RFR17665 W	9504X W75458	AVV1///85 AAU/23651 BE931/33 B7134037
			0.0040000.00	74444 AMMOCO46 DE711901 AMONADO DE064333 DE7193	ON REGANTAN KI	5491717 RE3/5	3/14 BF34332/ 8G33820/ 148/33 6W13434
			BE001925 AW	7365156 AW365154 AW606653 BF763109 BE931637 BE167	181 BE713879	BF354008 BF67	/8726 H90899 AW365145 W38382 AI498487
				600			

PCT/US02/29560

	409010	10331_1	AA059411 AI79	1714 BM014781 BGS42863 BG771232 AA429722 A1377 5263 A1494075 A1572127 AA420992 BF436083 A1648673 9169 A1758175 AA976350 BG701414 BF057794 AW1383 56883 BF435859 AA196423 AW237471 R99289 D61992	5 AA878813 BI4886 599 AA062583 BI54	514 BG/0 49631 Al	JUSSS AA128609 AV/U 185077 AA933879 AW	2879 AA731 140 A1300330 024454 AA193289 AA045194
5			BF027898 BG7	79448				
	409760	865166_1	A 4 20 20 40 TO 20	1C T020CA ALITRAGO? AAA77551				
	410099		AVOCECTA AND	CC247 AV75150R AA290026 RS3043 AA3313R7 AK0561	4R RI917678 BG81	9395 BG	:911971 BG820167 Al1	174254 AA348720 AA364503
	410033	16732_1	ANUDOUT ANT	03241 WA121220 WAT20250 INDOOR WADDING WADDING WADDING	20 00000024 842	24000 AL	663737 BC039709 W	2000 ALA39658 RESS1237
			BG714279 AW	193230 AA081774 H24222 AV727176 BF875715 AA0816	ON REMOOSA WAS	34000 AL	200101 00023703 77	2002 A 404C40 T22014
			AA283724 BF1	09530 A1457096 A1805992 BE467736 AA693467 A16975	33 A1887863 A11674	419 AW9	01380 VAA301169 RF1	UZ179 AAA04349 123011
10			OF237042 AA7	16077 AAG1700A AA16771A RE339675 AADRA61R AIA1R	634 T315R6 AA436	630 AI3	56472 AA705191 AV4Z	304 A1204699 A1041169
10			A 404 4 400 AVA	27081 AA788593 T32735 AI767935 AA747914 T03534	ALMOSORAR AT 1195	27 RF30	7037 AW901982 AW99	13370 AW901977 AW902071
			AAZTTAUZ AYY	12/081 AA/00393 132/30 MI/0/333 MA/4/3/4 103334/	ATT 303040 ALT 100	~~~~		
			W60090 N7990	6 D52685 T07735 BE702069 BE702172 T08671 BE7671	121 85/6/11/ 85/	0/113		
	456247	2142387_1	R10170 R0974	3				
			A1220117 AIRE	PETODALA ROZRELIA AZENDELA ODALEDIAR PERRELA CERT	AW571549 AW950	0042 AJD	89943 AA437280 AU1	50878 BF 197070 AJ 267984
16	412477	8669_2	AIZZUTTI AUGS	96688 AI433152 AI338921 AI620364 AI280197 AA65253	1 AIC7/039 AI3/2/	A7 AISX	350 AI281295 AI1486	21 N54787 AI338121
15			BF594181 BF1	90088 AI433132 AI330321 AI020304 AI200137 AA03233	11 MUI 1300 MINES	AL MOE	72CE AIA/910CE7 AA03	469 AH67868 AW148701
			AI281153 N511	99 A1087072 AA954788 AW069054 A1345309 BG52962	9 AL340 L33 Bruss	DO M 10	1303 MIC 13031 MASS	PECOCOD A1400E0042 A10E1ED2
			A1383720 BEO	17685 AW015498 AA937149 AA708346 AW771478 AW8	02508 H53334 AW	389204 /	444189530 M223855 W	1200000 WAA320042 WISO 1005
			AN/TINGENE DOS	963 AA13661 <i>A</i> W63767 AIG36893 AIG36063 AIA18730 N	99964 ALS68933 AL	915737 <i>f</i>	WUBUB91 AH 185356 NA	5550 N58513 N52624 NOUV31
			A1247247 TOE	CA DECORDES AISADESS AUXIDRICAS AAGGSSGA AARRSAS	7 AI073726 AA633	132 AA6	29674 AA629649 AA62	3656 AA5/8535 AH00/20
20			A1247 247 133	35786 AA994396 AA991209 AA948663 AA929054 AA92	7052 T97001 AAG2	8210 44	629296 AWR02267 AV	384129 RF744400 AA194110
20			AA804572 A10	35786 AA994396 AA991209 AA948003 AA929054 AA92	1995 101001 14495	021074	DESERVE PATROVERSON PAR	307123 DI 144400111101111
			AJ382839 AA 1	34837 AA406284 AI250750 R37035 AI525586 W01244				
	444105	649788_1	AW189097 Al1	23917 Al123926				
	406851	0_0	A A COOTE A DO	204				
			000000000000	940673 BG432524 BE157554 BG676980 AU144284 AI74	A ZENDZILIA EREZE	1693500	AW293668 AW371408	BE856107 Al338042
25	444726	3503_2	BG500003 BE	98246 BE673290 AW297653 AA156532 AI017342 AI916	TEA ALTONGAA ALTO	04202 A	957671 DERS7018 AL	107420 AI318157 AW204327
25			AW188320 All	198246 BE673290 AWZ97653 AA156532 AIU 17342 AI910	11 IN PEODE I IN PC10		******************************	41924C02 AMPAOCDA
			AW664668 AV	/274339 AA582788 AI345741 AW301433 AI873468 AW1	37388 BF / 18731 B	17/1841.	3 AA8/ 1433 BFUU 13/3	MIDS 4033 WANDADOO
			AUMONOMOS AU	/R/10306 AW/R/10173 RE673179 A/611327 AA705753 RE7	715478 AW849414	AWMAYJ	199 ANU85/39 AN 140043	10/412 M003003 M11104041
			A101240E A101	10074 A1744941 RE717113 RE717118 RE715564 AIR725	77 AA029457 CD03	CSB A1465	9558 BE/155// AAU43	413 81843813
		474445 4	DC444C00 AII	845895 AW178095 BE140914 BE140909 AW178107 AV	ULTRINGA AWRASER	3 RF349	267 AWR45898 AW845	811 AW845814 BF767720
20	454194	171445_1		043030 WALLOOSS DC 140314 DE 140303 VILLIANIO VI	***************************************			
30	406799	0_0	AA908548					
	413659	1526081_1	BE155647 BE	155627				
	454478	4273_16	AW796921 AV	V798102 AW805749 AW805872 BF985060 AW794380 B	F380449 AW79446	6 AW79	4538	
	TABLE 59	ıc.						
35)U.		sponding to an Eos probesel				
33	Pkey:	Uni	ing untimes cours	ne 7 digit numbers in this column are Genbank Identifier (Cli numbers "Dun	hom et	of "refers to the outlica	tion entitled "The DNA
	Ref:	Seq	uence source. I	te / digit numbers in this countril are demoark identities (ON HUNDONS. DUIN	along or a	a. Total a a la passas	
		seq	uence of human	thromosome 22" Dunham, et al. (1999) Nature 402:489-4	3 0.			
	Strand:	Indi	cates DNA strand	from which exons were predicted.				
	Nt_positio	on: Indi	cates nucleotide	positions of predicted exons.				
40	_							
. •	Pkey	Ref	Strand	Nt_position				
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941				
				121907-122035,122804-122921,124019-12416				
	402075	8117407	Plus	121307-122033,122004-122321,124013-12410				
4 -	401785	7249190	Minus	165776-165996,166189-166314,166408-16656				
45	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423				
	406433	9256507	Plus	58094-58565				
	401760	9929699	Plus	83126-83250,85320-85540,94719-95287				
	403903	7710671	Minus	101165-102597				
	404467	8077630	Minus	24951-25853				
50	404407	00//030	mu ius	24331-23003				
50								,
		A. ADOUT ET	CENEC HOOSE	ULATED IN BENIGN NEVI RELATIVE TO NORMAL TIS	SHES			
	TABLE	MA: ABOUT S	GENES UPREC	ad in benign nevi relative to normal tissues. These genes	were calected from	59680 c	onhesets on the Eas/A	ffymetrix Hu03 Genechip array.
	(abte ou	M IISIS 200011 53	genes opregual	obtained from this analysis was expressed as average into	encity (All a norma	dized val	e reflection the relative	level of mRNA expression.
55		pression data k	r each proceser	MISTREO DIGITI UIS BRIDINGS WAS EXPRESSED AS AVERAGE AND	cisil) (ra), a nomi		oc ranous 15 and renes 1	•
23	Pkey:			t identifier number				
	ExAccn:			number, Genbank accession number				
	Unigene	ID: Un	igene number					
	Unigene	Title: Un	igene gene title					
	R1;	700	erage of benign r	evi Als divided by the 90th percentile of normal tissue Als				
60	R2:	RV.	erage of benion r	evi Als divided by 90th percentile of normal tissue Als, wi	here the 15th percen	ntile of no	ormal tissue Als was su	ibtracted from both the
00	142.		merator and den					
	Pkey	ExAccn	UnigenelD	Unigene Title	R1		R2	•
				dopachrome tautomerase (dopachrome delta	8.69	9	5.62	
65	430377	NM_00192			8.37		13.47	
65	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)			4.78	
	430686	NM_00194	2 Hs.2633	desmoglein 1	7.26			
	406964	M21305		FGENES predicted novel secreted protein	6.50		3.73	
	426555		2 Hs.2053	tyrosinase (oculocutaneous albinism IA)	6.40	0	7.35	
				small inducible cytokine subfamily A (Cy	6.23	3	8.85	
70	429852				5.49		4.32	
70	430822		Hs.248017	glyceraldehyde-3-phosphate dehydrogenase				
	420208	BE276055	Hs.95972	sitver (mouse homolog) like	5.4		9.84	
	431360		7 Hs.251680	toricrin	3.8		3.00	
	421773		Hs.112457	ESTs	3.8	0	9.04	
			Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	3.7		4.23	
75	438380				3.2		2.34	
75	431089			ESTs. Weakly similar to unknown protein			3.20	
	420798		Hs.99936	keratin 10 (epidermolytic hyperkeratosis	3.0			
	442503	AF147078	Hs.150853	p53-responsive gene 5	2.8		5.01	
	405451			dihydropyrimidinase-like 3	2.8		2.85	
	452240		Hs.61232	ESTs	2.8		1.90	
80	402525			NM_002699":Homo sapiens POU domain, clas	2.7	18	2.72	
50	413171		Hs.75219	tyrosinase-related protein 1	2.6		5.58	
				Homo sapiens, Similar to RIKEN cDNA 1110	2.5		3.18	
	439496				2.4		2.38	
	422656	AI870435	Hs.1569	LIM homeobox protein 2	2.4		2.50	

	453317	MILE 002277	He 41000	the state of the s		
	420783	NM_002277 AI659838	Hs.41696 Hs.99923	keratin, hair, acidic, 1	2.34	3.76
	422511	AU076442	Hs.117938	lectin, galactoside-binding, soluble, 7	2.33	2.43
	427666	AI791495	Hs.180142	collagen, type XVII, alpha 1	2.28	2.00
5	459702	AJ204995	13.100142	calmodulin-like skin protein (CLSP) gb:an03c03.x1 Stratagene schizo brain S1	2.28	2.50
	451668	Z43948	Hs.326444	cartilage acidic protein 1	2.25 ° 2.23	1.85
	431703	AA514264	Hs.4437	triosephosphate isomerase 1	2.15	2.42 2.20
	453511	AL031224	Hs.33102	AP-2 beta transcription factor	2.13	2.20
10	401780			NM_005557*:Homo sapiens keratin 16 (foca	213	2.02
10	416640	BE262478	Hs.79404	neuron-specific protein	2.11	2.02
	444105	AW189097		ESTs	211	1.46
	428748	AW593206	Hs.98785	Ksp37 protein	2.09	1.52
	418067	Al127958	Hs.83393	cystatin E/M	2.09	2.32
15	417017 401781	AA976064	Hs.180842	ribosomal protein L13	2.08	2.52
13	407178	A 8405C54		Target Exon	2.02	2.03
	452308	AA195651 AI167560	Hs.61297	AP-2 beta transcription factor	1.88	217
	429348	AJ242859	Hs.199731	ESTs	1.84	2.38
	402880	14242000	113.133731	Langerhans cell specific c-type tectin Target Exon	1.83	3.26
20	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	1.69	2.10
	401963		1.5.55555	NM_006311:Homo sapiens nuclear receptor	1.69	2.20
	424010	AL080168	Hs.137556	Homo sapiens mRNA; cDNA DKFZp434A132 (fr	1.66 1.65	2.02
	432800	BE391046	Hs.278962	AIM-1 protein	1.61	2.05 2.83
~ -	400328	X87344		transporter 2, ATP-binding cassette, sub	1.57	2.27
25	412580	AA113262	Hs.17901	Homo sapiens, clone tMAGE:3937015, mRNA,	1.55	2.42
	435292	N20514	Hs.172965	ESTs	1.53	2.21
	408561	AI308037	Hs.84120	hypothetical protein MGC13016	1.52	2.01
	427923	AW274357	Hs.301406	hypothetical protein PP3501	1.47	271
30	447763	BE619911	Hs.115803	hypothetical protein	1.40	2.10 .
J U	454478 427289	AW805749		superoxide dismutase 2, mitochondrial	1.30	2.36
	430513	AJ097346 AJ012008	Un 344505	phosphoserine aminotransferase	1.24	2.02
	411388	X72925	Hs.241586 Hs.69752	G6C protein	1.20	2.18
	** 1000	~~******	113.03732	desmocallin 1	1.00	2.43
35	TABLE 6					
	Pkey: CAT num	umq	ua Eos probese	tidentifier number		
	Accessio		e cluster number bank accession i			
	7000000	i. Gen	Dank accession	numbers .		
40	Pkey	CAT Number	Accession			
	431089	125941_2		M063489 AA715980 BF001091 BF880066 AA666102 AA6219	AC A A A D 1 D 2 C	
	459702	539529_1	8G207209 BE	166299 Al204995 BG199355 AW969908 AA528756 AW4407	76 0104431020	
	444105	649788_1	AW189097 AI	123917 AI123926	1001011331	
15	407178	683007_1	AW235123 A			
45	454478	4273_16	AW796921 AV	N798102 AW805749 AW805872 BF985060 AW794380 BF380	0449 AW794466 A	W794538
	427289	1820_2	BC007350 BC	6766159 BG769338 BG761999 BG744385 BG770572 AW370	610 AW370581 A	A97R3S3 AW3279
			AW612968 A/	N530644 A1751211 N26980 A1394506 AA747849 RF154926 PI	F477185 AAR49R	47 P30135 A1750
			AVV012240 AV	A505495 AA515380 BG760793 AW370651 BG766029 AW370	595 BF229885 BC	3762422 BG7649
50			AV/U342U Hb	5047 AA485582 R56186 H90385 R55913 BI261497 BI018403	BF376945 T7557	78 BF933325 BF9
			DIVIDIZI NA	953 BF933343 BF932871 H08334 R14012 BF897622 T50816	i BG698803 BF34	0083 Z20199
	TABLE 6	OC:				
	Pkey:		ue number corre	sponding to an Eos probeset		
	Ref:	Secu	ence source Ti	he 7 digit numbers in this column are Genbank Identifier (GI) n		
55		seou	ence of human	phromosome 22° Dunham, et al. (1999) Nature 402:489-495.	umbers. 'Uunnan	n, et al." reters to
	Strand:	Indic	ates DNA strand	from which exons were predicted.		
	Nt_positio	n: Indic	ates nucleotide	positions of predicted exons.		
~ ^	Pkey	Ref	Strand	Nt_position		
50	405451	7622517	Minus	145949-146227		
	402525	9800048	Minus	19748-20683		
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941		
	401781	7249190		83215-83435,83531-83656,83740-83901,8423		
65	402880 401963	9920561	Minus	41555-41865		
0.5	401903	3126783	Plus	51382-51521		
						
	TABLE 0	Esta about 72 (ENES UPREG	JLATED IN BENIGN NEVI RELATIVE TO PRIMARY MELANC)MAS	
70	Core eve	raccina data for	sues abredarate	d in benign nevi relative to primary metanomas. Genes were s	elected from 5968	30 probesets on ti
. •	Pkey:	Unio	ua Eor omborot	blained from this analysis was expressed as average intensity	(Al), a normalized	value reflecting t
	ExAcon:	Even	notes Accession	identifier number		
	Unigenell	D: Linio	sue unumper chen veccezzion	number, Genbank accession number		
	Unigene 1		ene dene tide			
75	R1			vi Als divided by the 90th percentile of primary melanoma Als		
-	R2	aven	ige of benign ne	vi Als divided by the 90th percentile of primary melanoma Als.	where the 15th pr	ercentile of norma
		num	erator and denor	nen acor .		
20	Pkey	ExAcon	UnigenetD	Unigene Title	R1	R2
80	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.60	2.50
	424897	D63216	Hs.153684	frizzled-related protein	3.40	2.69
	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	2.90	3.25
	431089	BE041395		ESTs, Wealthy similar to unknown protein	2.82	1.56

: Eos probeset identifier number duster number ok accession numbers

BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA6211 AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492 BG207209 BE166299 A/204995 BG199355 AW969908 AA528756 AW440

NM_024638:Homo sapiens hypothetical prot C1002500:gi[6754254]ref]NP_034610.1] hea C4000447-gi[7705570]ref]NP_038851.1] KI baculoviral IAP repeat-containing 7 (fiv

cytochrome c-1.

Homo sapiens cDNA: FLJ22105 fis, clone H
KIAAN55 gene product
NM_005311:Homo sapiens nuclear receptor
NM_0074631:Homo sapiens myzovirus (influ

hypothetical protein DKFZp434F1819 NM_021158*:Norno sapiens protein kinase d macrophage mynistrytated alanine-rich C

ENSP00000174317":KIAA0303 (FRAGMENT).

ENSP0000174317-MAA0303 (FRAGMENT) Target Exon proteotipal protein 1 (Petizaeus Merzbac C4001432::gi6009515(bijli8AA84941.1) (AB gbHuman Evariable segment 5 to antith hypothetical protein FLU 13074 beta site APP-deaving enzyma 2 hypothetical protein PP3501 eutarpote translation initiation factor C120017077-gi73052(15)r@htp-(038599.1) k hypothetical protein PP3501 eutarpote translation initiation factor C120017077-gi73052(15)r@htp-(038599.1) k hypothetical 2-st Skratiaeuen gray (937217)

gbyt65g12.1 Stratagene oray (937217) polassum votage-gated channel, shaker-trinucleotide repeat containing 3 phosphosenne aminotransferase

matrix metalloproteinase 17 (membrane-in

hypothetical protein
ESTs, Weatry similar to C29149 proline-r
amytoid beta (A4) precursor protein-bind

zona pellucida glycoprotein 3A (sperm re Eos Control

F-box only protein 7 microphthalmia-associated transcription

Target Exon gb:Human mRNA for pre-mRNA splicing fact Target Exon

Target exon

NM_022355:Homo saplens putative dipeptid
hypothetical protein PP3501
gb:601275386F1 NIH_MGC_20 Homo saplens c
gb:TC8AP1E1967 Pediatric pre-8 cetl acut
existin 1 Jens pureful

Target Exon
ESTs, Weakly similar to BING1 [H.sapiens
cerold-lipofuscinosis, neuronal 2, late

small nuclear ribonucleoprotein 70kD pol leukocyte immunoglobulin-like receptor, gb;yd60d05.r1 Soares fetal liver spleen

ENSP00000034663:Zinc finger protein 131

ES19
hypothetical protein FLJ11006
NM_022490:Homo sapiens hypothetical prot
preferentially expressed antigen in mela
Homo sapiens mRNA full length insert cON

KIAA0468 gene product coronin, actin-binding protein, 28

cofilin 1 (non-muscle) **ESTs**

leukocyte tyrosine kinase

ESTs

ESTs

G protein-coupled receptor 27

C7002129*:gi]3638957|gb]AAC36301.1| (AC0 Target Exon natural killer-turnor recognition sequenc

AIM-1 protein

Target Exon ESTs

ESTs

calpain 3 (p94)

Target Exon

ESTs cytochrome c-1

256126 40300

129501

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i.112095 i.75061 i.192352

£1787

s.10043 s.271411 s.301406 s.93379

s.298184 s.21858 s.159581

k 278962

is 187461 Is.279175

5.241493

ts.5912 ts.166017

ts.161757

ts.158287 ts.24907

ts.161851

ts.301406

Hs.123164

Hs.25734 Hs.20478

Hs.174051 Hs.67846 Hs.210

Hs.278283

Hs.40527

Hs 47448

Hs.49344 Hs.30743 Hs.20034

	459702	539529_1		166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
	414221	685586_1	AA136653 AA	1136656 AW450979 AA984358 AA809054 AW238038 AAA92073 BE168945
	455657	1490185_1	BE065209 BE	5065364 BE065110 BE065111
_	419200	9531_1	BF036043 AV	V190446 BG194731 AW662036 A1445021 BE937550 AW818972 AW393132 AA834685 BF 112058 AV721682 H16423 A1270167 A1857345
5		-	AAG37302 AV	MR18444 REG207RD RC40RE7R RE15501D RI508271 RI509811 RE161728 AW578737 AW753711 AW3/9/07 AW301910 UG300000
-			AW028637 A	W994240 BF887392 BF790073 AW381624 AV727105 BF439618 AA443174 AW18009 N42850 AW5/3242 A41/258 AA463483 AW6/6131
			A1167170 AA	836627 AAA43828 AW592922 AA235129 AA730278 AW439062 AW474332 BIJU43239 AW474342 BIG/U8553 AWJ6242J BI-U9UU28
			RF827256 R1	16550 R39478 R39479 R94368 BG540916 BM314745 AA251087 D54231 D55274 BF085805 D31589 AW966405 AW994425 D81879
			RENGREAS AV	AGO 1107 AA 383529 RUD21552 R56420 N39976 AA 573281 HB2595 AA 234955 BE 093539 AW 367006 BF 358697 BF 366318 AA 663856
10			BE702000 R	F035969 AI267384 AI267232 BE348320 AA621574 AA861212 BF083343 BF083341 AV745131 D53074 AW954476 AW954472 AA376836
10			81/734531 D	53063 C14928 AA093287 AA062638 BC483558 BE940050 AA765964 T70171 BE938775 BE940057 D53502 AW373300 AL118798
			N4124331 D	A193411 AW444709 AW952455 A1887612 BF431948 BI496876 A1264159 BM128481 A1624657 A1689301 A1969467 AA861685 AA251595
			BM120/20 A	AB72090 AB26790 AA328366 BE827416 R75951 D56918 R68122 BE827384 AL118797 AI184164 AA164411 BI495332 BE858113
			AMOZOTO I M	0660 T69849 AW780389 C14667 BE934995 BI018652 R92801 AA164410 H00752 AW373305 AW373299 AW373302
16		740.0	ALCOJOOU FILE	C012195 NM_007126 AF 100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418
15	430540	713_2	8001/1/18	U120387 BG770238 BG686740 BG913323 B1759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847
			BM045810 A	196861 BE856897 AA463876 AI375927 AA648810 AA948193 AA490916 AI459993 AI458188 AI240408 AI191843 AI131029 AW768399
			A1//01/1 BF	190001 BEBS0097 AA403070 AD37327 AA00010 AA370133 AM30310 AA3333 AA30100 AE247400 AE104740 AE104747
			AJ365196 AV	V337984 AW026150 BE466591 BE674599 AIB18438 AA772197 AI651927 AW151143 B198825 BG819083 BM458764 BE903567
00			BE732715 B	M043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610
20			BE561530 B	E560537 BE903782 BE732947 BI2277204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420
			BE298109 A	W245422 AI423847 AI914618 H80534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE745965 BF743630 BE879296
			A1359493 BA	MO18598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM62953
			BG340524 V	V52648 AA113434 BE785431 BIO41981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BIO91658 N72512
			W58732 W8	5690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069
25			F13645 R41	394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114
			A1243844 A	AB09493 AA481029 AA825718 A1347866 A1431670 AA814435 A1251109 R07704 AA765606 AA724593 A1918399 A1537550 AA491103
			AW0081881	R07703 AA989120 AA745235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809
			BE002760 B	IG746251 BE962912 BM454584 AL134894 BF104082 HB0591
	434596	14701_1	AF147374 T	59538 T59589 T59598 T59542
30	427289	1820_2	BC007350 E	3G766159 BG769338 BG761999 BG744385 BG770572 AW370610 AW370581 AA978353 AW327973 AW402425 AI889380 AA868504
		-	AW612968	AA630644 A1751211 N26980 A1394506 AA747849 BF154926 BF477185 AA649647 R39135 A1750216 T35363 W36278 AWU/9375
			AW612240	AA505495 AA515380 BG760793 AW370651 BG766029 AW370595 BF229885 BG762422 BG764907 T50662 AA025671 AW815715
			AV703420 F	465047 AA485582 R56186 H90385 R55913 B1261497 B1018403 BF376945 T75578 BF933325 BF932853 BG502266 AW868934 AV683504
			Rt018121 N	A1953 RE93343 RE932871 H0R334 R14D12 RE897622 T50816 BG698803 BF340083 Z20199
35	400263	18977_1	711692 X51	IASS NM 001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE885804 BI868669 BG337216 AW629935
			BM016525	ALS60409 ALS62866 AL909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BL261304 BG770095 BI033486
			B1517580 B	G876485 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719
			RG876487	AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758
			DIMENAS	argazene awnasi ze nagsea awnosna i argazea fagi i bagaan 186105450 BG387343 BF569547 BF154671 BM007368 BF569385
40			BF772007 I	BI 199487 BF761700 BI 261519 BF944452 BF898506 AIO38390 BMO44934 AW381142 BG743618 BE769206 BE893973 BIO15047 BF886479
70			BE761350	BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503
	414500	622003 1		BG774174 BIO15084 DE385437 DE408833 RE387650
	414580	623093_1	BG333973	BE385437 BE408833 BE387650
45	437026	1240260_1	BG333973 AW976573	BE385437 BE408833 BE387650 AA742335 AA830000
45			BG333973 AW976573	BE385437 BE408833 BE387650
45	437026 419045	1240260_1 348516_2	BG333973 AW976573	BE385437 BE408833 BE387650 AA742335 AA830000
45	437026 419045 TABLE 6	1240260_1 348516_2 i2C:	BG333973 AW976573 BF981324	BE385437 BE408833 BE387650 AA742335 AA830000 BG723297 T85693 T81681 T81909
	437026 419045 TABLE 6 Pkey:	1240260_1 348516_2 i2C:	BG333973 AW976573 BF981324	BE385437 BE408833 BE387650 AA742335 AA830000 BG723297 T85693 T81681 T81909
45 50	437026 419045 TABLE 6	1240260_1 348516_2 :2C: Uni See	BG333973 AW976573 BF981324 ique number co quence source.	BE385437 BE408833 BE387650 AA742335 AA830000 BG723297 T85693 T81681 T81909 wresponding to an Eos probeset The 7 digit numbers in this cotumn are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
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	437026 419045 TABLE 6 Pkey: Ref:	1240260_1 348516_2 2C: Uni See sec Ind	BG333973 AW976573 BF981324 I ique number co quence source, quence of huma icates DNA stra	BE385437 BE40833 BE387650 AA742335 AA830000 BG723297 T85693 T81681 T81909 rresponding to an Eos probeset The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al. (1999) Nature 402:489-495. and from which exons were predicted.
50	437026 419045 TABLE 6 Pkey: Ref: Strand:	1240260_1 348516_2 2C: Uni See sec Ind	BG333973 AW976573 BF981324 I ique number co quence source, quence of huma icates DNA stra	BE385437 BE40833 BE387650 AA742335 AA830000 BG723297 T85693 T81681 T81909 rresponding to an Eos probeset The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al. (1999) Nature 402:489-495. and from which exons were predicted.
	437026 419045 TABLE 6 Pkey: Ref: Strand: Nt_positi	1240260_1 348516_2 2C: Uni See sec Indi ion: Indi	BG333973 AW976573 BF981324 I ique number co quence source, quence of huma icates DNA stra icates nucleotic	BE385437 BE408833 BE387650 AA742335 AA830000 BG723297 T85693 T81681 T81909 Interponding to an Eos probeset The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al. (1999) Nature 402:489-495. and from which exons were predicted. de positions of predicted exons.
50	437026 419045 TABLE 6 Pkey: Ref: Strand: Nt_positi	1240260_1 348516_2 2C: Uni Sec sec Ind ion: Ind	BG333973 AW976573 BF981324 I sique number co quence source, quence of huma icates DNA stra icates nucleotic Strand	BE385437 BE40833 BE387650 AA742335 AA830000 BG723297 T85693 T81681 T81909 rresponding to an Eos probeset The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA on chromosome 22" Dunham, et al. (1999) Nature 402:489-495. and from which exons were predicted. te positions of predicted exons.
50	437026 419045 TABLE 6 Pkey: Ref: Strand: Nt_positi Pkey 404356 401116	1240260_1 348516_2 2C: Uni Sec sec Ind ion: Ind Ref 7630858	BG333973 AW976573 BF981324 li ique number co quence of huma icates DNA stra icates nucleotic Strand Minus Plus	BE385437 BE408833 BE387650 AA742335 AA830000 BG723297 T85693 T81681 T81909 wresponding to an Eos probeset The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Identifier of the product of the publication entitled "The DNA in chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Identifier of the product of the publication entitled "The DNA in chromosome 22" Dunham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al. "refers to the publication entitled "The DNA in chromosome 22" Dunham, et al. "1999) Nature 1999 Nature
50	437026 419045 TABLE 6 Pkey: Ref: Strand: NL positi Pkey 404356	1240260_1 348516_2 2C: Uni Sec sec Ind ion: Ind Ref 7630858 9966559	BG333973 AW976573 BF981324 ique number co quence source. quence of huma icates DNA stra icates nucleotic Strand Minus	BE385437 BE40833 BE387650 AA742335 AA830000 BG723297 T85693 T81681 T81909 wresponding to an Eos probeset The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA in chromosome 27 Dunham, et al. (1999) Nature 402-489-495. In the positions of predicted exons. Nt_position 126433-126623
50	437026 419045 TABLE 6 Pkey: Ref: Strand: Nt_positi Pkey 404356 401116 404977 402181	1240260_1 348516_2 2C: Uni Sec sec Ind ion: Ref 7630858 9966559 3738341	BG333973 AW976573 BF981324 I ique number co quence source, quence of huma icates DNA str icates nucleotic Strand Minus Minus Minus	BE385437 BE40833 BE387650 AA742335 AA830000 BG723297 T85693 T81681 T81909 rresponding to an Eos probeset The 7 digit numbers in this coturns are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA on chromosome 22" Dunham, et al. (1999) Nature 402:489-495. and from which exons were predicted. te positions of predicted exons. Nt_position 126433-12623 123579-124447 43081-43229
50	437026 419045 TABLE 6 Pkey: Ref: Strand: Ni_positi Pkey 404356 401116 40497: 402181 405451	1240260_1 348516_2 IZC: Uni See sec Ind Idon: Ind Ref 7630858 9966559 3738341 875912 7622517	BG333973 AW976573 BF981324 I ique number co quence source, quence of huma icates DNA stra icates nucleotic Strand Minus Ptus Minus Ptus Ptus	BE385437 BE40833 BE387650 AA742335 AA830000 BG723297 T85693 T81681 T81909 wresponding to an Eos probeset The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA in chromosome 27 Dunham, et al. (1999) Nature 402:489-495. the positions of predicted exons. Nt_position 126433-126623 123579-124447 43081-43229 449746-450040
50	437026 419045 TABLE 6 Pkey: Ref: Strand: Nt_positi Pkey 404356 401116 404977 402181 405217	1240260_1 348516_2 2C: Uni See sec Ind Ion: Ind Ref 7630858 9966559 3738341 875912 7622517 9795981	BG333973 AW976573 BF981324 I ique number co quence source, quence of huma- icates DNA stri icates nucleotic Strand Minus Plus Minus Plus Minus Minus Minus	BE385437 BE40833 BE387650 AA742335 AA830000 BG723297 T8569 T81681 T81909 rresponding to an Eos probeset The 7 digit numbers in this coturns are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al. (1999) Nature 402:489-495. and from which exons were predicted. te positions of predicted exons. Nt_position 126433-126623 123579-124447 43081-43229 449746-450040 145949-146227 21521-21757
50	437026 419045 TABLE 6 Pkey: Ref: Strand: NL_positi Pkey 404356 401116 404977 402181 402217 402040	1240260_1 348516_2 2C: Uni See sex Ind Ind Ref 7630858 9966559 3738341 8575912 7622517 9795981 6758938	BG333973 AW976573 BF981324 ique number co quence source, quence of huma icates DNA stra icates nucleotic Strand Minus Plus Minus Plus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus	BE385437 BE40833 BE387650 AA742335 AA830000 BG723297 T85693 T81681 T81909 wresponding to an Eos probeset The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA in chromosome 27 Dunham, et al. (1999) Nature 402:489-495. the positions of predicted exons. Nt_position 126433-126623 123579-124447 43081-43229 449746-450040 14559-146227 21521-21757 22063-22999
50	437026 419045 TABLE 6 Pkey: Ref: Strand: NL_positi Pkey 404356 401116 40497: 402181 405451 402217 405040 403532	1240260_1 348516_2 2C: Uni See sec Ind on: Ind Ref 7630858 9966559 3738341 8575912 7622517 9795981 6758938 8076842	BG333973 AW976573 BF981324 ique number co quence source, quence of huma icates DNA stri icates nucleotic Strand Minus Plus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus	BE385437 BE40833 BE387650 AA742335 AA30000 BG723297 T8569 T81681 T81909 rresponding to an Eos probeset The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al. (1999) Nature 402:489-495. and from which exons were predicted. te positions of predicted exons. Nt_position 125433-125623 123679-124447 43081-43229 449746-450040 145549-146227 21521-21757 23063-23599 81750-81901
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50 55 60 65 70	437026 419045 TABLE 6 Pkey: Ref: Strand: Ni_positi 404356 401116 405451 405451 405451 405451 4056016 401626 40163 402934 405016 402934 405016 402934 405016 40350 40406 40406	1240260_1 348516_2 32C: Uni See Sec Ind (on: Uni Ref 7630858 9966559 3738341 8575912 7622517 9795981 6758938 8076842 8918414 7159748 33126783 2896643 8272661 7263904 8224409 7528342 8112966 812966	BG333973 AW976573 BF981324 ique number co quence source. quence of huma icates DNA str icates nucleotic Strand Minus Plus Minus Minus Minus Minus Minus Plus Minus Plus Minus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	BE35437 BE40833 BE387650 AA742335 AA30000 BG723297 T8593 T81681 T81909 rresponding to an Eos probeset The 7 digit numbers in this coturns are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al. (1999) Nature 402-489-495. and from which exons were predicted. te positions of predicted exons. Nt_position 126433-126523 123579-124447 43081-43229 449746-450040 145949-146227 21521-21757 23063-23999 81750-81901 101532-101852, 102006-102263 31755-32148 105911-107251 51392-51521 4727-4969 4134-1940 142689-142979 90999-94843 2365-2518 55513-55776 33611-38761 79689-79967 4677-6084 90692-91238 62537-62945,63155-63308 13735-137663155-63308 13735-137663155-63308 13735-137663155-63308 13735-137663155-63308 13735-137663155-63308
50 55 60 65 70	437026 419045 TABLE 6 Pkeyr. Ref: Ni_positi 100,000 11116 404917 402181 402417 402294 403294 403294 40506 401963 40294 40506 40303 404994 40506 404994 40506 404994 40506 404994 40506 404994 40506 404994 40506 404994 40506	1240260_1 348516_2 12C: Uni See See Ind Ind Ref 7630858 9966559 3738341 8575912 7622517 9795981 6758938 8076842 8918414 9838214 7159748 3126783 2996643 8272661 7263904 8272409 8724610	BG333973 AW976573 BF981324 ique number co quence source. quence of huma- icates DNA str- icates nucleotic Strand Minus Plus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Plus Minus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	BE38437 BE40833 BE387650 AA742335 AA30000 BG723297 T8569 T81681 T81909 **responding to an Eos probeset The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Durtham, et al." refers to the publication entitled "The DNA in chromosome 22" Durtham, et al. (1999) Nature 402-489-495. and from which exons were predicted. **Le positions of predicted exons.** NL_position 126433-126623 123579-124447 43081-43229 449746-450040 145949-146207 21521-21757 22053-23599 81750-81901 101532-101852-102006-102263 31755-32188 105911-107251 51382-515521 4727-4969 41341-41940 142689-142979 90999-94843 2356-2518 55513-55778 38611-38761 79689-79967 4677-6084 90693-91238 62537-62945,63155-6308 137536-137682,137920-138045 1415-2071 724447-72588,72673-77802,73119-73245
50 55 60 65 70	437026 419045 TABLE 6 Pkey: Ref: Strand: Ni_positi 404356 401116 404977 402181 405451 402217 406040 403532 402828 405776 401963 401963 401963 402994 405016 402911 403960 40490 405318 402343 40396 40490 405016 40490 4	1240260_1 348516_2 12C: Uni See Sec Ind (on: Ind Ref 7630858 9966559 3738341 8575912 7622517 9955891 6758938 8076842 818414 9838214 7159748 3126783 2996643 8272661 7263904 8224409 77528342 8112965 7230958 3638954 8099256 8576059 9796674 3082162 9796674 9838275	BG333973 AW976573 BF981324 I ique number co quence source, quence source, quence of huma icates DNA str icates nucleotic Strand Minus Plus Minus Plus Minus Minus Plus Minus Plus Minus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	BE38437 BE40833 BE387650 AA74233 AA830000 BG723297 T85693 T81681 T81909 **responding to an Eos probeset The 7 digit numbers in this column are Genbank Identifiar (GI) numbers. **Dunham, et al.** refers to the publication entitled **The DNA in chromosome 27 Dunham, et al.** (1999) Nature 402-489-495. and from which exons were predicted. **Le positions of predicted exons.** Nt. position 126433-126523 123379-124447 43081-43229 449746-45040 143349-146277 21521-21757 23053-23599 81750-81901 101532-101852 102006-102263 31755-32148 105911-107251 51382-51521 4727-4959 41341-41940 142689-142979 90999-34843 2365-2518 55513-55778 33611-38761 79689-79957 4677-6084 90693-91238 62537-62945-63155-63308 13755-137682,137980-73119-73245 34115-2071 72447-72588,72673-77800,73119-73245
50 55 60 65 70	437026 419045 TABLE 6 Pkeyr. Ref: Ni_positi 100,000 11116 404917 402181 402417 402294 403294 403294 40506 401963 40294 40506 40303 404994 40506 404994 40506 404994 40506 404994 40506 404994 40506 404994 40506 404994 40506	1240260_1 348516_2 12C: Uni See Sec Ind Ind Ind Ind Ind Ind Ind Ind Ind Ind	BG333973 AW976573 BF981324 ique number co quence source. quence of huma- icates DNA str- icates nucleotic Strand Minus Plus Minus Minus Minus Minus Minus Minus Minus Minus Minus Minus Plus Minus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	BE38437 BE40833 BE387650 AA742335 AA30000 BG723297 T8569 T81681 T81909 **responding to an Eos probeset The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Durtham, et al." refers to the publication entitled "The DNA in chromosome 22" Durtham, et al. (1999) Nature 402-489-495. and from which exons were predicted. **Le positions of predicted exons.** NL_position 126433-126623 123579-124447 43081-43229 449746-450040 145949-146207 21521-21757 22053-23599 81750-81901 101532-101852-102006-102263 31755-32188 105911-107251 51382-515521 4727-4969 41341-41940 142689-142979 90999-94843 2356-2518 55513-55778 38611-38761 79689-79967 4677-6084 90693-91238 62537-62945,63155-6308 137536-137682,137920-138045 1415-2071 724447-72588,72673-77802,73119-73245



404632 9796668 Plus 45096-45229

TABLE 63A: ABOUT 181 GENES UPREGULATED IN BENIGN NEVI RELATIVE TO MELANOMA METASTASES

Table 63A lists about 181 genes upregulated in berign nevi relative to melanoma metastases. Genes were selected from 59680 probesets on the Eos/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pitery: Unique Eos probeset identifier number

ExAcor: Exemplar Accession number, Genbank accession number

UniquenelD: Uniquene gene title

R1 average of benign nerit Als divided by the 90th percentile of melanoma metastasis AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator. 5

10

Unique Eos probeset identifier number
Exemplar Accession number, Genbank accession number
Unigene number
Unigene number
Unigene gene title
average of benign nevi Als divided by the 90th percentile of melanoma metastasis Als
average of benign nevi Als divided by the 90th percentile of melanoma metastasis Als
average of benign nevi Als divided by the 90th percentile of melanoma metastasis Als, where the 15th percentile of normal tissue Als was subtracted from both
the numerator and denominator

		the m	merator and deno	minator		
15		010110				
10	Pkey	ExAcon	UnigenelD	Unigene Tide	R1	R2
	401781	Cottai	ongcitto	Target Exon	19.33	19.21
	422511	AU076442	Hs.117938	coffagen, type XVII, alpha 1	13.54	14.18
	401780	M0010442	NS.111330	NM_005557°:Homo sapiens keratin 16 (foca	12.97	13.63
20		4522524	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	12.61	24 40
20	409601	AF237621	ns.00020	desmoplakin (OPI, OPII)	11.73	51.19 ; 6.91
	412635	NM_004415	11- 00000		10.18	14.08
	420783	Al659838	Hs.99923	tectin, galactoside-binding, soluble, 7	8.48	6.79
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito		9.62
25	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (ach	8.28	
25	430685	NM_001942	Hs.2633	desmoglein 1	7.26	5.64
	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	7.12	10.88
	442577	AA292998	Hs.163900	ESTs	7.01	6.59
	406964	M21305		FGENES predicted novel secreted protein	6.50	8.82
	401785			NM_002275":Homo saplens keratin 15 (KRT1	6.40	9.77
30	410001	AB041036	Hs.57771	kallikrein 11	6.18	6.16
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	5.73	16.57
	418686	Z36830	Hs.87268	annexin A8	5.32	5.27
	439496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN cDNA 1110	4.89	9.81
	452240	AI591147	Hs.61232	ESTs	4.89	6.67
35	402525			NM_002699*:Homo sapiens POU domain, clas	4.74	4.80
55	431360	NM_000427	Hs.251680	loricrin	4.66	3.98
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	4.63	5.69
	418067	Al127958	Hs.83393	cystatin E/M	4.56	6.78
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	4.56	5.73
40	418663	AK001100	Hs.41690	desmocolin 3	4.44	5.23
70		AY007220	Hs.288998	S100-type calcium binding protein A14	4.24	6.49
	419329			ESTs, Wealthy similar to DAP1_HUMAN DEATH	3.95	3.37
	439706	AW872527	Hs.59761		3.88	9.60
	421773	W69233	Hs.112457	ESTs	3.82	10.18
45	408536	AW381532	Hs.135188	ESTs	3.78	6.33
45	418394	AF132818	Hs.84728	Kruppel-like factor 5 (Intestinal)		4.92
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	3.77	
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	3.70	5.30
	424049	AB014524	Hs.138380	KIAA0624 protein	3.68	4.41
	421948	L42583	Hs.334309	keratin 6A	3.62	3.13
50	427666	AI791495	Hs.180142	catmodutin-like skin protein (CLSP)	3.59	4.40
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	3.48	6.09
	436895	AF037335	Hs.5338	carbonic anhydrase XII	3.42	3.28
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	3.28	3.89
	401760			Target Exon	3.21	7.11
55	431089	BE041395		ESTs, Wealdy similar to unknown protein	3.21	5.78
	434293	NM_004445	Hs.3796	EphB6	3.14	3.11
	412432	AA126311	Hs.9879	ESTs	3.14	4.85
	442503	AF147078	Hs.150853	p53-responsive gene 5	3.11	5.92
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	3.07	4.89
60	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	2.99	3.09
	433339	AF019226	Hs.8036	ofioblastoma overexpressed	2.96	2.75
	414876	AW950925	Hs.924	crystallin, mu	2.94	3.82
	437233	D81448	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	2.87	3.42
	424897	D63216	Hs.153684	frizzled-related protein	2.87	1.96
65	456034	AW450979		gb:ULH-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	2.73	2.54
	424364	AW383226	Hs. 163834	ESTs, Weakly similar to G01763 atrophin-	2.72	2.92
	427318	AF186081	Hs.175783	zinc transporter	2.71	2.21
	452887	AI702223	Hs.107253	hypothetical protein DKFZp761F24	2.67	6.47
	452308	AI167560	Hs.61297	ESTs	2.67	4.61
70	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.64	2.68
70	431369	8E184455	Hs.251754	secretory leukocyte protease inhibitor (2.57	3.91
	451541	BE279383	Hs.26557	plakophilin 3	2.49	5.47
		NM_002277		keratin, hair, acidic, 1	2.45	4.17
	453317	AF001691	Hs.74304	periplakin	2.42	4.90
75	412633		Hs.24395	small inducible cytokine subfamily 8 (Cy	241	2.68
13	417233				2.39	2.67
	424797	AA622394	Hs.153177	ribosomal protein S28	2.39	4.07
	424010		Hs.137556	Homo sapiens mRNA; cDNA DKFZp434A132 (fr	2.39	2.34
	453241	H58995	Hs.37648	ESTs	2.35	1.88
0.0	426451		Hs.169946	GATA-binding protein 3 (T-cell receptor	2.32	2.24
80	423467		Hs.129014	hypothetical protein FLJ20207	2.32	1.99
	432222			gb:an03c03.x1 Stratagene schizo brain S1		2.60
	430168			DKFZP43411735 protein	2.30	2.60 1.91
	457121	AJ743770	Hs.180513	ESTs, Weakly similar to KIAA0822 protein	2.28	1.91
				CO.C		

	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D hypothetical protein FLJ11036	2.27 2.27	8.50 2.21
	446989 429365	AK001898 AA451798	Hs.16740 Hs.99249	ESTs	2.25	2.54
	459702	Al204995	113.33243	gb:an03c03.x1 Stratagene schizo brain S1	2.25	2.35
5	420511	AF052692	Hs.98485	gap junction protein, beta 3, 31kD (conn	2.23	2.17
	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	2.23 2.21	3.23 2.74
	417017	AA976064	Hs.180842	ribosomal protein L13	221	1.68
	433124 430152	U51712 AB001325	Hs.13775 Hs.234642	hypothetical protein SMAP31 aquaporin 3	2.20	3.32
10	444726	NM_006147	113.251012	interferon regulatory factor 6	2.15	5.20
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	2.15	2.82
	425483	AF231022	Hs.158159	FAT tumor suppressor (Orosophila) homolo	2.14	2.96
	419912	AF249745	Hs.6066	Rho guarine nucleotide exchange factor (2.14 2.12	2.25 2.99
15	431441	U81961 AW189097	Hs.2794	sodium channel, nonvoltage-gated 1 alpha ESTs	2.11	2.98
13	444105 428748	AW593206	Hs.98785	Ksp37 protein	2.09	1.51
	456826	AI871742	Hs.302428	wingless-type MMTV integration site fami	2.09	3.25
	413163	Y00815	Hs.75216	protein tyrosine phosphatase, receptor t	2.09	4.97
20	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.06 2.06	5.68 2.04
20	430285	AI917602	Hs.106440	ESTs GPI-anchored metastasis-associated prote	2.05	5.92
	444781 451668	NM_014400 Z43948	Hs.11950 Hs.326444	cartilage acidic protein 1	2.04	2.19
	441134	W29092	Hs.346950	cellular retinoic acid-binding protein 1	2.04	3.08
	433428	T29975	Hs.33104	Huntingtin interacting protein C	2.04	1.63
25	425831	U46689	Hs.159608	aldehyde dehydrogenase 3 family, member	2.03	3.92
	446727	AB011095	Hs.16032	KIAA0523 protein	2.01 2.01	2.60 2.05
	431703 452554	AA514264 AW452434	Hs.4437 Hs.58006	triosephosphate isomerase 1 ESTs, Wealdy similar to ALU5_HUMAN ALU S	1.99	4.04
	439625	AF086453	Hs.58611	ESTs	1.99	2.31
30	402880			Target Exon	1.99	2.75
	428471	X57348	Hs.184510	stratifin	1.98	2.10
	413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	1.97 1.95	3.16 3.89
	452547	AA335295 NM 014214	Hs.74120	adipose specific 2 inositol(myo)-1(or 4)-monophosphatase 2	1.94	2.06
35	437679 429259	AA420450	Hs.5753 Hs.292911	Plakophilin	1.93	2.96
33	406387	741120100		Target Exon	1.92	2.97
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	1.91	3.46
	437202	AA326110		nuclear transcription factor Y, gamma	1.89	2.00
40	426150	NM_003658	Hs.167218	Bart-like homeobox 2	1.86 1.85	2.60 4.61
40	434574 446051	AI424458 BE048061	Hs.33470 Hs.37054	ESTs ephrin-A3	1.85	3.48
	424471	AA341329	Hs.311524	ESTs	1.84	2.62
	422106	D84239	Hs.111732	Fc fragment of IgG binding protein	1.83	4.69
4.5	451721	NM_006946	Hs.26915	spectrin, beta, non-erythrocytic 2	1.82	2.00
45	451849	AI199261	Hs.27191	hypothetical protein from clone 24796	1.81 1.79	2.31 3.07
	429348	AJ242859	Hs.199731	Langerhans cell specific c-type lectin ESTs	1.77	3.37
	423523 432543	AW299828 AA552690	Hs.193580 Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	1.76	2.46
	403828	74552654	100102120	C4000447*:gij7705570jrelJNP_038851.1 KI	1.73	2.06
50	412446	A1768015		ESTs	1.68	3.16
	420039	NM_004605		sulfotransferase family, cytosofic, 28,	1.67	2.22
	411274	NM_002776	Hs.69423	kallikrein 10	1.66 1.66	2.26 2.52
	401963 435016	AI284219	Hs.130749	NM_006311:Homo sapiens nuclear receptor ESTs, Weakly similar to 138022 hypotheti	1.65	2.20
55	437897	AA770561	Hs.146170	hypothetical protein FLJ22969	1.64	3.21
	419648	T73661	Hs.91877	thyroid hormone responsive SPOT 14 (rat)	1.63	2.94
	410545	U32324	Hs.64310	interleukin 11 receptor, alpha	1.62	2.58
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.62 1.60	3.92 3.43
60	456898	NM_001928 AB011086	Hs.155597 Hs.129739	D component of complement (adipsin) KIAA0514 gene product	1.60	2.18
00	423526 416305	AU076628	Hs.79187	coxsackie virus and adenovirus receptor	1.50	2.47
	413966	AA133935	Hs.173704	ESTs, Moderately similar to A53959 throm	1.59	2.99
	414217	A1309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	1.59	2.82
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	1,57	2.64
65	432647	AI807481	Hs.278581	fibroblast growth factor receptor 2 (bac junction plakoglobin	1,56 1,56	2.74 2.97
	429002 430171	AW248439 AF086289	Hs.2340 Hs.234766	skin-specific protein	1.54	2.18
	422717		Hs.119475	cold inducible RNA-binding protein	1.51	2.19
	414323			KIAA0273 gene product	1.51	3.73
70	423184		8 Hs.1624	ephrin-A1	1.50	2.18
	433101		Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	1.50	2.00
	424362		Me 4E0025	Homo sapiens mRNA; cDNA DKFZp586F0824 (f RAB25 RAB25, member RAS oncogene family	1.48 1.46	2.04 2.83
	433662 445431		Hs.150826 Hs.12701	plasmotipin	1.46	2.00
75	456906		Hs.156637	Cas-Br-M (murine) ectropic retroviral tr	1.44	2.04
,,	442599		Hs.324051	RelA-associated inhibitor	1.42	3.50
	445656	W22050	Hs.21299	ESTs. Weakly similar to AF151840 1 CGI-8	1.42	2.53
	444672		Hs.11669	taminin, alpha 5	1.40	2.36
80	447990	BE048821	Hs.20144	small inducible cytokine subfamily A (Cy Integrin, bela 4	1.40 1.39	2.29 2.86
٥0	418462 453023			serine protease inhibitor, Kunitz type,	1.38	2.28
	416340		Hs.79226	fasciculation and elongation protein zet	1.38	2.24
	433417			Homo sapiens, Similar to RIKEN cDNA 5830	1.38	2.14
				507		

					4 00	0.24	
	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	1.36	2.34	
	432894	AW167668	Hs.279772	brain specific protein	1.36	5.09	
	439733	AL365412	Hs.107203	hypothetical protein from EUROIMAGE 1759	1.36	2.00	
_	454478	AW805749		superoxide dismutase 2, mitochondrial	1.35	2.85	
5	423515	AA327017	Hs.176594	ESTs	1.35	2.45	
-	436663	AW410458	Hs.5258	chromosome 11 open reading frame2	1.35	2.07	
	404246			Target Exon	1.34	2.96	
	411939	A1365585	Hs. 146246	ESTs	1.33	2.31	
	409178	BE393948	Hs.50915	kallikrein 5	1.33	2.03	
10	427795	BE268268	Hs.180842	ribosomal protein L13	1.33	2.29	
10					1.32	2.78	
	447299	AF043897	Hs.18075	chromosome 9 open reading frame 3	1.32	3.37	
	447330	BE279949	Hs.18141	ladinin 1	1.31	2.71	
	433399	N46406	Hs.84700	similar to phosphatidylcholine transfer			
1.5	403986			Target Exch	1.31	2.09	
15	407597	AA043925	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	1.30	2.28	
	450796	NM_001988	Hs.25482	envoplakin	1.30	3.45	
	415550	L13720	Hs.78501	growth arrest-specific 6	1.29	2.76	
	415512	Y16270	Hs.78482	paralemmin	1.26	2.49	
	430513	AJ012008	Hs.241586	G6C protein	1.26	3.07	
20	422581	NM_016339	Hs.118562	Link guarrine nucleotide exchange factor	1.23	2.04	
	420048	AW206824	Hs.25766	ESTs	1.23	2.01	
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	1.23	2.22	
	430560	Z28942	Hs.243960	N-myc downstream-regulated gene 2	1.23	2.42	
	426377	AK001921	Hs.169575	hypothetical protein MGC2550	1.23	2.20	
25	402218	AWOISEI	115.103313	NM_022165":Homo sapiens Lin-7b protein (1.23	2.01	
23		A14004670	Un OCAE	Homo sapiens mRNA for KIAA1741 protein,	1.18	2.24	
	413944	AW001579	Hs.9645		1.16	2.16	
	414186	U33446	Hs.75799	protease, serine, 8 (prostasin)			
	426068	AF029778	Hs.166154	jagged 2	1.15	2.07	
20	431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	1.14	2.33	
30	411388	X72925	Hs.69752	desmocollin 1	1.00	2.61	
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	1.00	2.63	
	TABLE 63	3B:					
	Pkey:	Unio	que Eos probeset ide	ntifier number			
35	CAT num		e cluster number				
	Accession	n: Gen	bank accession num	bers			
	Pkey	CAT Number	Accession				
	412636	1438_1	M77830 NM 004	415 AF139065 RG6R1115 RG740377 RI712964 RG000	1656 AA128476	D BI438324 H27408 BE931630 BE167165 AW370827 AW37	0813
40	412000	1400_1	105211 RC69886	5 BG740734 BG680618 BG739778 BI765807 BM3534	03 DE 1353310	AW1777RA AW2057R9 AW951576 AWR48592 RF 182164	
70							
			DE140300 DE040	107 PINCOAAE DINCOAAA DE360093 DE720006 DE7200	UJ BMJ3J240 160 BE71515A	BE082584 BE082576 BE004047 AAR57316 BI039774 BE71	3818
			BF149266 8E940	1187 B1060445 B1060444 BF350983 BE720095 BE7200	369 BE715154	BE082584 BE082576 BE004047 AA857316 BI039774 BE71	3818
			BF149266 BE940 BE713548 AW17	1187 B1060445 B1060444 BF350983 BE720095 BE7200 0253 BE160433 B1039775 AW886475 BM462504 BE9	369 BE715154 31734 BF1492	BE082584 BE082576 BE004047 AAB57316 BI039774 BE71 64 AA340777 BF381183 BG621737 AU127260 AW364859	
			BF149266 BE940 BE713548 AW17 BF993352 BG223	1187 B1060445 B1060444 BF350983 BE720095 BE720 0253 BE160433 B1039775 AW886475 BM462504 BE9 3489 BE819009 BF381184 BE715956 R58704 AA8522	069 BE715154 31734 BF1492 112 AW366566	BE082584 BE082576 BE004047 AAB57316 BI039774 BE71 64 AA340777 BF381183 BG621737 AU127260 AW364859 BI090358 BF087707 BE819046 BE819005 AA377127 BE01	3467
			BF149266 BE940 BE713548 AW17 BF993352 BG223 BE819069 BE819	1187 B1060445 B1060444 BF350983 BE720095 BE7200 0253 BE160433 B1039775 AW886475 BM462504 BE3- 4889 BE819009 BF381184 BE715956 R58704 AA8522 3048 B1036306 BG390973 B1040954 BF919911 AU140	069 BE715154 31734 BF1492 112 AW366566 1155 AI951766	BE082584 BE082576 BE004047 AAB57316 BI039774 BE7 64 AA340777 BF381163 BG621737 AU127260 AW364859 B0990358 BF087707 BE819048 BE819005 AA377127 BE0 A1434518 AW804674 BF752969 BE837009 BE925826 BF14	3467
45			BF149266 8E940 BE713548 AW17 BF993352 BG223 BE819069 BE819 AW995615 BE81	1187 B1060445 B1060444 BF350983 BE720095 BE720 0253 BE160433 B1039775 AW886475 B1462504 BE9 3489 BE819009 BF381184 BE715956 R58704 AAS22 1048 B1036306 BG990973 B1040954 BF919911 AU140 4264 B1039782 AU140407 BE144243 BE709863 BF98	369 BE715154 31734 BF1492 112 AW366566 1155 AI951766 15642 BE00192	BE082584 BE082576 BE004047 AAS57316 B1039774 BE71 64 AA340777 BF381183 BG621737 AU127260 AW364859 B0090358 BF087707 BE819046 BE819005 AA377127 BE01 A4434518 AW804674 BF752369 BE837009 BE925826 BF14 23 BF933510 AW265328 BG436319 BE182166 AW365175	3467
45			BF149266 8E940 BE713548 AW17 BF993352 BG223 BE819069 BE819 AW995615 BE81 AW847688 BE81	1187 BIOGO445 BIOGO444 BF350983 BE720095 BE7200 0253 BE160433 BI039775 AW886475 BM462504 BE9 1489 BE819009 BF381184 BE715956 F58704 AAB522 9048 BI036306 BG990973 BID40954 BF919911 AU140 4264 BI039782 AU140407 BE144243 BE709863 BF9 8280 AW177933 BF873679 AW178000 BE082526 BF	369 BE715154 31734 BF1492 112 AW366566 1155 AI951766 15642 BE00192 476866 BF086	BE082584 BE082576 BE004047 AAS57316 BI039774 BE7164 AA340777 BF381183 BG621737 AU127260 AW364859 BI090358 BF087707 BE819046 BE819005 AA377127 BE01 AI434518 AW804674 BF752969 BE837009 BE925826 BF14 33 BF933510 AW265328 BG436319 BE182166 AW365175 994 BF592276 BE082507 BE082514 BE082505 BF873693	3467
45			BF149266 8E940 BE713548 AW17 BF993352 BG223 BE819069 BE819 AW995615 BE81 AW847688 BE81 AW068840 AW84	1187 B1060445 B1060444 BF350933 BE720095 BE7200 9489 BE819009 BF381184 BE715956 F58704 AA85250 9489 BE819009 BF381184 BE715956 F58704 AA85250 9488 B1039506 BG990973 B1040954 BF919911 AU140 4264 B1039782 AU140407 BE144243 BE709863 BF98 8280 AW177933 BF873679 AW178000 BE082526 BF- 17678 BF804153 AW385157 BE813330 BE002030 AW	369 BE715154 31734 BF1492 112 AW366566 1155 A1951766 15642 BE00192 476866 BF086 7365153 BE184	BE082584 BE082576 BE004047 AAS57316 BI039774 BE7164 AA340777 BF381183 BE621737 AU127260 AW364859 BI090358 BF087707 BE619046 BE819005 AA377127 BE01 AI434518 AW804674 BF752969 BE837009 BE925826 BF1423 BF933510 AW265328 BG436319 BE182165 AW365175 B994 BF592276 BE082507 BE082514 BE082505 BF873693 1941 BF749421 BE184520 BF839562 BE184933 BF842254	73467 19265
45			BF149266 BE940 BE713548 AW17 BF993352 BG223 BE819069 BE819 AW995615 BE81 AW847688 BE81 AW68840 AW84 BE698470 BE93	1187 B1060445 B1060444 BF350983 BE720095 BE7200 0253 BE160433 B1039775 AW886475 BM462504 BE9, 3489 BE819009 BF381184 BE715956 R58704 AAS22, 2048 B1035006 BG990973 B1040954 BF919911 AU140 4264 B1039782 AU140407 BE144243 BE709863 BF98 8280 AW177933 BF873679 AW178000 BE082526 BF- 17678 BF804153 AW365157 BE813930 BE002030 AW 1048 BF999889 B7368816 BE184924 BE159646 BE7	269 BE715154 31734 BF1492 212 AW366566 1155 Al951766 15642 BE00192 476866 BF086 1365153 BE184 14632 BE18494	BE082584 BE082576 BE004047 AAS57316 BI039774 BE7164 AA340777 BF381183 BE621737 AU127260 AW364859 BI090358 BF087707 BE819046 BE81905 AA377127 BE01 AI434518 AW804674 BF752969 BE837009 BE925826 BF1423 BF933510 AW265328 BG436319 BE182166 AW365175 9944 BF592276 BE082507 BE082514 BE08250 BF873693 1941 BF749421 BE184920 BF839562 BE184933 BF642254 BB05986845 AA151128 AA099891 W39488 C04715 BF096	73467 19265
			BF149266 8E940 BE713548 AW17 BF993352 BG223 BE819069 BE815 AW995615 BE81 AW068840 AW84 BE698470 BE93 BE865341 AW79	1187 BIOGO445 BIOGO444 BF-35093 BE720095 BE7200 0253 BE160433 BI039775 AW886475 BM462504 BE9 1489 BE819009 BF-381184 BE715956 FS8704 AAB529 048 BE036306 BG990973 BIO40954 BF919911 AU140 4264 BI039782 AU140407 BE144243 BE709863 BF98 8280 AW177933 BF873679 AW178000 BE082526 BF- 17678 BF804153 AW355157 BE813930 BE002303 AW1048 BF99889 BF368816 BE184924 BE159646 BE71 9304 ALBO3116 BE149760 BE705967 BE705966 BE7	269 BE715154 31734 BF1492 212 AW366566 1155 Al951766 15642 BE00192 476866 BF086 1365153 BE184 14632 BE18494 05968 AW8487	BE082584 BE082576 BE004047 AAS57316 BI039774 BE74 64 AA340777 BF381183 BG621737 AU127260 AW364859 BI090358 BF087707 BEB19046 BE819005 AA377127 BE01 AI434518 AW804674 BF752969 BE837009 BE925826 BF1 38 BF933510 AW265328 BG436319 BE182166 AW365175 994 BF592276 BE082507 BE082514 BE082505 BF873693 I941 BF749421 BE184920 BF83962 BE184933 BF842254 I88 BG986845 AA131128 AA099891 W39488 C04716 BF02723 AW376699 AW376817 AW376697 BC005097 BF75111	73467 19265 1124
45			BF149266 BE940 BE713548 AW177 BF993352 BE819069 BE819 AW995615 BE81 AW847688 BE81 AW068840 AW84 BE698470 BE985341 AW79 BE669084 AW84	1187 BIGG0445 BIGG0444 BF-350983 BE720095 BE7200 9189 BE60433 BI039775 AW886475 BM462504 BE9 91489 BE819009 BF-381184 BE715956 FS8704 AA8522 9048 BI036306 BG990973 BI040954 BF919911 AU140 4264 BI039782 AU140407 BE144243 BE709865 BF98 8280 AW177933 BF873879 AW178000 BE082526 BF- 17678 BF804153 AW385157 BE813330 BE002030 AW 1048 BF999889 BF368816 BE184924 BE159646 BE7 19304 ALBO3116 BE149760 BE705967 BE705966 BE7 18371 AW376782 AW848789 AW849074 AW381413 B	069 BE715154 31734 BF1492 112 AW366566 1155 AI951766 15642 BE00192 476866 BF086 476856 BF184 4632 BE1849 05968 AW8487 F927725 BF09	BE082584 BE082576 BE004047 AAS57316 BI039774 BE7164 AA340777 BF381183 BG621737 AU127260 AW364859 BI090358 BF087707 BE819046 BE819005 AA377127 BE01 A434518 AW804674 BF752969 BE837009 BE925826 BF143 BF933510 AW265328 BG436319 BE182166 AW365175 B994 BF592756 BE082507 BE082514 BE082505 BF873693 1941 BF749421 BE184920 BF839562 BE184933 BF842254 BB6986845 AA131128 AA099891 W39488 C04715 BF09673 AW376699 AW376817 AW376697 BG005097 BF75113 4211 AW997139 BE885474 BE185187 BE156621 BF75113 4211 AW997139 BE885474 BE185187 BE156621 BF75108	73467 19265 1124
			BF149266 BE940 BE713548 AW177 BF993352 BG223 BE819069 BE819 AW995615 BE81 AW06840 AW8- BE698470 BE93 BE865341 AW79 BE696084 AW8- BE713297 BE71	1187 BIOGO445 BIOGO444 BF-360983 BE720095 BE7200 0253 BE160433 BIO39775 AW885475 BM462504 BE9. 0253 BE160433 BIO39775 AW885475 BM462504 BE9. 0348 BIO36306 BG990973 BIO40954 BF919911 AU140 4264 BIO39702 AU140407 BE144243 BE793653 BF88 0260 AW177933 BF873679 AW178000 BE082526 BF- 17678 BF804153 AW365157 BE13930 BE002030 AW 1048 BF999898 BF368816 BE184924 BE159646 BE71 9304 AL603116 BE149760 BE705967 BE705966 BE7 0371 AW375782 AW848789 AW89074 AW381413 BI 02598 BE179915 AW799309 BF872345 BF088676 BE7	269 BE715154 31734 BF1492 112 AW366566 1155 AI951766 15642 BE00192 476656 BF086 4632 BE1849- 4632 BE1849- 59568 AW648 F927725 BF09	BE082584 BE082576 BE004047 AA557316 BI039774 BE7: 46 AA340777 BE381183 BE6621373 AU127260 AW364859 BI090358 BF087707 BE819046 BE819005 AA377127 BE0; A434518 AW804674 BF752969 BE837009 BE252826 BF1: 38 BF933510 AW265328 B62436319 BE182166 AW365175 994 BF592276 BE082507 BE082514 BE082505 BF873693 1941 BF749421 BE184920 BF83962 BE189333 BF842254 BB 6936845 AA131128 AA099991 W39488 C04715 BF096 723 AW376699 AW376817 AW376697 BC005097 BF75111 4211 AW997139 BE685474 BE185187 BE156621 BE71508 998 BG005197 BF350088 BE715196 BE715155 BF752396	73467 19265 1124
			BF149266 BE940 BE713548 AW171 BF993352 BG223 BE819069 BE815 AW995615 BE81 AW947688 BE81 AW668840 AW84 BE696084 AW79 BE696084 AW79 BE713297 BE713	1187 BIOGO445 BIOGO444 BF-35093 BE720095 BE7200 0253 BE160433 BI039775 AW886475 BM462504 BE9 1489 BE819009 BF-381184 BE715956 FS8704 AAB529 1648 BIO36306 BG990973 BI040954 BF919911 AU140 14264 BI039782 AU140407 BE144243 BE709863 BF98 14264 BI039782 AU140407 BE144243 BE709863 BF98 14280 AW177933 BF873679 AW178000 BE082526 BF- 147678 BF804153 AW355157 BE813930 BE002030 AW- 1048 BF999889 BF368816 BE184924 BE159646 BE71 19304 ALBO3116 BE149760 BE705967 BE705966 BE7- 18371 AW376782 AW848789 AW84974 AW36143 BI 1298 BE179915 AW799309 BF872345 BF088676 BE7- 1199 BF752409 BE006561 BG959922 BF094833 BF08	069 BE715154 31734 BF1492 112 AW366566 1155 AI951766 15642 BE00192 476866 BF086 1365153 BE184 4632 BE1849- 05968 AW8487 15927725 BF09 05939 AW7522 14748 BF09456	BE082584 BE082576 BE004047 AAS57316 BI039774 BE74 64 AA340777 BF381183 BG621737 AU127260 AW364859 B090358 BF087707 BEB19046 BE819005 AA377127 BE01 A434518 AW804674 BF752969 BE837009 BE925826 BF14 38 BF933510 AW265328 BG436319 BE182166 AW365175 994 BF592276 BE082507 BE082514 BE082505 BF873693 1941 BF749421 BE184920 BF83962 BE184933 BF842254 188 BG986845 AA131128 AA099891 W39488 C04715 BF5076 723 AW376599 AW376817 AW376697 BC005097 BF75111 4211 AW997139 BE865474 BE185187 BE15662 1BE71508 599 BG005197 BF350086 BE715196 BE715155 BF752396 133 AW377699 AW507238 BE082519 AW377700 BF349467	73467 19265 1124 5
			BF149266 BE940 BE713548 AW171 BF993352 BG223 BE819069 BE815 AW995615 BE81 AW947688 BE81 AW668840 AW84 BE696084 AW79 BE696084 AW79 BE713297 BE713	1187 BIOGO445 BIOGO444 BF-35093 BE720095 BE7200 0253 BE160433 BI039775 AW886475 BM462504 BE9 1489 BE819009 BF-381184 BE715956 FS8704 AAB529 1648 BIO36306 BG990973 BI040954 BF919911 AU140 14264 BI039782 AU140407 BE144243 BE709863 BF98 14264 BI039782 AU140407 BE144243 BE709863 BF98 14280 AW177933 BF873679 AW178000 BE082526 BF- 147678 BF804153 AW355157 BE813930 BE002030 AW- 1048 BF999889 BF368816 BE184924 BE159646 BE71 19304 ALBO3116 BE149760 BE705967 BE705966 BE7- 18371 AW376782 AW848789 AW84974 AW36143 BI 1298 BE179915 AW799309 BF872345 BF088676 BE7- 1199 BF752409 BE006561 BG959922 BF094833 BF08	069 BE715154 31734 BF1492 112 AW366566 1155 AI951766 15642 BE00192 476866 BF086 1365153 BE184 4632 BE1849- 05968 AW8487 15927725 BF09 05939 AW7522 14748 BF09456	BE082584 BE082576 BE004047 AAS57316 BI039774 BE74 64 AA340777 BF381183 BG621737 AU127260 AW364859 B090358 BF087707 BEB19046 BE819005 AA377127 BE01 A434518 AW804674 BF752969 BE837009 BE925826 BF14 38 BF933510 AW265328 BG436319 BE182166 AW365175 994 BF592276 BE082507 BE082514 BE082505 BF873693 1941 BF749421 BE184920 BF83962 BE184933 BF842254 188 BG986845 AA131128 AA099891 W39488 C04715 BF5076 723 AW376599 AW376817 AW376697 BC005097 BF75111 4211 AW997139 BE865474 BE185187 BE15662 1BE71508 599 BG005197 BF350086 BE715196 BE715155 BF752396 133 AW377699 AW507238 BE082519 AW377700 BF349467	73467 19265 1124 5
50			BF149266 BE940 BE713548 AW17 BF993352 BG222 BE819069 BE819 AW995615 BE81 AW068840 AW84 BE698470 BE931 BE865341 AW79 BE696084 AW784 BE713297 BE71 BF93817 BF81 BF993817 BF81	1187 BIOGOA45 BIOGOA44 BF-35093 BE720095 BE7200 0253 BE160433 BI039775 AW886475 BM462504 BE9 1489 BE819009 BF-381184 BE715956 FLS8704 AAB522 048 BI036306 BG990973 BI040954 BF919911 AU140 4264 BI039782 AU140407 BE144243 BE709865 BF98 2280 AW177333 BF873875 AW178009 BE082526 BF7 17678 BF804153 AW365157 BE813930 BE002030 AW 1048 BF993899 BF368816 BE184924 BE159646 BE71 9304 AL603116 BE149760 BE705967 BE705966 BE7 18371 AW376782 AW848789 AWB49074 AW361413 BI 1298 BE179915 AW99309 BF872345 BF088676 BE7 1190 BF752409 BE006561 BG959922 BF0948673 BF0 103 A392926 AU158477 BI467252 AU159919 A176081	269 BE715154 21734 BF1492 112 AW366566 1155 AI951766 15642 BE00192 476866 BF086 7365153 BE184 4632 BE18494 55968 AW848 F927725 BF09 15939 AW752 14748 BF09456 16 BF082516 A	BE082584 BE082576 BE004047 AAS57316 BI039774 BE7164 AA340777 BF381183 BG621737 AU127260 AW364859 BI090358 BF087707 BE819046 BE819005 AA377127 BE07 AL434518 AW804674 BF752969 BE837009 BE925826 BF143 BF933510 AW265328 BC436319 BE182166 AW365175 B948 BF592276 BE082507 BE082514 BE082505 BF873693 I941 BF749421 BE184920 BF839562 BE184933 BF842254 I8 BC986845 AA131128 AA059891 W39488 C04715 BF096 BF33 AW376697 AW376697 B005097 BF751115 4211 AW997139 BE865474 BE185187 BE156621 BE71508 599 BG005197 BF350086 BE715196 BE715155 BF752396 I3 AW377699 AW507238 BE082519 AW377700 BF349467 IA39101 AA451922 AJ340326 AJ590375 B1791553 Al700953	73467 19265 1124 5
50			BF149266 BE940 BE713548 AW17 BF993352 BG22: BE819069 BE815 AW995615 BE81 AW066840 AW84 BE698470 BE93 BE865341 AW79 BE696084 AW84 BE713297 BE71: BF093817 BF831 AI190590 AIS94 AI142882 AA039	1187 BIOGO445 BIOGO444 BF-360983 BE720095 BE7200 0253 BE160433 BIO39775 AW885475 BM462504 BE9 0253 BE160433 BIO39775 AW885475 BM462504 BE9 0348 BE819009 BF-381184 BE715956 FR8704 AA8529 0348 BIO36306 BG990973 BIO40954 BF919911 AU140 4264 BIO39782 AU140407 BE144243 BE70963 BF98 0280 AW177933 BF873679 AW178000 BE0082506 BF1 17678 BF804153 AW365157 BE813930 BE002030 AW 1048 BF993898 BF368816 BE184924 BE159646 BE71 19304 AL603116 BE149760 BE705967 BE705966 BE7 18371 AW376782 AW848789 AW849074 AW361413 BI 12289 BE179915 AW799399 BF872345 BF088676 BE7 1190 BF752409 BE006561 BG959922 BF084833 BF09 101 BR392926 AU158477 BI467252 AU159919 AT6081 1975 AA946935 AA644381 BM314884 AA702424 AM11	369 BE715154 31734 BF1492 112 AW36566 1155 AI951766 15642 BE00192 476866 BF086 1365153 BE1B4 4632 BE1849- 05968 AW848 F927725 BF09 05939 AW752: 14748 BF09456 6 BF082516 A 7612 AW19055	BE082584 BE082576 BE004047 AA557316 BI039774 BE7: 46 AA340777 BE381183 BE621373 AU127260 AW364859 BI090358 BF087707 BE819046 BE819005 AA377127 BE0; AI434518 AW804674 BF7572969 BE837009 BE252826 BF1; 38 BF933510 AW265328 B6243619 BE182166 AW365175 994 BF592276 BE082507 BE082514 BE082505 BF873693 1941 BF749421 BE184200 BF83962 BE184933 BF842234 B8 G936845 AA131128 AA099891 W39488 C04715 BF096 723 AW376699 AW376817 AW376697 BC005097 BF75111; 4211 AW997139 BE6825474 BE185187 BE156621 BE71508 99 BC005197 BF350086 BE715196 BE715155 BF752396 13 AW377699 AW607238 BE082519 AW377700 BF349467 1439101 AA451923 AI340326 AI590975 B1791553 AI70963 15 AI220573 AI304772 AI270345 AI6273383 AA552300 A991	73467 49265 1124 5 9
			BF149266 BE940 BE713548 AW17 BF993352 BG22: BE819069 BE813 AW995615 BE81 AW068840 AW8- BE698470 BE93: BE865341 AW79 BE6960B4 AW84 BE713297 BE713 BF093817 BE713 A1190590 AI5544 AI142882 AN094 AI142882 AN094 AI146807 AI34	1187 BIOGO445 BIOGO444 BF-360983 BE720095 BE7200 0253 BE160433 BIO39775 AW886475 BM462504 BE9 1489 BE819009 BF-381184 BE715956 FS8704 AAB529 1489 BE819009 BF-381184 BE715956 FS8704 AAB529 14648 BIO36306 BG990973 BIO40954 BF919911 AU140 14624 BIO36306 BG990973 BIO40954 BF919911 AU140 14624 BIO39782 AU140407 BE144243 BE709863 BF98 147678 BF804153 AW355157 BE813930 BE002030 AW 1048 BF999889 BF368816 BE184924 BE159646 BE71 19304 ALBO3116 BE149760 BE705967 BE705966 BE77 18371 AW376782 AW848789 AW84978 AW561413 BI 2398 BE179915 AW799309 BF872345 BF088676 BE71 1190 BF752409 BE006561 BG959922 BF094833 BF08 103 AJ392926 AU158477 B1467252 AU159919 AJ76081 1903 AJ392926 AU158477 B1467252 AU159919 AJ76081 1907 BYS0700 AA149191 AA026864 AI8300049 AW7801	369 BE715154 31734 BF1492 112 AW36566 1155 AI951766 155642 BE00192 476866 BF086 1365153 BE184 14632 BE18494 15968 AW848 1F927725 BF09 15939 AW752 14748 BF09456 16 BF082516 AW19055 14315 AU718449 14315 AU718449	BE082584 BE082576 BE004047 AAS57316 BI039774 BE7. 40 AA340777 BF381183 BG621737 AU127260 AW364859 BI090358 BF087707 BEB19046 BE819005 AA377127 BE01 AI434518 AW804674 BF752269 BE837009 BE925826 BF1 AI434518 AW804674 BF752269 BE837009 BE925826 BF1 38 BF933510 AW265328 BG436319 BE182166 AW365175 994 BF592276 BE082507 BE082514 BE082505 BF873693 I941 BF749421 BE184920 BF83962 BE184933 BF842254 I88 BG986845 AA131128 AA099891 W39488 C04715 BF75296 P23 AW376599 AW376817 AW376697 BC005097 BF75111 4211 AW997139 BE865474 BE185187 BE15621 BE71508 E99 BG005197 BF350086 BE715196 BE715155 BF752396 E30 AW377699 AW507238 BE082519 AW377700 BF349467 IA39101 AA451923 AJ340326 AJ590975 BI791553 AJ700963 E3 AU275739 AW507238 BE082519 AW377700 BF349467 IA39101 AA451923 AJ340326 AJ590975 BI791553 AJ700963 E5 AU220573 AJ304772 AJ270345 AJ627383 AA552300 AJ911 INS B19984 AJ858282 BI466588 AJ860584 AJ025932 AA02604	73467 19265 1124 5 9 702 7
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A081626 AA370719 AA	73467 19265 1124 5 9 9 3 7702 7 7 52 2 7 7 52 104327 104647
50 55 60 65 70 75	456034 432222 459702 444726 444105 455797	685586_1 539529_1 539529_1 3503_2 649788_1 1511159_1	BF 149266 BE940 BF 713548 AW17 BF993352 BG222 BE819069 BE813 AW995615 BE81 AW968840 AW84 BE698470 BE931 BE698470 BE931 BE69808A AW84 BF713297 BE713 BF093817 BF831 A190590 A15544 A1142882 AA039 AW166807 AI34 AA703222 AA653 AA065527 AA78 BG881425 BE70 AW7999118 BF00 AW7999118 BF00 BG984933 BE71 BE001925 AW38 BG940189 AW066468 BG949330 BE71 BE001925 AW38 BG207209 BE16 BG225209 BE16 BG225209 BE16 BG225209 BE16 BG225209 BE16 BG235209 BE16 BG24549405 AW64 AW849405 AW64 AW849405 AW84 AW189097 AI12 BE091833 BE00 BE091833 BE00 AA358674 AI13 AA258674 AI13 AA2787270 AW54	1187 BIOGOA4S BIOGOA44 BF-360983 BE720095 BE7200 0253 BE160433 BIO39775 AW886475 BM462504 BE9 2489 BE819009 BF-381184 BE715956 R58704 AAB52 25048 BIO36306 BG990973 BIO40954 BF919911 AU140 2464 BIO36306 BG990973 BIO40954 BF919911 AU140 2464 BIO36306 BG990973 BIO40954 BF919911 AU140 2464 BIO36306 BG990973 BIO40954 BF919911 AU140 24654 BIO39782 AU140407 BE144243 BE709863 BF98 2828 AW177933 BF873679 AW178000 BE082525 BF1 267678 BF804153 AW355157 BE813930 BE002030 AW 1048 BF999889 BF368816 BE184924 BE159646 BE71 9304 ALBO3116 BE149760 BE705967 BE705966 BE71 2371 AW376782 AW848789 AW84974 AW361413 BI 2398 BE179915 AW799309 BF872345 BF088676 BE71 21190 BF752409 BE006551 BG959922 BF094833 BF09 203 AJ392926 AU158477 B1467252 AU159919 AJ76081 2075 AA946936 AA644381 BM314884 AA702424 Ak11 25078 W95070 AA149191 AA026864 AI830049 AW780 2109 W19287 W02155 AW150038 AA022701 T87181 26078 R29904 BG680059 BG676647 BF764409 AA026 27996 BE002273 AW879451 AJ571075 BE067768 AV7 28392 AJ915556 AW105614 AI887258 AI53857 BE9264 27978 BE185750 BE714064 BE713903 BE713868 BE7 25972 BF927780 AW853812 BE925515 BG577012 BG7 27834 BI040941 AA337270 AW384371 AW847442 BI0 24441 AW996245 BE71801 AJ284090 BE064323 BE7 2573 BE872225 AW391912 BE925515 BG677012 BG7 263489 AA715980 BF001091 BF880066 AA666102 AM 26529 AI204995 BG193355 AW969908 AA528756 AW 265299 AI204995 BG193355 AW969908 AA528756 AW 26529 AI204995 BG193355 AW969908 AA528756 AW 26529 AI204995 BG193355 AW969908 AA528756 AW 26529 AI204995 BG193355 AW969908 AA528756 AW 26529 AI204995 BG193355 AW969908 AA528756 AW 26529 AI204995 BG193355 AW969908 AA528756 AW 26529 AI204995 BG193355 AW969908 AA528756 AW 26529 AI204995 BG193355 AW969908 AA528756 AW 26529 AI204995 BG193355 AW969908 AA528756 AW 26529 AI204995 BG193355 AW969908 AA528756 AW 26529 AI204995 BG193355 AW969908 AA528756 AW 26529 AI204995 BG193355 AW969908 AA528756 AW 26529 AI204995 BG193355 AW969908 AA528756 AW 26529 AI204995 BG193356 AW66969 BG70708 BF0 274339 AA582788 AI345741 AW301433 AI873468 AW 28345 AF745097 W84430 AI304351 B	369 BE715154 31734 BF1492 112 AW366566 1155 AB51766 1155 AB51766 1155 AB51766 1155 AB51766 1155 AB51766 1155 AB51766 1155 AB51766 1155 AB51766 1155 AB51766 1155 AB51766 1155 AB51766 1155 AB5176 1156 AB5176 1156 AB5176 1156 AB5176 1156 AB5176 1156 AB5176 1156 AB5176 1156 AB5176 1156 AB5176 1156 AB5176 1156 AB5176 1156 AB5176 1156 AB5176 1156 AB5176 1156 AB5176 1156 AB5176 1156 AB5176 1156	BE082584 BE092576 BE004047 AA557316 BI039774 BE7: 40 AA340777 BE381183 BG621737 AU127260 AW364859 BI090358 BF087707 BE819046 BE819005 AA377127 BE01 A434518 AW804674 BF757269 BE837009 BE292826 BF14 38 BF933510 AW265328 BG436319 BE182166 AW365175 994 BF592276 BE082507 BE082514 BE082505 BF673693 1941 BF749421 BE184920 BF83962 BE184933 BF642254 BB G936864 SA A131128 AA099891 W39488 CO4715 BF076 723 AW376699 AW376817 AW376697 BG005097 BF751111 4211 AW997139 BE885474 BE185167 BE15651 BE71508 399 G0005197 BF350008 BE715196 BE715155 BF752396 33 AW377699 AW507238 BE082519 AW377700 BF349467 1439101 AA451923 AJ34072 AL7937345 AI627383 AA552300 A991 AB19294 AI658282 BE168588 AI860584 AI025932 AA02604 FF082491 AW021347 A1568096 BE933862 AA088866 D120 434 BF082513 AV94095 AIZ70027 AI635878 AA128330 B1762795 BG287391 AW798780 BE706045 BE926470 32 N29754 CO3378 N84767 AA131077 H30146 BE714290 BC319486 AA247658 AW798883 AW103521 BF989173 164 BE713810 AW365151 BG355489 BE005272 BF915937 164 BE713810 AW365151 BG355489 BE005272 BF915937 164 BE713810 AW365151 BG355489 BE005272 BF915937 164 BE713810 AW365151 BG355489 BE005272 BF915937 164 BE713810 AW365151 BG355489 BE005272 BF915937 164 BE713810 AW365151 BG355489 BE005272 BF915937 164 BE713810 AW365151 BG355489 BE005272 BF915937 164 BE713810 AW365151 BG355489 BE005272 BF915937 164 BE713810 AW365151 BG355489 BE005272 BF915937 164 BE713810 AW365151 BG355489 BE005272 BF915937 164 BE713810 AW365151 BG355489 BE005272 BF915937 164 BE713810 AW3651515 BG355489 BE005272 BF915937 164 BE713810 AW3651515 BG355489 BE005272 BF915937 164 BE713810 AW3651515 BG355489 BE005272 BF915937 164 BE713810 AW3651515 BG355489 BE005272 BF915937 164 BE713810 AW3651515 BG355489 BE005272 BF915937 164 BE713810 AW3651515 BG355489 BE005272 BF915937 164 BE713810 AW3651515 BG355489 BE005272 BF915937 164 BE713810 AW3651515 BG355489 BE005272 BF915937 164 BE713810 AW3651515 BG355489 BE005272 BF915937 164 BE713810 AW3651515 BG355489 BA077157 BE00300 BG681378 BE714290 1656 W35048 W25458 AW177785 AA025851 BE931733 BF1 168 B	73467 19265 1124 5 9 9 3 7702 7 7 52 2 7 7 52 104327 104647



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5	412446	63467 _1 (3E090279 BG6976 3C021735 Al66921 3F960659 AA9879 3E090026 BF9431	H10757 R10703 C01061 R27637 A827230 AW151953 60 AW877265 B1818938 BF528291 AW953624 R57461 2 Al 120184 A1769949 BC701002 BE 184363 BE819031 07 Z41449 BF908059 BF908053 BF908049 BC699424 B 58 A1632924 BF512340 BF952021 BF960776 BF943437	BF969694 BG702238 BF090049 BF9633 BF908060 BF962832 BF95202 BF942847 A1768015 F09778	018 BF961912 BF943013 AA934514 AA151245 0 BF963134 BK035538 BF908052 BF908057					
	424362	2318_7	4A617929 BF9470 AF284421 AL1376 A1 534638 T97116	01 B1035448 BE935876 AW890837 AW898604 BF95740 46 BG542551 AI278088 AI423919 AI274095 BE838965 AW855182 C02210 AI783480 AW024874	05 BF963433 8G704815 BE839174 BE839102 BF9245						
	454478	4273_16	AW796921 AW798	102 AW805749 AW805872 BF985060 AW794380 BF38	0449 AW794466 AW794538						
10	TABLE 63C										
	Pkey: Ref:	 Ey: Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <u>Nature</u> 402:489-495. 									
15	Strand: Indicates DNA strand from which exons were predicted. NL position: Indicates nucleotide positions of predicted exons.										
	Pkey 401781	Ref 7249190		position 15-83435,83531-83656,83740-83901,8423							
20	401780	7249190	Minus 283	97-28617,28920-29045,29135-29296,2941							
	401785	7249190		776-165996,166189-166314,166408-16656							
	402525 401760	9800048 9929699		48-20683 26-83250,85320-85540,94719-95287							
	402880	9926561		55-41865							
25	406387	9256180		229-116371,117512-117651							
	403828	9838214		55-32148 182-51521							
	401963 404246	3126783 7406725		62-51521 177-82628,82721-82817,82910-83071,8314							
	403986	8576059	Plus 908	92-91238							
30	402218	7689783	Ptus 127	² 677-127886							
35	Table 64A Eos/Affym	fists about 929 g etrix Hu03 Gene el of mRNA exp Uniqu Exern	penes downregulat chip array. Gene e ression. ne Eos probeset ide	GULATED IN PRIMARY MELANOMAS AND/OR MELAN ed in primary melanomas and/or melanoma melastases i expression data for each probeset obtained from this anal entifier number mber, Genbank accession number	relaine to normal skin. Genes	MGLB 2616C160 BOLD 23000 PLONESSIZ OU DIG					
40	Unigene T	Mor Union	ene gene title		and malanama matastas	ie Ale					
	R1 R2	90th	percentile of norma	al skin Als divided by the 90th percentile of primary melar al skin Als divided by the 90th percentile of primary melar	noma and melanoma melasias noma and melanoma melasias	is Als, where the 15th percentile of normal tissue					
	R2	Alsv	eas subtracted from	both the numerator and denominator							
45					RI	R2					
45	Pkey	ExAccn	UnigenelD Hs.99949	Unigene Title prolactin-induced protein	27.72	20.12					
	420813 408591	X51501 AF015224	Hs.46452	mammaglobin 1	26.40	24.26					
	431360	NM_000427	Hs.251680	toricrin	26,16	20.45					
60	401781			Target Exon	19.68 18.12	19.56 10.36					
50	412636	NM_004415	U= 20400C	desmoplakin (DPI, DPII) lipophilin B (uteroglobin family member)	16.61	18.06					
	429441 418067	AJ224172 Al127958	Hs.204096 Hs.83393	cystatin E/M	16.00	25.32					
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	15.64	11.81					
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	15.03	37.51 14.86					
55	401780	********	11- 113400	NM_005557":Homo sapiens keratin 16 (foca S100 calcium-binding protein A7 (psorias	14.20 13.95	28.08					
	422168 420783	AA586894 AI659838	Hs.112408 Hs.99923	tectin, galactoside-binding, soluble, 7	13.52	18.85					
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	13.14	13.81					
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	12.78	6.35					
60	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (ach	12.78 12.67	15.22 13.24					
	428824 453309	W23624 Al791809	Hs.173059 Hs.32949	ESTs defensin, beta 1	12.02	12.42					
	446227	AI281459	Hs.270114	ESTs	11.79	12.32					
	421948	L42583	Hs.334309	keratin 6A	11.58	9.02					
65	432877	AW974111	Hs.292477	ESTs	11.18 11.04	11.30 11.07					
	412047 407230	AA934589 AA157857	Hs.49696 Hs.182265	ESTs keratin 19	10.79	11.40					
	421296	NM_002666		perilipin	10.73	7.94					
	410001	AB041036	Hs.57771	kaflikrein 11	10.72	10.70					
70	418026	8E379727	Hs.83213	fatty acid binding protein 4, adipocyte	10.33 10.09	7.16 9.67					
	447966 401203	AA340605	Hs.105887	ESTs, Weakly similar to Hornolog of rat Z Target Exon	9.95	7.37					
	452308	AI167560	Hs.61297	ESTs	9.71	20.05					
	425580	L11144	Hs.1907	galanin	9.66	8.41					
75	433124	U51712	Hs.13775	hypothetical protein SMAP31	9.50	4.96 6.34					
	420919	M57892	Hs.100322	carbonic anhydrase VI	9.41 9.36	10.58					
	443162 427656		Hs.9029 Hs.180142	DKFZP434G032 protein calmodulin-like skin protein (CLSP)	9.19	11.73					
	431369		Hs.251754	secretory leukocyte protease inhibitor (8.85	17.76					
80	408536	AW381532	Hs.135188	ESTs	8.82	26.43					
	430686			desmoglein 1	8.73 8.69	6.58 6.81					
	436895		Hs.5338 Hs.41690	carbonic anhydrase XII desmocollin 3	8.61	9.15					
	418663	ANUU1100	F15.4 1030								
				589							



	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	8.51	13.13
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	8.44 8.39	9.61 5.13
	430130	AL137311	Hs.234074 Hs.163900	Homo sapiens mRNA; cDNA DKFZp761G02121 (ESTs	8.34	7.92
5	442577 437191	AA292998 NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	8.16	10.08
,	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	8.04	7.55
	413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	7.68	7.81
	452240	AJ591147	Hs.61232	ESTs	7.63	9.39
10	442757	A1739528	Hs.28345	ESTS	7.62 7.51	7.31 6.17
10	450680 456525	AF131784 AW468397	Hs.25318 Hs.100000	Homo sapiens clone 25194 mRNA sequence S100 calcium-binding protein A8 (calgran	7.49	7.12
	407328	AA508857	113.100000	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.35	7.20
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	7.16	8.39
	417240	N57568	Hs.48028	EST	7.13	15.05
15	410052	AA525225	Hs.334630	Homo sapiens cDNA FLJ14462 fis, clone MA	7.13 7.06	7.28 6.93
	431842	NM_005764	Hs.271473	epithelial protein up-regulated in carci alcohol dehydrogenase 1B (class I), beta	7.06 7.03	7.85
	426488 439394	X03350 AA149250	Hs.4 Hs.56105	ESTs	7.00	4.53
	422963	M79141	Hs.13234	ESTs	6.99	5.30
20	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	6.97	20.68
	410530	M25809	Hs.64173	ATPasa, H transporting, lysosomal (vacuo	6.96	7.04
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	6.96 6.94	6.68 6.68
	427890	AA435761	LL 20100E	ESTs Homo sapiens cDNA FLJ11346 fis, clone PL	6.84	8.44
25	432374 429624	W68815 AA458648	Hs.301885 Hs.99476	ESTs, Weakly similar to 1313184B alpha1	6.83	6.37
23	451029	AA852097	Hs.25829	ras-related protein	6.81	8.96
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	6.80	7.68
	439496	BE616501	Hs.32343	Horno sapiens, Similar to RIKEN cDNA 1110	6.77	14.06
20	431713	AK000388	Hs.267997	EHM2 gene	6.72 6.71	7.11 7.17
30	451253 414987	H48299 AA524394	Hs.26126 Hs.294022	ctaudin 10 hypothetical protein FLJ14950	6.67	11.68
	400304	AF005082	Hs.113261	Homo sapiens skin-specific protein (xp33	6.64	7.90
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	6.60	7.29
	424364	AW383226	Hs.163834	ESTs, Wealty similar to G01763 atrophin-	6.58	6.78
35	421773	W69233	Hs.112457	ESTs	6.55	17.59
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol	6.55 6.55	6.79 8.97
	411388	X72925	Hs.69752	desmocoliin 1 NM_002275":Homo sapiens keratin 15 (KRT1	6.51	9.94
	401785 406867	AA157857	Hs.182265	keratin 19	6.50	6.23
40	429504	X99133	Hs.204238	lipocafin 2 (oncogene 24p3) (NGAL)	6.43	6.79
	426106	AI678765	Hs.21812	ESTs	6.41	7.69
	413172	M38180	Hs.38586	hydroxy-delta-5-steroid dehydrogenase, 3	6.39	7.09
	407395	AF005082	U- 542405	gb:Homo sapiens skin-specific protein (x	6.39 6.36	7.71 9.23
45	422166 437176	W72424 AW176909	Hs.112405 Hs.42346	S100 calcium-binding protein A9 (calgran calcineurin-binding protein calsarcin-1	6.30	5.45
73	440383	AA884208	Hs.30484	ESTs	6.26	6.25
	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	6.22	10.13
	418686	Z36830	Hs.87268	annexin A8	6.19	6.14
50	440116	A1798851		hemoglobin, gamma G	6.18 6.19	4.28 6.91
50	424049	AB014524	Hs.138380 Hs.1076	KIAA0624 protein small proline-rich protein 1B (comifin)	6.18 6.17	7.42
	417366 432543	BE185289 AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	6.16	6.86
	414449	AA557660	Hs.76152	decorin	6.15	3.93
	441188	AW292830	Hs.255609	ESTs	6.12	6.68
55	424008	R02740	Hs. 137555	putative chemokine receptor; GTP-binding	6.12	5.33
	431319	AA873350	Hs.302232	ESTs ESTs	6.11 5.97	6.84 6.20
	444105 428358	AW189097 AA993222	Hs.101915	Stargardt disease 3 (autosomal dominant)	5.94	5.15
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	5.71	5.83
60	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	5.69	4.49
	428666	AL080190	Hs. 189242	Homo sapiens mRNA; cDNA DKFZp434A202 (fr	5.65	5.16
	410541	AA065003	Hs.64179	syntenin-2 protein	5.62 5.61	5.84 5.75
	431926		Hs.239483	gb:EST384816 MAGE resequences, MAGL Homo Human clone 23933 mRNA sequence	5.60	5.76
65	430332 444945		Hs.156457	hypothetical protein FLJ22408	5.53	9.25
05	430714		Hs.287601	Homo sapiens cDNA FLJ13830 fis, clone TH	5.48	5.38
	435538		Hs.4930	low density tipoprotein receptor-related	5.46	3.19
	414407		Hs.76704	ESTs	5.43	5.29
70	417035		Hs.22968	Homo sapiens done IMAGE:451939, mRNA se	5.40 5.40	5.40 3.87
70	442315 416931		Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z adipose most abundant gene transcript 1	5.39	9.12
	431048		Hs.80485 Hs.249129	cell death-inducing DFFA-like effector a	5.39	6.06
	436090		Hs.332879	EST	5.37	5.33
	411274	NM_00277	6 Hs.69423	kaltikrein 10	5.37	5.97
75	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	5.36	9.35
	406706		Hs.231581	myosin, heavy polypeptide 1, skeletal mu	5.34 5.32	4.08 10.40
	430171		Hs. 234766	skin-specific protein lg superfamily receptor LNIR	5.32 5.31	6.01
	452747 426451		Hs.61460 Hs.169946	GATA-binding protein 3 (T-cell receptor	5.31	3.81
80	414602			Homo sapiens mRNA; cDNA DKFZp564B1264 (f	5.26	5.92
	424399			AI905687:IL-BT095-190199-019 BT095 Homo	5.25	16.94
	430071	AA355986		transcription factor 8 (represses interl	5.20 5.18	5.01 6.38
	431416	AA532718	Hs.178604	ESTs	5.18	5.38
				600		

	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	5.17	5.72
	446082 430699	AI274139 AW969847	Hs.156452 Hs.292718	ESTS	5.16	5.14 4.97
	434525	W01370	Hs.46824	ESTs, Weakly similar to RET2_HUMAN RETIN ESTs	5.14 5.12	4.97 6.18
5	426101	AL049987		Homo sapiens mRNA; cDNA DKFZp564F112 (fr	5.11	3.79
	419648	T73661	Hs.91877	thyroid hormone responsive SPOT14 (rat)	5.08	13.64
	438962 419912	BE046594	Hs.6066	gb:hn41c11x1 NCI_CGAP_RDF2 Homo sapiens	5.08	4.09 4.77
	420583	AF249745 H77859	Hs.65450	Rho guanine nucleotide exchange factor (reticulon 4	5.08 5.06	4.77 5.56
10	432125	AW972667	Hs.183006	Homo sapiens cONA FLJ12300 fis, clone MA	5.05	6.32
	445263	H57646	Hs.42586	KIAA1560 protein	5.03	5.22
	407839	AA045144	Hs.161566	ESTS	5.03	5.27
	434293 427850	NM_004445 AA416756	Hs.3796 Hs.161051	Eph86 ESTs, Moderately similar to ALU6_HUMAN A	5.03 4.99	4.91 16.04
15	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	4.94	8.14
	445493	AI915771		metaflothionein 1E (functional)	4.93	4.33
	429365	AA451798	Hs.99249	ESTs	4.90	5.19
	412633 448490	AF001691 AJ523897	Hs.74304 Hs.271692	periptakin ESTs, Weakly similar to 138022 hypotheti	4.90 4.85	11.71 4.88
20	408491	A1088063	Hs.7882	ESTs	4.80	4.39
	430168	AW968343	Hs.145582	OKFZP43411735 protein	4.80	6.05
	407102	AA007629		glycerol-3-phosphate dehydrogenase 1 (so	4.78	7.23
	421998 422633	R74441 X56832	Hs.118804	poly(A)-binding protein, nuclear 1 enolase 3, (beta, muscle)	4.77 4.72	4.78 6.24
25	444930	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	4.71	3.72
	439652	W67826	Hs.55412	ESTs, Wealdy similar to K1CJ_HUMAN KERAT	4.70	3.60
	450626	AW190989	Hs.1508	insufin-degrading enzyme	4.68	5.14
	456898 408239	NM_001928 AA053401	Hs.155597	D component of complement (adipsin) ESTs, Moderately similar to ALU7_HUMAN A	4.68 4.67	15.83 6.17
30	415192	D17793	Hs.78183	aldo-keto reductase family 1, member C3	4.64	4.48
	443827	AI087867	Hs.134667	ESTs	4.63	5.06
	431441	U81961	Hs.2794	sodium channel, nonvollage-gated 1 alpha	4.63	8.48
	408741 427318	M73720 AF186081	Hs.646 Hs.175783	carboxypeptidase A3 (mast cell) zinc transporter	4.63 4.62	3.19 3.57
35	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	4.62	5.14
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	4.61	6.80
	437233	D81448	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	4.60	6.19
	446525 402294	AW967069	Hs.211556	hypothetical protein MGC5487 Target Exon	4.59 4.57	2.45 5.47
40	424098	AF077374	Hs.139322	small proline-rich protein 3	4.57	5.12
	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	4.57	4.76
	418021	M15881	Hs.1137	uromodulin (uromucoid, Tamm-Horstall gly	4.54	4.49
	422068 414798	AJ807519 AJ286323	Hs.104520 Hs.97411	Homo sepiens cDNA FLJ 13694 fis, clone PL hypothetical protein MGC12335	4.54 4.53	4.32 3.04
45	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein-2	4.53	2.91
	400109			Eos Control	4.52	3.94
	407242	M18728	11- 272022	gb:Human nonspecific crossreacting antig	4.51	4.07
	431901 435992	AW295050 AI033259	Hs.272023 Hs.118317	transforming, acidic coiled-coil contain Homo sapiens cDNA FLJ12088 fis, clone HE	4.50 4.50	4.16 4.77
50	447365	BE383676	Hs.334	Rho guanine nucleolide exchange factor (4.50	3.99
	449785	AI225235	Hs.288300	hypothetical protein FUJ23231	4.49	4.02
	424620	AA101043	Hs.151254	katlikrein 7 (chymotryptic, stratum com	4.47	5.43
	432559 459290	AW452948 NM_001546	Hs.257631 Hs.34853	ESTs inhibitor of DNA binding 4, dominant neg	4.47 4.45	3.10 3.17
55	422313	AF045941	Hs.115166	sciellin	4.45	5.07
	416305	AU076628	Hs.79187	coxsackie virus and adenovirus receptor	4.44	5.25
	432314 441633	AA533447 AW958544	Hs.312989 Hs.112242	ESTs	4.44 4.43	3.52 2.64
	424670	W61215	Hs.116651	normal mucosa of esophagus specific 1 epithelial V-like antigen 1	4.42	4.27
60	414489	AI620677	Hs.73105	ESTs	. 4.41	3.77
	413040	AA193338	Hs.12321	sodium calcium exchanger	4.36	4.58
	426974 448249	AB002298 AW855331	Hs.173035 Hs.337124	KIAA0300 protein ESTs	4.35 4.35	4.97 4.49
	451743	AW074266	Hs.23071	ESTs	4.34	4.52
65	427919	AA173942	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	4.33	3.94
	422305	AI928242	Hs.293438	ESTs, Highly similar to AF198488 1 trans	4.32	7.20
	408104 447945	AW972927 AI922838	Hs.293968 Hs.9670	ESTs ESTs, Wealdy similar to ALU1_HUMAN ALU S	4.31 4.30	3.53 3.72
	439349	A1660898	Hs.6834	ESTs	4.29	4.16
70	433339	AF019226	Hs.8036	glioblastoma overexpressed	4.29	3.94
	427074	AA527435	Hs.178589	hepatocellular carcinoma antigen gene 52	4.28	4.97
	453574	AJ767947	Hs.50841	ESTs	4.25	3.66
	410677 424833	NM_003278 NM_003894		tetranectin (plasminogen-binding protein period (Drosophila) homelog 2	4.25 4.22	17.64 3.13
75	426248		Hs.293668	ESTs 2	4.21	4.09
	410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	4.19	276
	406805	A1686003	Hs.296031	ESTs	4.19	3.87
	438533 451831	AJ440266 NM_001674	Hs.170673 Hs.460	ESTs, Wealdy similar to 124832 hypotheti activating transcription factor 3	4.18 4.18	5.93 4.74
80	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	4.17	2.83
	434936	AJ285970	Hs.183817	ESTs	4.17	4.39
	430361	AI033965	Hs.239926	sterol-C4-methyl oxidase-like	4.17	2.38
	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	4.16	5.15

	421978	AJ243662	Hs.110196	NICE-1 protein	4.15	8.07
	437135	AL038624	Hs.208752	ESTs, Wealthy similar to ALU8_HUMAN ALU S	4,14	4.92
	442554	AW467376	Hs.129640	ESTs	4.12	4.00
	451814	AA847992	Hs.137003	ESTs	4,11	4.58
5	410023	AB017169	Hs.57929	slit (Orosophila) hornolog 3	4,10	3.92
	457121	AI743770	Hs. 180513	ESTs, Weakly similar to KIAA0822 protein	4.09	3.19
	426539	AB011155	Hs.170290	discs, targe (Drosophila) homolog 5	4.09	3.69
	430191	A1149880	Hs.188809	ESTs	4.07	4.49
	430433	AA478883	Hs.273766	ESTs	4.07	3.74
10	425992	AA367069	Hs.100636	ESTs	4.06	4.37
	428931	AA994979	Hs.98967	ATPase, HQ-transporting, lysosomal, non	4.05	4.15
	452392	L20815	Hs.507	comeodesmosin	4.04	11.00
	402845	400.0		ENSP00000246267:KIAA0444 PROTEIN (FRAGME	4.03	4.18
	439873	BE159253	Hs.300638	ESTs	4.03	3.86
15	432305	M62402	Hs.274313	Insufin-like growth factor binding prote	4.02	8.79
	420789	A1670057	Hs.199882	ESTs	4.02	4.34
	453560	AA348626	Hs.5890	hypothetical protein FLJ23306	4.02	5.13
	428957	NM_003881	Hs.194679	WNT1 inducible signating pathway protein	4.01	4.29
	429556	AW139399	Hs.98988	ESTs	4.01	4.59
20	448585	AB020676	Hs.21543	KIAA0869 protein	4.01	4.52
20	403710	ABUZBOTG	113.21343		4.00	3.31
	423634	AW959908	Un 4500	C4000160:gi]12735793 ref)XP_011928.1 pr		6.61
	421485		Hs.1690	heparin-binding growth factor binding pr	3.98	
		AA243499	Hs.104800	hypothetical protein FLJ 10134	3.98	3.79
25	437611	AA897108	H- 170155	gb:am08a06.s1 Soares_NFL_T_GBC_S1 Home s	3.97	4.24
25	426500	NM_014638	Hs.170156	KIAA0450 gene product	3.96	4.93
	448710	T62926	Hs.304184	ESTs	3.96	4.54
	408199	AA132637	Hs.15396	Homo sapiens, clone IMAGE:3948909, mRNA,	3.95	5.57
	428340	AF261088	Hs.154721	aconitase 1, soluble	3.94	3.24
30	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	3.94	9.16
20	456972	AI054347	Hs.2017	ribosomal protein L38	3.93	4.37
	418381	AA682393	Hs.119237	ESTs	3.93	3.45
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	3.92	15.00
	456332	AA228357		gb:nc39d05.r1 NCI_CGAP_Pr2 Homo sapiens	3.91	4.88
25	445607	AA488107	Hs.30156	ESTs, Weakly similar to unnamed protein	3.91	3.19
35	426411	AK000708	Hs.169764	hypothetical protein FLJ20701	3.90	4.50
	446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega	3.90	3.89
	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	3.89	5.11
	452894	AI598065	Hs.61558	ESTs	3.88	3.73
40	430570	A417881	Hs.292464	ESTs	3.87	4.47
40	439625	AF086453	Hs.58611	ESTs	3.86	4.81
	418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (p	3.85	3.01
	431247	ALD21578	Hs.278489	matrilin 4	3.85	3.35
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	3.85	5.15
4-	441319	AI354869	Hs.133081	ESTs, Wealdy similar to T08700 hypotheti	3.84	5.03
45	452877	AI250789	Hs.32478	ESTs	3.84	3.26
	444252	R21135	Hs.54985	ESTs	3.83	5.58
	416265	AA177088	Hs.190065	ESTs	3.82	3.87
	418875	W19971	Hs.233459	ESTs	3.80	2.92
	440509	BE410132	Hs.134202	ESTs, Wealdy similar to T17279 hypotheti	3.80	4.36
50	442503	AF147078	Hs.150853	p53-responsive gene 5	3.80	7.53
	427081	AI474533	Hs.170528	ESTs, Moderately similar to ALUC_HUMAN!	3.77	4.81
	458222	AW139592		hypothetical protein DKFZp434K1421	3.77	3.56
	445107	Al208121	Hs.147313	ESTs, Wealdy similar to 138022 hypotheti	3.77	3.20
	435283	A1480319	Hs.120058	ESTs	3.76	3.76
55	436557	W15573	Hs.5027	ESTs, Wealdy similar to A47582 B-cell gr	3.76	2.65
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	3.75	7.59
	434206	AW136973		ESTs, Weakly similar to \$69890 mitogen i	3.72	3.96
	424824	AI217440	Hs.143873	ESTs	3.72	3.52
	457411	AW085961	Hs.130093	iroquois-class homeobox protein IRX2	3.71	3.05
60	452241	AL050204	Hs.28540	Homo sapiens mRNA; cDNA DKFZp586F1223 (f	3.70	4.84
	421845	AW021631	Hs.16515	ESTs	3.69	3.59
	413922	AI535895	Hs.221024	ESTs	3.68	4.22
	422746	NM_004484	Hs.119651	glypican 3	3.68	4.29
	433934	AW273261	Hs.216292	ESTs	3.68	4.39
65	452547	AA335295	Hs.74120	adipose specific 2	3.66	12.23
	400295	W72838		AI905687:1L-BT095-190199-019 BT095 Homo	3.66	9.25
	419098	AA234041	Hs.87271	ESTs	3.66	4.94
	417054	AF017060		aldehyde oxidase 1	3.65	4.51
	423974	AL118754		gb:DKFZp761P1910_r1 761 (synonym: harry2)	3.65	4.32
70	431362		Hs.293560	ESTs	3.65	3.73
	420506		Hs.194613	ESTs	3.65	3.25
	448065		Hs.172759	ESTs, Moderately similar to ALU7_HUMAN A	3.64	4.62
	437457		Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-	3.64	4.54
_	451951	AW082B70	Hs.210954	ESTs	3.64	3.69
75	435679		Hs. 120451	ESTs, Weakly similar to unnamed protein	3.64	3.39
. •	412676			gap junction protein, alpha 1, 43kD (con	3.62	3.62
	412668			hypothetical protein FLJ14621	3.62	4.22
	413899		Hs.75608	tight junction protein 2 (zona occludens	3.62	3.06
	444726			interferon regulatory factor 6	3.59	10.65
80	428722		Hs.190787	fissue inhibitor of metalloproteinase 4	3.59	3.31
	429973		Hs. 164680	ESTs	3.59	3.71
	452413		Hs.215030	ESTs	3.58	4.66
	416157			transforming growth factor, beta recepto	3.58	4.44
					0.00	4. ***

	420207	41024633	Hs.105607	bicarbonate transporter related protein	3.57	3.74
	430397 411939		Hs.146246	ESTs	3.57	12.42
	450353		Hs.103296	ESTs, Weakly similar to \$65657 atpha-1C-	3.57	4.11
	432406	AI340571	Hs.343666	KIAA0969 protein	3.57	2.84
5	439609	AW971945	Hs.293236	ESTs	3.56	3.14
-	435381	AW136397	Hs.175382	ESTs	3.56	3.48
	410173	AA706017	Hs.119944	ESTs	3.56	3.37
	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	3.56	9.93 4.24
10	413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fis, clone L	3.55 3.55	4.77
10	434360	AW015415	Hs.127780	ESTs	3.53	5.65
	423973	AF038461	Hs.136574 Hs.159183	arachidonate 12-lipoxygenase, 12R type KJAA0754 protein	3.52	4.79
	425681 428382	AB018297 AF007132	Hs.184019	Homo sapiens clone 23551 mRNA sequence	3.51	4.45
	451184	T87943	15.10-0.5	transcription factor 7-like 2 (T-cell sp	3.51	3.63
15	448496	BE379077	Hs.130849	ESTs, Weakly similar to 138022 hypotheti	3.51	3.30
	425831	U46689	Hs.159608	aldehyde dehydrogenase 3 family, member	3.48	8.66
	428232	BE272452	Hs.183109	monoarrine oxidase A	3.48	9.54
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	3.48 3.48	6.05 7.86
20	401760			Target Exon	3.47	3.67
20	427899	AA829285	Hs.332053	serum armytoid A1	3.46	3.85
	451767	AI525014	Hs.187328 Hs.30792	ESTs hook2 protein	3.45	5.66
	452849 427408	AF044924 AA583206	Hs.2156	RAR-related orphan receptor A	3.45	5.02
	447165	AL042400	Hs.75668	Homo sapiens, Similar to RIKEN cDNA 1700	3.45	3.61
25	422083	NM_001141	Hs.111256	aractidonate 15-lipoxygenase, second typ	3.45	7.71
	420876	AA918425	Hs.177744	ESTs	3.44	8.46
	421114	AW975051	Hs.293156	ESTs, Weakly similar to 178885 serine/th	3.44	4.47
	426233	AA372796	Hs.269339	ESTs, Weakly similar to AF161356 1 HSPC0	3.44	3.96
20	428221	U96781	Hs.183075	ATPase, Ce transporting, cardiac muscle,	3.42 3.42	4.32 6.35
30	403593	44/000044	U- 100044	Target Exon	3.42	3.34
	423467	AK000214	Hs.129014 Hs.19385	hypothetical protein FLJ20207 CGI-58 protein	3.41	2.44
	447731 456327	AA373527 H68741	Hs.38774	ESTs	3.40	3.46
	413880	AI660842	Hs.110915	interleukin 22 receptor	3.37	3.61
35	429501	A1700588	Hs.293388	ESTs, Weakly similar to A34612 zinc fing	3.37	3.44
	437575	AW954355	Hs.36529	hypothetical protein MGC11242	3.36	4.87
	420231	R06866	Hs.19813	ESTs	3.36	8.60
	424010	AL080188	Hs.137556	Homo sapiens mRNA; cDNA DKFZp434A132 (fr	3.36	6.20
40	426789	F06596	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	3.34 3.34	3.40 3.35
40	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	3.34	4.06
	420693	NM_001972		elastase 2, neutrophil transmembrane 4 superfamily member 3	3.33	4.36
	418318 413163	U47732 Y00815	Hs.84072 Hs.75216	protein tyrosine phosphatase, receptor t	3.32	9.47
	428496	AA769986	Hs.185802	ESTs	3.32	3.88
45	416349	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	3.31	4.01
	409095	AW337272	Hs.293656	ESTs, Moderately similar to S72481 proba	3.31	3.31
	443072	AI937532		gb:wp78d02.x1 NCI_CGAP_Bm25 Homo sapien	3.31	4.40
	437596	AA761490		ESTs, Moderately similar to S65657 alpha	3.30	5.31 3.47
50	444094	A1695764	Hs.202394	ESTs	3.29 3.29	3.76
50	437150	R51407	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	3.28	4.30
	407334 423017	AA494411 AW178761	Hs.296031 Hs.227948	ESTs serine (or cysteine) proteinase inhibito	3.28	3.78
	447875	R22029	Hs.13905	ESTs	3.28	3.44
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	3.27	3.71
55	411962	AA099050		gb:zk85d12.r1 Soares_pregnant_uterus_NbH	3.27	4.28
	424395	AA165082	Hs.146388	microtubule-associated protein 7	3.27	3.82
	400494			ENSP00000238970°:CIG30 (Fragment).	3.27	2.60
	430418	R98852	Hs.36029	heart and neural crest derivatives expre	3.26 3.26	6.19 4.24
60	409231	AA446644	Hs.692 Hs.4285	GA733-2 antigen; epithelial glycoprotein Homo sapiens cDNA: FLJ22505 fis, clone H	3.26	5.17
UU	434952 445234	T10269 AW137636	Hs.146059	ESTs	3.25	5.59
	426150	NM_003656		Bartl-like homeobox 2	3.25	5.21
	400076	1100000		Eas Control	3.25	3.60
	421462	AF016495	Hs. 104524	адиарогіл 9	3.25	3.93
65	420677	AW086215	Hs.246096	ESTs	3.25	3.53
	424125		Hs.1735	inhibin, beta B (activin AB beta polypep	3.24	3.88
	443672		Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	3.24 3.24	5.64 4.13
	420682		Hs.88602	ESTS	3.23	4.90
70	423725		Hs.132127	hypothetical protein LOC57822 ESTs	3.23	3.97
70	431157 440469		Hs.132678	gb;ny40e07.s1 NCI_CGAP_Pr12 Homo sapiens	3.23	3.39
	449961			ESTs	3.21	5.36
	407948			ICEBERG caspase-1 inhibitor	3.21	4.61
	400835			chromosome 2 open reading frame 2	3.21	3.62
75	413329		Hs.133539	ESTs	3.21	3.43
	414825		Hs.77432	epidermal growth factor receptor (avian	3.21	3.72
	450860			integrin, beta 8	3.20 3.19	5.89 6.84
	444816		Hs.283742	H.sapiens mRNA for retrotransposon ESTs, Weakly similar to ALUB_HUMAN !!!!	3.19	3.59
80	453855 432278			hypothetical protein FLJ23563	3.19	3.51
OU	43227			ESTs	3.18	5.50
	41848			CO34 antigen	3.18	3.65
	40852		Hs.46320	Small proline-rich protein SPRK (human,	3.18	7.43

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	435337	AI078307	Hs.134317	ESTs, Weakly similar to PC4259 ferritin	3.17	3.51
	445502	AW379160	Hs.12813	DKFZP434J214 protein	3.17	3.62
	412477	AA150864		microsomal glutathione S-transferase 1	3.17 3.16	5.39 3.60
5	421757	Z20897	Hs.296259	paraoxonase 3	3.16	5.56
,	413835 420309	AJ272727 AW043637	Hs.249163 Hs.21766	fatty acid hydroxylase ESTs, Wealdy similar to ALU5_HUMAN ALU S	3.15	1.99
	444895	AI674383	Hs.22891	solute carrier family 7 (cationic amino	3.15	4.45
	414869	AA157291	Hs.21479	ubinuclein 1	3.13	4.40
4.0	412947	AA122277		gb:zk97e09.s1 Soares_pregnant_uterus_NbH	3.13	3.30
10	443265	AJ916207	Hs.9167	SH3 domain binding glutamic acid-rich pr	3.12 3.11	4.62 11.54
	421335	X99977	Hs.103505	ARS component B	3.10	2.85
	401905 443514	BE464288	Hs.141937	ENSP00000252232":Sterol regulatory eleme ESTs	3.09	3.66
	418817	AA913229	Hs.19339	ESTs	3.08	3.88
15	434727	H43374	Hs.7890	Homo sapiens mRNA for KIAA1671 protein,	3.08	4.18
-	435858	AF254260	Hs.283009	tuftelin 1	3.08	3.96
	430285	A1917602	Hs. 106440	ESTs	3.07	3.30
	448106	AI800470	Hs.171941	ESTS	3.07 3.07	5.19 3.85
20	432908 450086	AI861896 AW016343	Hs.233301	ESTs ESTs	3.07	1.38
20	451529	AI917901	Hs.208641	ESTs	3.07	3.29
	418443	NM_005239	Hs.85146	v-ets avian erythroblastosis virus E26 o	3.06	4.12
	426848	H72531	Hs.36190	ESTs	3.05	4.34
25	429506	D49835	Hs.171942	ras responsive element binding protein 1	3.05 3.05	3.97 3.29
25	425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha ESTs, Weakly similar to ALU1_HUMAN ALU S	3.05	3.89
	413822 434230	R08950 AA551569	Hs.272044	hypothetical protein PRO2822	3.04	3.63
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	3.04	8.09
	415696	AI821552	Hs.188682	ESTs	3.03	3.43
30	449618	A1076459	Hs.15978	KIAA1272 protein	3.01	3.29
	414665	AA160873		serum amytoid A1	3.01	9.22 3.30
	446682	AW205632	Hs.211198	ESTs	3.00 2.99	3.74
	443801 412446	AW206942 AI768015	Hs.253594	intron of: trichorhinophalangeal syndro ESTs	2.99	4.47
35	449271	AW338067	Hs.7869	Homo sapiens cDNA FLJ11946 fis, clone HE	2.99	4.35
	435702	AI033647	Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	2.98	3.49
	403180			Target Exon	2.98	3.92
	434442	AA737415		ESTs	2.98	3.61 3.86
40	439593	BE073597	Hs.124863	ESTs gb:RC2-BT0318-241199-011-410 BT0318 Homo	2.98 2.98	3.49
40	410453 414766	AW749036 AW293452	Hs.16228	gp:RC2-810316-241139-011410 B10316 R0110 ESTs	2.97	3.63
	432566	AW439330	Hs.256889	ESTs, Weakly similar to 2109260A B cell	2.97	3.99
	451541	BE279383	Hs.26557	plakophilin 3	2.97	6.90
	452195	AA994712	Hs.116878	ESTs	2.97	3.30
45	401747			Homo sapiens keratin 17 (KRT17)	2.97	4.10
	431316	AA502663	Hs.145037	ESTs	2.96 2.95	3.05 7.12
	445437 421690	AI224165 AW162667	Hs.148725 Hs.106857	ESTs calbindin 2, (29kD, calretinin)	2.95	5.68
	456371	S76825	Hs.89695	insulin receptor	2.94	4.59
50	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	2.94	4.12
	436664	AW197887	Hs.253353	ESTs	2.93	3.57
	406962	M13485		gb:Human metallothionein I-B gene, exon	2.93	2.66 7.48
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.92 2.92	3.28
55	428769 414629	AW207175 AA345824	Hs.106771 Hs.76688	ESTs carboxylesterase 1 (monocyte/macrophage	2.92	3.48
33	444204	Al129194	Hs.143040	ESTs	2.92	3.92
	421407	T82331	Hs.18227B	ESTs, Weakly similar to CGHU6C collagen	2.91	6.55
	453180	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	2.90	3.92
60	429538	BE182592	Hs.139322	small proline-rich protein 2A	2.88	4.75 6.74
60	452554	AW452434	Hs.58006	ESTs, Weakly similar to ALU5_HUMAN ALU S Homo saplens cDNA: FLI21498 fis, clone C	2.88 2.87	3.97
	417184 412093	N52510 BE242691	Hs.268597 Hs.14947	ESTs	2.86	3.48
	424135	AW994455		Homo sapiens mRNA; cDNA DKFZp762H106 (fr	2.86	3.32
	437167	AL050184	Hs.21610	DKFZP434B203 protein	2.86	3.87
65	454065	BE394588		gb:601311808F1 NIH_MGC_44 Homo sapiens c	2.86	3.43
	420230	AL034344	Hs.284186	forkhead box C1	2.85	3.67
	403108			ENSP0000241415":Hypothetical 67.7 kDa p	2.85 2.84	2.62 3.35
	434433 420544		Hs.98732	gb:hh70e05.y1 NCl_CGAP_GU1 Homo sapiens Homo sapiens Chromosome 16 BAC clone CIT	2.83	2.66
70	429429		Hs.334437	hypothetical protein MGC4248	2.83	3.59
	451721			spectrin, beta, non-erythrocytic 2	2.83	3.36
	424982	U94777		phosphorylase, glycogen; muscle (McArdle	2.83	4.50
	429259			Plakophilin	2.81	4.81
75	423523			ESTs ESTs	2.80 2.80	7.08 3.39
13	433637 452089		Hs.102307 Hs.271492	ESTs, Weakly similar to PC4211 hepatocel	2.80	3.62
	441187			hypothetical protein FLJ22174	2.80	3.52
	421965			gb:EST14128 Testis tumor Homo sapiens cD	2.79	3.49
	432098	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	2.79	2.31
80	429128			ESTs	2.78	4.17
	438913		Hs.172445	ESTs	2.77 2.76	3.65 3.79
	445029 419923			midline 2 ESTs	2.76	3.00
	415343	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	113.120213			

	416508	R39769	Hs.56406	ESTs, Moderately similar to ALUB_HUMAN A	2.76	3.59
	412507	L36645	Hs.73964	EphA4	2.76	3.90
	446339	AL046962	Hs.14845	forkhead box O3A	2.75	3.50
5	433710 432375	AI341667 BE536069	Hs.188920 Hs.2962	ESTs S100 calcium-binding protein P	2.75 2.74	3.33 5.77
-	409213	U61412	Hs.51133	PTK6 protein tyrosine kinase 6	2.74	3.76
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	2.74	8.19
	408839	AW277084		gb:xp61h09.x1 NCI_CGAP_Ov39 Homo sapiens	2.73	3.93
10	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	2.73	11.46
10	444026	AA205759	Hs.10119	hypothetical protein FLJ 14957	2.73	6.17
	433713 453317	AW976511 NM_002277	Hs.112592 Hs.41696	ESTs	2.72	3.42 4.76
	408493	BE206854	Hs.46039	keratin, hair, acidic, 1 phosphoglycerate mutase 2 (muscle)	2.72 2.72	3.74
	432947	AA570710	Hs.270998	ESTs, Weakly similar to 138022 hypotheti	2.72	3.44
15	421428	U26726	Hs.1376	hydroxysteroid (11-beta) dehydrogenase 2	2.72	4.95
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.72	4.29
	435016	AL284219	Hs.130749	ESTs, Weakly similar to I38022 hypotheti	2.71	4.45
	449667	AB023227	Hs.23860	KIAA1010 protein	2.71	3.72
20	407112 433848	AA070801 AF095719	Hs.51615 Hs.93764	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.70 2.70	3.82 2.76
20	430152	AB001325	Hs.234642	carboxypeptidase A4 aquaporin 3	2.69	4.26
	456063	NM_006744	Hs.76461	retinal-binding protein 4, interstitial	2.69	6.72
	424471	AA341329	Hs.311524	ESTs	2.68	4.57
25	453201	AI432195	Hs.135098	ESTs	2.68	3.69
25	450912	AW939251	Hs.25647	v-los FBJ murine osteosarcoma viral onco	2.68	4.25
	404996 409453	AJ885516	Hs.95612	Target Exon ESTs	2.67	4.28
	430937	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	2.65 2.65	6.51 3.78
	452887	AI702223	Hs. 107253	hypothetical protein DKFZp761F241	264	6.38
30	444169	AV648170	Hs.58756	ESTs	2.64	3.40
	428500	AI815395	Hs.184641	falty acid desaturase 2	2.64	3.47
	408395	BE072425	Hs.44579	hypothetical protein FLJ20199	2.64	4.01
	432093 451621	H28383	Un 20770	gb:y152c03.r1 Soares breast 3NbHBst Homo	2.63	4.08
35	447335	AJ879148 BE617695	Hs.26770 Hs.286192	fatty acid binding protein 7, brain hypothetical protein FLJ20940	2.62 2.61	2.51 3.62
55	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.61	3.68
	431166	AW971186	Hs.293839	ESTs	2.61	3.33
	440659	AF134160	Hs.7327	claudin 1	2.61	3.53
40	413542	BE295928	Hs.75424	inhibitor of DNA binding 1, dominant neg	2.61	4.48
40	413956	AI821351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.60	3.51
	407299 449539	AA460205 W80363	Hs.289770 Hs.58446	ESTs, Weakly similar to I38022 hypotheti	2.59	3.82
	413884	AI668892	Hs.239758	ESTs hypothetical protein FLJ12389 similar to	2.58 2.58	4.05 4.19
	445620	AI245225	Hs.17441	ESTs	2.57	3.44
45	433688	AA628467	Hs.112572	Homo sapiens cDNA FLJ 14130 fis, clone MA	2.56	3.57
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ 10570 fis, clone NT	2.56	3.47
	407083	248511		H.sapiens XG mRNA (clone PEP11)	2.55	3.61
	406790	AA293303	16- 55070	ribosomal protein L27a	2.54	4.36
50	450472 410310	Al190071 J02931	Hs.55278 Hs.62192	ESTs coagulation factor III (thromboplastin,	2.54 2.54	4.30 3.82
-	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	2.54	3.44
	430821	AA487264	Hs.154974	Homo sapiens mRNA; cDNA DKFZp667N064 (fr	2.54	4.55
	402575			Rho GTPase activating protein 1	2.53	5.47
55	429554	NM_012275	Hs.207224	Interleukin 1, delta	2.53	2.40
23	431631	AA548906	Hs.122244	ESTs	2.52	3.79
	408806 420235	AW847814 AA256756	Hs.75608 Hs.31178	Homo sapiens cDNA: FLJ21532 fis, clone C ESTs	2.52	4.51
	436314	A1983409	113.31110	ESTS	2.51 2.51	4.21 3.11
	432906	BE265489	Hs.3123	lethal giant larvae (Drosophila) homolog	2.50	5.62
60	429547	AW009166	Hs.99376	FGENESH predicted novel secreted protein	2.49	2.60
	410532	T53088	Hs.155376	hemoglobin, beta	2.49	4.73
	413475	AW021488	Hs.26981	ESTs	2.49	3.90
	429325	AW088739	Hs.243770	ESTs	2.48	3.71
65	424504 414320	AW865388 U13616	Hs.151076 Hs.75893	KIAA1243 protein ankyrin 3, node of Ranvier (ankyrin G)	2.48 2.48	4.16 3.80
-	423929	M69136	Hs.135626	chymase 1, mast cell	2.48	3.47
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	2.47	2.09
	444935	AA262449	Hs.223569	ESTs	2.47	5.96
70	445389	NM_016831		period (Drosophila) homolog 3	2.47	3.41
70	437897	AA770561	Hs.146170	hypothetical protein FL122969	2.47	6.80
	446292 409178	AF081497 BE393948	Hs.279682	Rh type C glycoprotein	246	7.37
	452865	AI924046	Hs.50915 Hs.119567	kallikrein 5 ESTs, Weakly similar to A47582 B-cell gr	2.46 2.46	5.59 6.03
	447179		Hs.157299	ESTs	2.46	3.23
75	414459		Hs.76171	CCAAT/enhancer binding protein (C/EBP),	2.46	3.25
	428188	M98447	Hs.22	transglutaminase 1 (K polypeptide epider	2.45	3.94
	428593		Hs.185973	degenerative spermatocyte (hornolog Droso	2.44	2.17
	436009		Hs.120925	ESTs	2.44	2.94
80	412810 416749		Hs.74615 comp Hs.79732	platelet-derived growth factor receptor, fibulin 1	243	3.61
50	444672		Hs.11669	laminin, alpha 5	243 242	4.46 6.39
	433143		Hs.294035	ESTs, Weakly similar to ALUS_HUMAN ALU S	2.42	3.45
	406997			metallothionein IV	2.42	3.92

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	433404	NA 004430	U- 1694	anhii 44	2.41	4.34
	423184 421321	NM_004428 NM_005309	Hs.1624 Hs.103502	ephrin-A1 glutamic-pyruvate transaminase (alanine	241	5.08
	456826	AJ871742	Hs.302428	wingless-type MMTV integration site fami	241	3.92
_	428897	AJ245719	Hs.194385	hypothetical protein FLJ20234	2.41	5.18
5	400232			NM_001895".Homo sapiens casein kinase 2,	2.41	3.82
	421481	AW391972	Hs. 104696	KIAA1324 protein	2.40	4.03
	442083	R50192	Hs.165062	ESTs	2.39	4.21
	422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	2.39	8.60
10	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.39	2.57
10	457008	AA410446	Hs.112011	ESTs. Weakly similar to unknown (H.sapie	2.39	3.85
	418355	L42563	Hs.1165	ATPase, H? transporting, nongastric, atp	2.38	3.84
	431179 432563	AI338644 NM_013261	Hs.195432 Hs.198468	aldehyde dehydrogenase 2 family (mitocho	2.37	7.89 3.77
	402338	MM_013201	115.130400	peroxisome proliferative activated recep Target Exon	2.37 2.37	3.46
15	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.37	4.57
••	435723	AW975895	Hs.307486	ESTs	2.37	6.39
	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	2.37	3.92
	409212	A1082423	Hs.141892	ESTs	2.36	3.79
••	451323	Al903313	Hs.34579	ESTs, Moderately similar to ALUS_HUMAN A	2.35	3.29
20	400307	AF005081		Homo sapiens skin-specific protein (xp32	2.35	9.96
	421993	R22497	Hs.110571	growth arrest and DNA-damage inducible,	2.35	5.16
	451092	AI207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein,	2.34	5.24
	445948	BE409053	Hs.299629	peroxisomal long-chain acyl-coA thioeste	2.34	3.77
25	424425	AB031480	Hs.146824	SPR1 protein	2.34	4.43
23	426050 425180	AF017307 U00115	Hs.166096 Hs.155024	E74-like factor 3 (ets domain transcript	2.34	5.64
	422106	D84239	Hs.111732	B-cell CLL/lymphoma 6 (zinc finger prote Fc fragment of tgG binding protein	2.33 2.33	3.51 6.95
	423503	M92843	Hs.343586	zinc finger protein homologous to Zfp-36	2.33	5.57
	453999	BE328153	Hs.240087	ESTs	2.32	3.40
30	419358	178763	Hs.90063	neurocalcin detta	2.32	6.72
	430468	NM_004673	Hs.241519	angiopoietin-like 1	2.32	3.90
	456876	AL044870	Hs.208780	ESTs, Weakly similar to T29647 hypotheti	2.32	3.27
	454947	AW846590		gb:QV0-CT0180-011099-025-d07 CT0180 Homo	2.32	4.43
25	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	2.31	7.22
35	438282	BE268288	Hs.195432	aldehyde dehydrogenase 2 family (mitocho	2.31	3.34
	420202	AL036557	Hs.95910	putative lymphocyte G0/G1 switch gene	2.31	8.47
	419245 444920	AI732742	Hs.87440	ESTs	2.31	3.39
	417314	AW450967 N68168	Hs.235240	ESTs	2.30	3.30
40	409586	AL050214	Hs.55044	gb:za11c01.s1 Soares fetal fiver spleen DKFZP586H2123 protein	2.30 2.30	3.12 3.52
	433662	W07162	Hs.150826	RAB25 RAB25, member RAS oncogene family	2.29	6.11
	451176	AA046457	Hs.60677	ESTs	2.29	6.59
	410531	AW752953		gb:QV0-CT0224-261099-035-g02 CT0224 Homo	2.29	3.29
	425982	R05327	Hs.189726	ESTs	2.29	3.37
45	435684	NM_001290	Hs.4980	LIM domain binding 2	2.29	4.54
	453003	AAB08466	Hs.103395	hypothetical protein FLJ14146	2.28	3.70
	434411	AA632649	Hs.201372	ESTs	2.28	4.40
	407394	AF005081		gb:Homo sapiens skin-specific protein (x	2.28	10.57
50	411579 401205	AC005258	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	2.28	4.06
50	443102	AI247472	Hs.132965	Target Exon ESTs	2.27	2.71
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.27 2.26	5.66 3.94
	434987	AW975114	15.1415	ESTs	2.26	3.72
	415477	NM_002228	Hs.78465	v-jun avian sarcoma virus 17 oncogene ho	2.26	3.42
55	423515	AA327017	Hs.176594	ESTs	2.25	6.21
	434903	AF161369	Hs.187763	Homo sapiens HSPC106 mRNA, partial cds	2.25	3.62
	443049	AI028613	Hs.132343	ESTs	2.25	3.13
	444637	T19101	Hs.11494	fibulin 5	2.24	6.43
60	41,0026	AI912061	Hs.55016	hypothetical protein FLJ21935	2.23	3.31
ou	418629	BE247550	Hs.86859	growth factor receptor-bound protein 7	2.23	4.17
	429587 431986	AA283969	Hs.334706	Homo sapiens cDNA FLJ11801 fis, clone HE	2.23	3.79
	409571	AA536130 AA504249	Hs.149018 Hs.187585	Novel human gene mapping to chomosome 20	2.22	3.54
	446051	BE048061	Hs.37054	ESTs ephrin-A3	2.22 2.22	3.87 4.57
65	422418	AK001383	Hs.116385	himself and a serie Cl. 140CO4	2.21	4.25
	453023	AW028733	Hs.31439	serine protease inhibitor, Kunitz type, ESTs	2.21	5.07
	435748	AA699756	Hs.117335	ESTs (2.20	3.35
	420105	AW015571	Hs.32244	ESTs, Weakly similar to FMOD_HUMAN FIBRO	2.19	6.55
30	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	2.19	3.51
70	433052	AW97 1983	Hs.293003	ESTs, Weakly similar to PC4259 ferritin	2.19	3.32
	430310	U60115	Hs.239069	four and a half LIM domains 1	2.19	3.83
	447205	BE617015	Hs. 11006	ESTs, Moderately similar to T17372 plasm	2.19	15.65
	449967	R40978	Hs.271498	ESTs, Moderately similar to ALU1_HUMAN A	2.18	3.54
75	452689	F33868	Hs.284176	transferrin	2.18	3.30
, 5	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	2.18	3.77
	432647 401192	AI807481	Hs.278581	fibroblast growth factor receptor 2 (bac	2.18	5.64
	421752	AK001521	Hs.107882	Target Exon hypothetical protein FLJ 10659	2.17 2.16	3.33
_	456646	AJ243662	Hs.110196	NICE-1 protein	2.16	3.44 2.39
80	421263	AB020638	Hs.103000	KIAA0831 protein	2.16	3.37
	445656	W22050	Hs.21299	ESTs, Weakly similar to AF151840 1 CGI-8	2.16	5.17
	450624	AL043983	Hs.125063	Homo sapiens cDNA FLJ13825 fis, clone TH	2.15	3.87
	429350	AI754634	Hs.131987	ESTs	2.15	3.90

	448144	AW169230		ESTs, Moderately similar to PC4259 ferri	2.14	3.28
	429002	AW248439	Hs.2340	junction plakoglobin	2.14	5.05
	429297	XB2494	Hs.198862	fibulin 2	2.14	4.32
5	452093 428848	AA447453 NM_000230	Hs.27860 Hs.194236	Homo sapiens mRNA; cDNA DKFZp585M0723 (I teptin (murine obesity homolog)	2.14 2.14	3.99 3.39
•	407584	W25945	Hs.8173	hypothetical protein FLJ10803	214	3.38
	453155	AF052126	Hs.552	steroid-5-alpha-reductase, alpha polypep	2.14	2.51
	453283	AA694386	Hs.290914	ESTs	213	3.28
10	456906	AF117646	Hs.156637	Cas-Br-M (murine) ectropic retroviral tr	2.13	3.76
IU	414815 417155	AW292140 175125	Hs.130286	ESTs	213	4.16
	416673	177052	Hs.299148 Hs.14039	hypothetical protein FLJ21801 ESTs	2.13 2.13	3.57 3.43
	452208	AA024792	Hs.31895	hypothetical protein MGC4093	2.12	5.67
1.5	413966	AA133935	Hs.173704	ESTs, Moderately similar to A53959 throm	212	4.76
15	430967	H16791	Hs.100895	ESTs	2.12	2.64
	429015 439518	BE168484	Hs.194737	KIAA0453 protein	212	3.30
	426468	W76326 AA379306	Hs.117558	gb:zd60d04.r1 Soares_felal_heart_NbHH19W ESTs	211 210	2.59 3.56
	407555	248511	15.11750	gb:H.sapiens XG mRNA (clone PEP11).	210	3.66
20	418226	AA424202	Hs.83834	cytochrome b-5	2.10	5.14
	423441	R68649	Hs.278359	absent in melanoma 1 like	2.10	3.64
	436961 432633	AW375974	Hs.156704	ESTs	210	3.21
	426102	AI796390 AF200496	Hs.210667 Hs.166371	ESTs interleukin 1, zeta	2.10 2.09	2.58 3.77
25	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.09	3.85
	437124	AAS54458		KIAA0666 protein	2.09	3.35
	407757	BE048414	Hs.165215	hypothetical protein MGC5395	2.08	4.41
	407815	AW373850	Hs.183860	hypothetical protein FLJ20277	2.08	5.01
30	443906 423887	AA348031 AL080207	Hs.7913 Hs.134585	ESTs DKFZP434G232 protein	2.08 2.08	3.40 3.92
-	406400	10000201	(13.154505)	kallikrein 8 (neuropsin/ovasin) (KLK8)	2.08	3.92 4.19
	437704	AA766142	Hs.131810	ESTs, Moderately similar to ALU1_HUMAN A	2.07	3.30
	412533	AA679863	Hs.69606	ESTs	2.07	3.39
35	426310	NM_000909	Hs.169266	neuropeptide Y receptor Y1	2.06	3.55
55	411821 442599	BE299339 AF078037	Hs.72249 Hs.324051	three-PDZ containing protein similar to ReIA-associated inhibitor	2.06 2.06	4.98 7.23
	432212	AW137742	10.01.403.	ESTs	2.04	3.52
	453469	AB014533	Hs.33010	KIAA0633 protein	2.04	4.01
40	443652	AI080692	Hs.134229	ESTs, Weakly similar to 154401 hypertens	2.04	3.36
40	452955 424464	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.03	3.64
	408702	R68537 AW959893	Hs.17962 Hs.27099	ESTs hypothetical protein FLJ23293 similar to	2.03 2.03	4.36 3.31
	439908	AI168031	Hs.155507	ESTs	2.03	3.83
45	412825	AW167439	Hs.190651	Homo sapiens cDNA FLJ13625 fis, clone PL	2.02	5.56
45	406784	AI144297	Hs.169401	apolipoprotein E	2.02	3.40
	427309 453195	NM_005714 BE241876	Hs.175218	potassium channel, subfamily K, member 7	2.02	4.58
	404246	DE241070	Hs.32352	hypothetical protein DKFZp434K1210 Target Exon	2.02 2.01	3.57 7.30
	443679	AK001810	Hs.9670	hypothetical protein FLJ10948	201	5.81
50	410669	AW805749		superoxide dismutase 2, mitochondrial	2.01	3.05
	446193	AI279390	Hs.144658	ESTs, Weakly similar to T17257 hypotheti	2.01	2.32
	449228 434346	AJ403107 AA630445	Hs. 148590	protein related with psoriasis	2.00 2.00	5.10
	456098	AW747800	Hs.55016	ESTs hypothetical protein FLJ21935	2.00	3.51 4.96
55	452467	AW500815		ESTs	2.00	4.66
	442866	AJ743317	Hs.283622	ESTs, Weakly similar to ALU5_HUMAN ALU S	1.98	3.72
	434699 417553	AA643687	Hs.149425	Homo sapiens cONA FLJ11980 fis, clone HE	1.98	3.11
	449142	L09190 R15913	Hs.194987	trichohyafin ESTs	1.98 1.98	2.09 3.50
60	407597	AA043925	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA	1.98	6.25
	429299	A1620463	Hs.347408	hypothetical protein MGC13102	1.97	3.77
	423031	AI278995		ESTs	1.97	3.62
	433495 430420	AW373784 AW140027	Hs.71 Hs.26373	alpha-2-glycoprotein 1, zinc	1.96	4.57
65	420139	NM_005357	Hs.95351	Homo sapiens cDNA: FLJ23449 fis, clone H lipase, hormone-sensitive	1.96 1.95	6.09 5.77
05	418462	BE001596	Hs.85266	integrin, beta 4	1.95	6.09
	447261	NM_006691	Hs. 17917	extracellular link domain-containing 1	1.95	3.33
	437220	AL117542	Hs.334305	GS1999full	1.94	3.45
70	407601 443595	AC002300 AF169312	Hs.37129 Hs.9613	sodium channel, nonvoltage-gated 1, beta	1.94	5.46
. •	409007	AL122107	Hs.49599	PPAR(gamma) angiopoietin related protein Homo sapiens mRNA; cDNA DKFZp434G0827 (f	1.94 1.94	4.67 3.59
	408717	AF045458	Hs.47061	unc-51 (C. elegans)-like kinase 1	1.94	4.29
	420055	NM_001487	Hs.94572	GCN5 (general control of arnino-acid synt	1.94	3.38
75	430392	NM_000627	Hs.241257	latent transforming growth factor beta b	1.93	3.75
,,	425078 423527	NM_002599 AI206965	Hs. 154437 Hs. 105861	phosphodieslerase 2A, cGMP-stimutated hypothetical protein FLJ13824	1.93 1.93	4.06 4.70
	447151	AI022813	Hs.92679	Homo sapiens clone CDABP0014 mRNA sequen	1.93	4.70 3.77
	422101	AW404176	Hs.111611	ribosomal protein L27	1.91	3.18
80	456653	A1807519	Hs.104520	Homo sepiens cDNA FL113694 fis, clone PL	1.91	3.41
ου	443444 420924	AW952619 R01026	Hs.17235	Homo sapiens clone TCCCIA00176 mRNA sequ	1.91	3.52
	426048	A1768853	Hs.245321 Hs.134478	ESTs ESTs	1.91 1.90	3.22 3.56
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	1.90	4.15

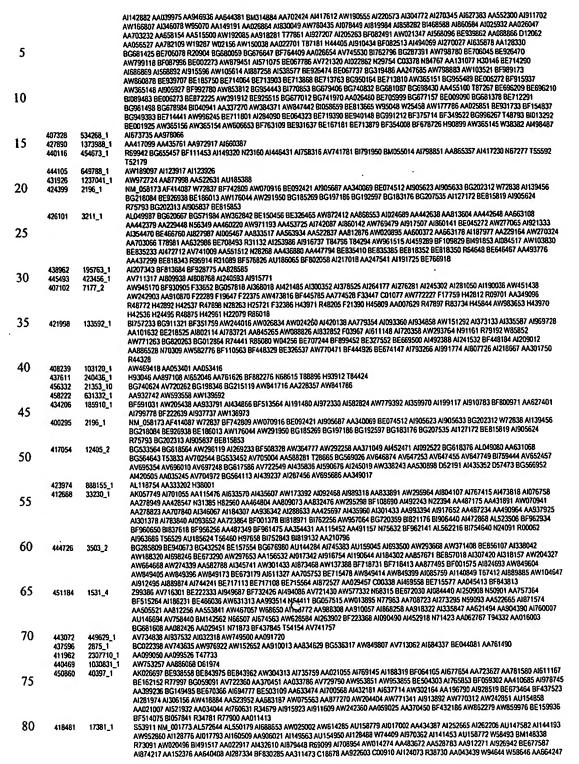
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.90	5.88
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	1.90	2.28
	418418	R61527	Hs.237517	ESTs	1.90	3.56
_	449372	AA001266	Hs.133521	ESTs	1.89	3.90
5	438752	AW238673	Hs.145038	ESTs	1.89	5.24
	428193	NM_004235		Kruppel-like factor 4 (gut)	1.89	5.21
	433251	AB040955	Hs.322735	KIAA1522 protein	1.89	5.00
	430560	Z28942	Hs.243960	N-myc downstream-regulated gene 2	1.89	7.09
• •	427795	BE268268	Hs.180842	ribosomal protein L13	1.89	4.51
10	410209	AI583661	Hs.60548	hypothetical protein PRO1635	1.89	3.35
	449243	AW295031	Hs.198671	ESTs	1.89	4.26
	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	1.88	6.20
	443932	AW888222	Hs.9973	tensin	1.88	9.28
1.5	427929	BE613835	. Hs.181159	Homo sapiens mRNA; cDNA DKFZp434F0217 (f	1.87	4.25
15	400078			Eos Control	1.07	6.73
	422639	AI929377	Hs.173724	creatine kinase, brain	1.87	5.51
	447374	AF263462	Hs.18376	KIAA1319 protein	1.87	3.42
	430346	AK000331	Hs.297641	KIAA0462 protein	1.87	4.15
20	428223	AA424313	Hs.98402	ESTs	1.87	3.70
20	408792	L29433	Hs.47913	coagulation factor X	1.87	4.08
	433855	AA834082	Hs.307559	ESTs	1.87	4.16
	451583	A1653797	Hs.24133	ESTs	1.87	3.81
	426377	AK001921	Hs.169575	hypothetical protein MGC2550	1.86	5.55
25	431647	AL138578	Hs.266738	hypothetical protein dJ796117.1	1.86	3.74
25	422055	NM_014320	Hs.111029	putative heme-binding protein	1.86	4.68
	425750	AL050276	Hs.42400	zinc finger protein 288	1.86	4.04
	422491	AA338548	Hs.117546	neuronatio	1.86	4.37
	438942	AW875398	Hs.6451	PRO0659 protein	1.85	5.06
20	400198			Eos Control	1.85	5.22
30	427136	AL117415	Hs.173716	a disintegrin and metalloproteinase doma	1.85	3.41
	427605	NM_000997	Hs.337445	ribosomal protein L37	1.85	4.73
	418253	AA215539	Hs.283643	Homo sapiens cDNA FLJ11606 fis, clone HE	1.84	5.94
	441912	AA971484	Hs.159938	ESTs	1.84	3.73
35	421632	AA825426	Hs.334689	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.83	3.62
33	440602	AI743491	Hs.292692	ESTs .	1.83	2.39
	431882	NM_001426	Hs.271977	engraited hornolog 1	1.83	3.30
	420772	AW752656	Hs.222707	KIAA1718 protein	1.83	3.73
	429197	H24471	Hs.26930	ESTs, Weakly similar to T20272 hypotheti	1.82	341
40	450796	NM_001988	Hs.25482	envoplakin	1.82	7.73
70	426928 415409	AF037062 AW993701	Hs.172914	retinal dehydrogenase 5 (11-cis and 9-ci	1.82	3.38
	401131	AW993/01		NS1-associated protein 1	1.82	3.60
	421324	BE257515	Hs.103503	NM_001651*:Homo sapiens aquaporin 5 (AOP	1.82	5.53
	400079	0023/313	HS.103303	deoxyribonuclease Hike 2	1.61 1.81	5.53
45	430513	AJ012008	U- 241505	Eos Control		6.79
43	426508	W23184	Hs.241586 Hs.170171	G6C protein	1.81	7.49 3.55
	425883	AL137708	Hs.161031	glulamate-ammonia ligase (glutamine synt	1.81 1.80	5.43
	429191	AF065215	Hs.198161	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	1.79	5.90
	432417	AL040350	Hs.162203	phospholipase A2, group IVB (cytosolic)	1.79	3.63
50	406467	74000	113.102203	ESTs, Wealdy similar to atternatively sp Target Exon	1.79	4.16
•	444135	AK000374	Hs.10346	hypothetical protein FLJ20154	1.79	3.32
	426402	BE387327	Hs.80475	polymerase (RNA) II (DNA directed) polyp	1.78	3.51
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	1.78	3.72
	425880	X01630	Hs.160786	argininosuccinate synthetase	1.78	3.29
55	400300	X03363	14.100700	HER2 receptor tyrosine kinase (c-erb-b2,	1.78	3.44
	451304	M92642	Hs.26208	collagen, type XVI, alpha 1	1.78	3.57
	400082			Eos Control	1.78	3.82
	446603	NM_014835	Hs.15519	oxysterol-binding protein-related protei	1.77	3.48
	425415	M13903	Hs.157091	involucin	1.77	4.64
60	400083			Eos Control	1.77	6.31
	427620	NM_003705	Hs.179866	solute carrier family 25 (mitochondrial	1.76	3.47
	446971	AI652143	Hs.288382	hypothetical protein FLJ13111	1.76	4.21
	429807	AK002138	Hs.306227	Homo sapiens cDNA FLJ11276 fis, clone PL	1.76	2.63
	446560	AK001567	Hs.311002	Homo sapiens cDNA FLJ10705 fis, clone NT	1.76	3.82
65	412824	AW958075	Hs.11261	small proline-rich protein 2A	1.76	4.31
	439927	AA854650	Hs.124597	ESTs	1.75	3.63
	410223	S73775	Hs.60708	calsequestrin 1 (fast-twitch, skeletal m	1.75	3.79
	414500	W24087	Hs.76285	DKFZP564B167 protein	1.75	3.55
70	448182	AF244137	Hs.20597	host cell factor homolog	1.75	3.40
70	439651	AF085480	Hs.56255	ESTs	1.75	2.55
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	1.75	3.54
	424389	AA339786		lymphocyte-specific protein 1	1.75	4.48
	450837	D58463	Hs.85969	hypothetical protein FLJ12270	1.74	3,40
75	425920	AL049977	Hs.162209	daudin 8	1.74	3.33
75	435680	H50946	Hs.284183	Homo sapiens galectin-related inhibitor	1.74	3.47
	439639	AA370045	Hs.6607	AXIN1 up-regulated	1.73	5.22
	416950	AL049798	Hs.80552	demaiopontin	1.73	4.99
	400199			Eos Control	1.73	6.25
QΛ	409737	AB011539	Hs.56186	EGF-like-domain, multiple 3	1.73	4.28
80	424420	BE614743	Hs.146688	prostaglandin E synthase	1.72	3.42
	421545	AA292810	Hs.90034	hypothetical protein FLJ21916	1.72	2.12
	414323	NM_014759		KIAA0273 gene product	1.71	4.82
	407228	M25079	Hs.155376	hemoglobin, beta	1.70	7.02

	406643	N77976	Hs.347939	hemoglobin, alpha 2	1,70	3.60
	447299	AF043897	Hs. 18075	chromosome 9 open reading frame 3	1.70	5.10
	439733	AL365412	Hs.107203	hypothetical protein from EUROIMAGE 1759	1.69	2.92
_	415512	Y16270	Hs.78482	paratemmin	1.69	4.92
5	407100	R29657		gb:F1-1179D 22 week old human fetal live	1.69	3.96
	425503	W92517	Hs.158203	actin binding LIM protein 1	1.68	5.97
	433738	A1684802	11- 247000	ESTS	1.68	2.88
	406791 428975	A1220684 NM_004672	Hs.347939 Hs.194694	hemoglobin, alpha 2	1.68	3.44
10	435661	AF220263	Hs.193920	mitogen-activated protein kinase kinase MOST2 protein	1.68 1.67	2.74 3.56
10	459317	BRCA1b	115.150520	Eos Control	1.67	3.34
	426923	AF112977	Hs.172887	phytanoyl-CoA hydroxylase (Refsum diseas	1.67	4.53
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	1.67	3.36
	417029	AW952192	Hs.273385	guanine nucleotide binding protein (G pr	1.67	5.22
15	437201	F29279	Hs.171625	hypothetical protein MGC14697	1.67	5.75
	454478	AW805749		superoxide dismutase 2, mitochondrial	1.67	4.55
	406710	A1708347	Hs.184014	ribosomal protein L31	1.66	3.80
	431593 457820	NM_002108 AA341497	Hs.276590 Hs.31408	ESTS PAR (PAR SIA CYPACE)	1.66 1.66	2.45 2.44
20	441899	A1372588	Hs.8022	RAR (RAS Eke GTPASE) TU3A protein	1.66	4.06
	414185	U33446	Hs.75799	protease, serine, 8 (prostasin)	1.65	6.52
	418116	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot	1.65	3.44
	403105			Target Exon	1.64	4.12
25	450014	N41322	Hs.18441	ESTs	1.64	2.90
25	436685	W28661	Hs.5288	Homo sapiens mRNA; cDNA OKFZp434M245 (fr	1.64	4.49
	401429	11107000		C14001067;pi 4126465 dbi BAA36581.1 (AB	1.64	3.82
	420983 433126	W95228 AB021262	Hs.100764	cathepsin G	1.64	3.64
	428150	AW950547	Hs.99816 Hs.70312	beta-catenin-interacting protein ICAT cytochrome c oxidase subunit VIIa polype	1.63 1.63	3.29 7.05
30	412295	AW088826	15.70012	poly(A)-binding protein, nuclear 1	1.63	4.01
	430831	AA703239	Hs.269804	ESTs, Wealthy similar to ALU1_HUMAN ALU S	1.63	3.60
	429348	AJ242859	Hs.199731	Langerhans cell specific c-type lectin	1.62	2.64
	407082	247055		gb:Human partial cDNA sequence, famesyl	1.62	2.13
25	452556	H78517	Hs.33905	ESTs	1.62	4.64
35	415688	AA166963		gb:zo86d01.s1 Stratagene ovarian cancer	1.62	3.33
	446515 445919	AL048875 T53519	Hs.334592	hypothetical protein DKFZp5661133	1.62	3.66
	447330	8E279949	Hs.18141	hypothetical protein MGC14141 ladinin 1	1.62 1.61	5.65 5.61
	412374	X01388	Hs.73849	apolipoprotein C-III	1.61	5.18
40	400229			NM_021724*:Homo saplens nuclear receptor	1.61	3.57
	414814	D14697	Hs.77393	famesyl diphosphate synthese (famesyl	1.61	2.08
	424397	A1950320		gb:wp08d10.x1 NCI_CGAP_Kid12 Homo sapien	1.60	3.59
	451335	AB023192	Hs.26285	imidazoline receptor candidate	1.60	5.54
45	426156	BE244537	Hs.167382	natriuretic peptide receptor A/guanylate	1.60	4.79
43	456267 436950	A1127958 L05779	Hs.83393 Hs.113	cystatin E/M	1.60 1.60	2.50
	421397	\$67368	Hs.103998	epoxide hydrolase 2, cytoplasmic gamma-aminobutyric acid (GABA) A recepto	1.60	3.98 3.28
	419092	J05581	Hs.89603	mucin 1, transmembrane	1.60	3.69
	440160	BE560269	Hs.7010	NPD002 protein	1.59	2.49
50	417481	AA203281	Hs.6191	ESTS	1.59	3.60
	406778	H06273	Hs.101651	Homo sapiens mRNA; cDNA DKFZp434C107 (fr	1.58	3.98
	402991	4140000000	11- 100544	Target Exon	1.58	3.36
	425169 446429	AW292500 AI681807	Hs.128514 Hs.201391	ESTs ESTs	1.58 1.58	4.00
55	426445	AA378739	Hs.187711	ESTs	1.57	3.20 3.63
	425196	AL037915	Hs.155097	carbonic anhydrase II	1.57	3.44
	422581	NM_016339	Hs.118562	Link guanine nucleotide exchange factor	1.57	3.55
	440054	AW661947	Hs.6891	splicing factor, arginine/serine-rich 6	1.56	3.39
60	415988	BE407713	Hs.78943	bleomycin hydrolase	1.56	2.43
60	441860	AW451330	Hs.348198	hypothetical protein FLJ 20262	1.55	3.38
	428462	AI571486	Hs.30258	ESTs	1.55	3.65
	449518 420075	BE395253 AF142482	Hs.30861 Hs.203846	ESTs TEA domain family member 3	1.55 1.55	3.80 3.81
	406799	AA908548	113.200070	gb:og83g12.s1 NCI_CGAP_Ov8 Homo sapiens	1.54	3.87
65	450787	AB006190	Hs.25475	aquaporin 7	1.54	4.06
	419659	AB023206	Hs.92186	Leman coiled-coil protein	1.54	3.82
	408543	N78098	Hs.44289	ESTs	1.54	3.10
	410169	AI373741	Hs.59384	hypothetical protein MGC3047	1.54	4.73
70	426068	AF029778	Hs.166154	jagged 2	1.54	4.82
70	432191	AA043193	Hs.273186	hypothetical protein, done Telethon(Ita	1.54	5.83
	415166 410048	NM_003652 W76467	Hs.78068 Hs.343874	carboxypeptidase Z proline oxidase homolog	1.54 1.54	4.58 4.66
	430502	AI123657	Hs.127264	ESTs, Weakly similar to JC5314 CDC28/cdc	1.53	3.41
	433640	AW390125	Hs.240443	Homo sapiens cONA: FLJ23538 fis, clone L.	1.53	4.57
75	413353	AW293542	Hs.75309	eukaryotic translation elongation factor	1.53	3.59
	431021	AI869664		thiosulfate sulfurtransferase (rhodanese	1.53	3.73
	431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	1.52	6.09
	433019	AI208513	Hs.279915	translocase of inner mitochondrial membr	1.52	4.49
80	406801	AW242054 AA531527	Hs.190813	ribosomal protein L9	1.51	5.56
00	427461 432894	AW167668	Hs.332040 Hs.279772	hypothetical protein MGC13010 brain specific protein	1.51 1.51	3.77
	415550	L13720	Hs.78501	growth arrest-specific 6	1.50	6.72 4.02
	424707	BE061914	Hs.10844	Homo sapiens cDNA FLJ14476 fis, clone MA	1.49	4.02

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	445624	AW140103	Hs.78880	ilvB (bacterial acetolactate synthase)-l	1.48	3.61	
	445071	A1280246	Hs.149504	ESTs	1.48	3.39	
	440763	AB028988	Hs.7407	KIAA1065 protein	1.48	4.03	•
_	451988	AF263928	Hs.27410	papillomavirus regulatory factor PRF-1	1.47	3.58	
5	427841	AW883367		hypothetical protein MGCS306	1,47	3.61	
	426335	AI054347	Hs.2017	ribosomal protein L38	1.47	3.76	
	454098	W27953	Hs.292911	Plakophilin	1,46	2.95	
	456766	R87310	Hs.7740	oxysterol binding protein-like 1			
	440526	AI832243	113.1170		1.46	3.40	
10	452586		Un 200042	ESTs	1.46	3.38	
10		AW958479	Hs.289043	spindlin	1.45	3.48	
	433399	N46406	Hs.84700	similar to phosphatidylcholine transfer	1.45	3.44	
	430238	N72519	Hs.236545	hydroxyacid oxidase 2 (long chain)	1.45	4.00	
	425456	T70445	Hs.157850	ribosomal protein L9	1,45	4.79	
	411085	AF022991	Hs.68398	period (Drosophila) homotog 1	1.45	4.43	
15	433638	AW872507	Hs.3462	cytochrome c oxidase subunit VIIc	1.44	3.89	
	445156	N89367	Hs.12373	adenylate cyclase 6	1,44	3.60	
	446576	AI659477		dystroglycan 1 (dystrophin-associated of	1.44	3.07	
	440433	AA252452	Hs.7187	hypothetical protein FLJ 10707			
	434536	H14486	Hs.3903		1.43	3.67	
20	423513			Cdc42 effector protein 4; binder of Rho	1.42	3.35	
20		AF035960	Hs.129719	transglutaminase 5	1.42	3.18	
	418681	AA287786	Hs.23449	insufin receptor tyrosine kinase substra	1.42	3.38	
	421935	AA131632	Hs.109672	CMP-NeuAC:(beta)-N-acetylgalactosaminide	1,41	4.04	
	406712	M31212	Hs.77385	myosin, light polypeptide 6, atkati, smo	1.41	4.27	
25	413944	AW001579	Hs.9645	Homo sapiens mRNA for KIAA1741 protein,	1.41	3.80	
25	435879	AW084463	Hs.30002	SH3-containing protein SH3GLB2; KIAA1848	1.41	3.55	
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	1.40	4.07	
	412669	AW880841	Hs.96908	p53-induced protein	1.40	3.59	
	415523	ALD42003	Hs.296847	cell matrix adhesion regulator			
	406713	U02629	Hs.77385		- 1.40	4.38	
30	439606			myosin, light polypeptide 6, alkali, smo	1.39	4.03	
50		W79123	Hs.58561	G protein-coupled receptor 87	1.39	3.65	
	430135	NM_000035	Hs.234234	aldolase B, fructose-bisphosphate	1.37	3.99	
	422682	W05238	Hs.94316	ESTs, Weakly similar to T31613 hypotheti	1.36	3.30	
	408198	AA131111		gb:zo16b06.r1 Stratagene colon (937204)	1.36	3.33	
25	419600	AA448958	Hs.91481	NEU1 protein	1,35	3.49	
35	437141	BE304917	Hs.31097	hypothetical protein FLJ21478	1.34	3.47	
	408250	R92918	Hs.19597	KIAA1694 protein	1.34	3.89	
	430012	NM_015373	Hs.227637	chromosome 22 open reading frame 2	1.32	4.24	
	425183	W76098	Hs.19223	HCCA2 protein	1.32		
	427706	AW971225	Hs.293800			3.52	
40	438303	AB028998		ESTs, Weakly similar to ALU1_HUMAN ALU S	1.32	3.50	
10	406800		Hs.6147	KIAA1075 protein	1.32	3.71	
		AA505535		gb:nh84h10.s1 NCI_CGAP_Br1.1 Homo sapien	1.32	3.65	
	442533	AA161224	Hs.8372	ubiquinol-cytochrome c reductase (6.4kD)	1,32	4.14	
	428475	AF172940	Hs.184542	CGI-127 protein	1.31	3.43	
4.5	406742	AJ468091	Hs.279860	turnor protein, translationally-controlle	1.30	3.34	
45	432295	BE091049	Hs.343665	ribosomal protein \$15a	1.30	3.29	
	422959	AV647015		paired immunoglobulin-like receptor beta	1.28	3.53	
	402956	•		ENSP00000244002*:KIAA1335 protein (Fragm	1.24	3.38	
	406743	AA911568	Hs.279860	tumor protein, translationally-controlle	1.24	3.70	
	437142	AI791617	Hs.145068				
50	424372	AW952803	Hs.21732	ESTs, Moderately similar to A46010 X-lin	1.23	3.48	
•	414716			Homo sapiens cDNA FLJ11780 fis, clone HE	1.18	2.44	,
		AF199598	Hs.97044	Kv channel-interacting protein 2	1.18	3.43	·
	431931	AB035302	Hs.272212	cadherin 9, type 2 (T1-cadherin)	1,15	2.49	
	406587			C15000544*:gij5454148trefjNP_006368.1 U	1.06	2.25	
55	409574	AW419080	Hs.250645	ESTs	1.00	3.60	
55	417435	NM_005181	Hs.82129 ·	carbonic anhydrase III, muscle specific	1.00	3.44	
	402075			ENSP00000251056":Plasma membrane calcium	1.00	3.37	
	422330	D30783	Hs.115263	epiregulin	1.00	3.35	
	418986	AI123555	Hs.81796	ESTs .	1.00	3.28	
	404175			Target Exon	1.00	3.08	
60	452640	AA027115	Hs.100206	ESTs, Weakly similar to A53856 anyl-acyl	1.00	2.82	
	443564	AI921685	Hs.199713	ESTs			
	******	1.000	165.155715	LUIS	1.00	2.51	
	TABLES	en.					
	TABLE 64						
65	Pkey:		ue Eos probeset ider	tifier number			
65	CAT num		e cluster number	•			
	Accession	n: Gent	bank accession numb	ners			
	Pkey	CAT Number	Accession				
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3	412233	100032_1	4 4 4 6 4 C 2 2 1 D C	-140E3E A1003444 A1703734 AAQ4E3EE AWRRRRS A1837857 FRWK/ AI611148 AI/WWW AVYWS/04 NOLID I K/313Z WWW.
	•		AMPRIAGE D	CONNEN DICANINGA DYAAAA DOGORO WOANGE RE707744 REROQANI HE327552 BEDDYDUU AIA32366 AI241532 DE440104 AI2UDU (4
			AAB86528 N	0302 AW582776 BF110563 BF448329 BE326537 AW770471 BF444926 BE674147 AI793266 AI991774 AI807726 AI218667 AA301750
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20	424397	893246_1	AI950320 A	
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	431021	10409_1	NM_003312	BC010148 AK000862 D87292 BG709214 BF972766 BG740474 B1771592 B1159859 B1820468 B1523933 A1869664 AA314620 BF724353 IG195282 B1524679 BF435589 A1300546 AA481682 AW780207 A1800832 A1380540 BE722877 AW300707 AA941445 AW015893 A1381541
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40	TABLE 6			
	Pkey:	. Ur	ique number co	rresponding to an Eos probeset The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA"
	Ref:	56	quence source.	in chromosome 22 Dunham, et al. (1999) Nature 402:489-495.
	Strand:	tne	ficates DNA stra	and from which exons were predicted.
45	Nt_positi	on: tn	ficates nucleotic	le positions of predicted exons.
	~	D./	Chand	No applies
	Pkey 401781	Ref 7249190	Strand Minus	NL_position 83215-83435,83531-83656,83740-83901,8423
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
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	403593	6862650	Minus	62554-62712,69449-59602
	400494	9714719	Plus	169845-170272
	400835			89366-89622
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00	401905	8671966	Plus	153965-154441,156599-156819
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65	401905 403180 401747 403108 404996 402575 402338 401205	8671966 7523976 9789672 8980955 6007890 9884830 6957691 9743388	Plus Minus Minus Plus Plus Minus	15365-154441,156599-156819 63603-63759 118596-118816,119119-119244,119609-11976 93253-93867 37999-38145,38652-38998,39727-39872,4055 1093742-1093883
65	401905 403180 401747 403108 404996 402575 402338	8671966 7523976 9789672 8980955 6007890 9884830 6957691 9743388 9719502	Plus Minus Minus Plus Plus Minus Minus Plus	153965-154441,156599-156819 63603-63759 118596-118816,119119-119244,119609-11976 93253-93667 37999-38145,38652-38998,39727-39872,4055 109742-109883 36915-37250 167373-167433,167936-168031
	401905 403180 401747 403108 404996 402575 402338 401205 401192 406400 404246	8671966 7523976 9789672 8980955 6007890 9884830 6957691 9743388 9719502 9256298 7406725	Plus Minus Minus Plus Plus Minus Minus Plus Minus Plus Minus Plus Minus Plus Plus	153965-154441,156599-156819 63603-63759 118596-118816,119119-119244,119609-11976 93253-93667 37999-38145,38652-38998,39727-39872,4055 109742-109883 36915-37250 167373-167433,167936-168031 69559-70101 1553-1712,1878-2140,4252-4385,5922-6077 82477-82628,82721-82817,82910-83071,8314
65 70	401905 403180 401747 403108 404996 402575 402338 401205 401192 406400 404246 401131	8671966 7523976 9789672 8980955 6007890 9884830 6957691 9743388 9745529 97556298 7406725 8699812	Plus Minus Minus Plus Plus Minus Minus Plus Minus Plus Minus Plus Plus Plus Minus	15365-154441,156599-156819 63603-63759 118596-118818,119119-119244,119609-11976 93253-93867 37999-38145,38652-38998,39727-39872,4055 109742-109883 36915-37250 167373-167433,167936-168031 69559-70101 1553-1712,1878-2140,4252-4385,5922-6077 82477-82628,82721-82817,82910-83071,8314 94802-94987,95804-95887,95322-96487,9759
	401905 403180 401747 403108 404996 402575 402338 401205 401192 406400 404246 401131	8671966 7523976 9789672 8980955 6007890 9884830 6957691 9743388 9719502 97406725 8699812 9795551	Plus Minus Minus Plus Plus Minus Minus Plus Minus Plus Minus Plus Minus Plus Plus Plus Minus	153965-154441,156599-156819 63603-63759 118596-118818,119119-119244,119609-11976 93253-93667 37999-38145,38652-38998,39727-39872,4055 109742-109883 36915-37250 167373-167433,167936-168031 69559-70101 1553-1712,1878-2140,4252-4385,5922-6077 82477-82628,827271-82817,82910-83071,8314 94802-94987,95804-95887,96323-96487,9759 182212-1822958
	401905 403180 401747 403308 404996 402575 401205 401192 406400 404246 401131 406467 403105	8671966 7523976 9789672 8980955 6007890 9884830 6957691 9743388 9719502 9256298 7406725 8699812 9795551 8980016	Plus Minus Minus Plus Plus Minus Minus Minus Minus Plus Minus Plus Plus Minus Plus Minus Plus Minus Minus	153965-154441,156599-156819 63603-63759 118596-118816,119119-119244,119609-11976 93253-93567 37999-38145,38652-38998,39727-39872,4055 109742-109883 36915-37250 167373-167433,167936-168031 69559-70101 1553-1712,1878-2140,4252-4385,5922-6077 82477-82628,82721-82817,82910-83071,8314 94802-94987,95804-95887,95323-96487,9759 182212-182958
70	401905 403180 401747 403108 404996 402575 402338 401205 401192 406400 404246 401131 406467 403105 401425 401425 401425	8671966 7523976 9789672 8980955 6007890 9884830 9743388 9719502 9256298 7406725 8699812 9795551 9880016 9817890 7631064	Plus Minus Minus Plus Plus Minus Minus Plus Minus Plus Minus Plus Minus Plus Plus Plus Minus	153965-154441,156599-156819 63603-63759 118596-118818,119119-119244,119609-11976 93253-93667 37999-38145,38652-38998,39727-39872,4055 109742-109883 36915-37250 167373-167433,167936-168031 69559-70101 1553-1712,1878-2140,4252-4385,5922-6077 82477-82628,82727-82817,82910-83071,8314 94802-94987,95804-95887,96323-96487,9759 182212-182958 145287-145744 86946-87579 161294-161579
	401905 403180 401747 403108 404996 402575 402138 401205 406400 402464 401131 406467 403105 4040295	8671966 7523976 9789672 8980955 6007890 9884830 6957691 9743388 9719502 9256298 7406725 68998016 8980016 8217690 7631064 59408727	Plus Minus Minus Plus Plus Minus Minus Plus Minus Plus Minus Plus Minus Minus Minus Minus Minus Minus	153965-154441,156599-156819 63603-63759 118596-118818,119119-119244,119609-11976 93253-93567 37999-38145,38652-38998,39727-39872,4055 109742-109883 36915-37250 167373-167433,167936-168031 69559-70101 1533-1712,1878-2140,4252-4385,5922-6077 82477-82628,82727-82817,82910-83071,8314 94802-94987,95804-95887,96323-96487,9759 182212-182958 145287-145744 86946-87579 161294-161579 135901-136035
70	401905 403180 403187 404956 402573 401205 401192 406404 401131 404246 401131 404246 40299 40299 402995 402587	8671966 7523976 9789672 8980875 6607893 9884830 6957691 9715082 9715082 975525 7406725 7406726 9898016 981277830 981277830 981277830	Plus Minus Minus Plus Plus Minus Minus Minus Minus Minus Plus Minus Plus Minus Plus Minus Minus Minus Minus Minus Minus Minus Minus Minus	15365-15441,15659-156819 63603-63759 118596-118818,119119-119244,119609-11976 93253-93567 37993-38145,38652-38998,39727-39872,4055 109742-109383 36915-37250 167373-167433,167936-168031 69559-70101 1553-1712,1878-2140,4252-4385,5922-6077 82477-82628,82721-82817,82910-83071,8314 94002-94987,95504-95887,95323-96487,9759 182212-182958 145287-145744 86946-87579 161294-161579 135901-136035 120577-120718
70	401905 403180 401747 403108 404996 402575 402138 401205 406400 402464 401131 406467 403105 4040295	8671966 752396 9789672 8980955 6007890 9848430 6957691 9743388 9719502 9256298 7406725 6859812 9795551 8859812 9795551 8980016 8217890	Plus Minus Minus Plus Plus Minus Minus Plus Minus Plus Minus Plus Minus Minus Minus Minus Minus Minus	153965-154441,156599-156819 63603-63759 118596-118818,119119-119244,119609-11976 93253-93567 37999-38145,38652-38998,39727-39872,4055 109742-109883 36915-37250 167373-167433,167936-168031 69559-70101 1533-1712,1878-2140,4252-4385,5922-6077 82477-82628,82727-82817,82910-83071,8314 94802-94987,95804-95887,96323-96487,9759 182212-182958 145287-145744 86946-87579 161294-161579 135901-136035

TABLE 55A: ABOUT 838 GENES DOWNREGULATED IN BENIGN NEVI RELATIVE TO NORMAL SKIN
Table 55A lists about 838 genes downregulated in benign nevi relative to normal skin. Genes were selected from 59880 probesets on the Eos/Alfymetrix Hu03 Genectrip array. Gene
expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

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Pkey: ExAcon: UnigenetD: Unigene Title: R1: R2: 5

Unique Eos probeset identifier number
Exemplar Accession number, Genbank accession number
Unigene number
Unigene number
Unigene gene title
90th percentille of normal skin Als divided by the average of benign nevi Als
90th percentille of normal skin Als divided by the average of benign nevi Als, where the 15th percentile of normal tissue Als was subtracted from both the numerator and denominator

••	Pkey	ExAcon	UnigenelD	Unigene Tide	R1	R2
10	420813	X51501	Hs.99949	prolactin-induced protein	27.72	28.59
	408591	AF015224	Hs.46452	mammaglobin 1	26.40	28.34
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	21.33	21.57
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	18.06	18.96
15	429441 428087	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	16.61	18.06
13	407245	AA100573 X90568	Hs.182421 Hs.172004	troponin C2, fast titin	14.70 13.08	14.60 13.84
	428824	W23624	Hs.173059	ESTs	12.89	13.36
	428330	1.22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	12.78	13.98
	444816	Z48633	Hs.283742	H.sapiens mRNA for retrotransposon	12.26	9.86
20	453309	AI791809	Hs.32949	defensin, beta 1	12.02	10.62
	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALUS_HUMAN A	11.90	10.86
	446227	AI281459	Hs.270114	ESTs	11.79	12.32
	413902	AU076743	Hs.75613	CD36 antigen (collagen type I receptor,	11.19	10.82
25	432877	AW974111	Hs.292477	ESTs	11.18	11.30
25	426752	X69490	Hs.172004	titin	10.97	12.63
	427899	AA829286	Hs.332053	serum amyloid A1	10.85	13.85
	407230 451029	AA157857	Hs.182265	keratin 19	10.79	11.40
	421296	AA852097 NM_002666	Hs.25829 Hs.103253	ras-related protein penlipin	10.78 10.73	10.35 11.25
30	431211	M86849	Hs.323733	gap junction protein, bela 2, 26kD (conn	10.75	7.24
	422633	X56832	Hs.118804	enclase 3, (beta, muscle)	10.57	9.92
	405121			mitogen-activated protein kinase 8 inter	10.41	10.54
	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	10.26	23.20
	420859	AW468397	Hs.100000	S100 catcium-binding protein A8 (calgran	10.25	9.45
35	410850	AW362867	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	10.15	9.88
	416931	D45371	Hs.80485	adipose most abundant gene transcript 1	10.13	11.58
	447966	AA340605	Hs.105887	ESTs, Wealthy similar to Homolog of rat Z	10.09	5.51
	401203			Target Exon	9.95	10.74
40	425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	9.94	11.47
40	425580	L11144	Hs.1907	galanin	9.66	6.60
	414092 420919	Z14244 M57892	Hs.75752 Hs.100322	cytochrome c oxidase subunit VIIb	9.45	6.44
	443162	T49951	Hs.9029	carbonic anhydrase VI	9.41	10.49
	430154	AW583058	Hs.234726	DKFZP434G032 protein serine (or cysteine) proteinase inhibito	9.36 8.91	10.58 10.27
45	452322	BE566343	Hs.28988	glutaredoxin (thioftransferase)	8.90	7.26
	430071	AA355986	Hs.232068	transcription factor 8 (represses interl	8.86	8.94
	417240	N57568	Hs.48028	EST	8.81	18.90
	415477	NM_002228	Hs.78465	v-jun avian sarcoma virus 17 oncogene ho	8.72	6.86
60	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (8.39	10.26
50	408491	AI088063	Hs.7882	ESTs	8.00	8.20
	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	7.99	8.14
	409738	8E222975	Hs.56205	insulin induced gene 1	7.95	7.75
	428221 451831	U96781	Hs.183075	ATPase, Ca transporting, cardiac muscle,	7.89	8.86
55	410867	NM_001674 X63556	Hs.460 Hs.750	activating transcription factor 3 fibrillin 1 (Marfan syndrome)	7.7 9 7,76	7.51 7.55
00	444984	H15474	Hs.132898	fatty acid desaturase 1	7.75	5.64
	413076	U10564	Hs.75188	weet (S. pombe) homolog	7.68	5.65
	410532	T53088	Hs.155376	hemoglobin, beta	7.64	4.73
	442757	AI739528	Hs.28345	ESTS	7.62	7.66
60	412047	AA934589	Hs.49696	ESTs	7.61	7.48
	410052	AA525225	Hs.334630	Homo sapiens cDNA FLJ14462 fis, clone MA	7.52	7.28
	439394	AA149250	Hs.56105	ESTs	7.52	6.72
	442941	AU076728	Hs.8867	cysteine-rich, angiogenic Inducer, 61	7.51	6.27
65	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	7.51	4.10
65	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (catgran	7.49	8.08
	407334	AA494411	Hs.296031	ESTs	7.48	6.78
	414449 432305	AA557660	Hs.76152	decorin	7.39	8.30
	407328	M62402 AA508857	Hs.274313	insufin-like growth factor binding prote	7.38	8.79
70	431842	NM_005764	Hs.271473	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.35	7.20 6.93
, ,	426488	X03350	Hs.4	epithelial protein up-regulated in carci alcohol dehydrogenase 18 (class I), beta	7.06 7.03	7.85
	445502	AW379160	Hs.12813	DKFZP434J214 protein	7.01	6.63
	419285	D31887	Hs.89868	KIAA0062 protein	7.01	5.82
	409024	AW883529	Hs.173830	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.99	4.58
75	422963	M79141	Hs.13234	ESTs	6.99	4.08
	447918	Al129320	Hs.115175	ESTs, Highly similar to JC5818 gamma-act	6.98	6.49
	410530	M25809	Hs.64173	ATPase, H transporting, lysosomal (vacuo	6.96	7.04
	444381	BE387335	Hs.283713	ESTs, Weakly similar to \$64054 hypotheti	6.95	8.08
9Λ	417993	AW963705	Hs.301183	molecule possessing ankyrin repeats indu	6.94	7.12
80	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	6.94	6.79
	427890 444207	AA435761		ESTs	6.94	6.68
	4444	AI565004		cathepsin O (lysosomal aspartyl protease	6.93	4.66
	442083	R50192	Hs.165062	ESTs	6.92	6.92

	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	6.87	5.07
	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin 86) kinas	6.87	4.99
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	6.84	5.33
•	414841	H55601	Hs.77490	glutathione S-transferase theta 1	6.84	3.47
5	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	6.79	7.14
	427704 431713	AW971063 AK000388	Hs.292882 Hs.267997	ESTs EHM2 gene	6.72 6.72	7.30 7.10
	451253	H48299	Hs.26126	claudin 10	6.71	7.20
	453187	AI161383	Hs.34549	ESTs, Highly similar to \$94541 1 clone 4	6.68	3.02
10	400304	AF005082	Hs.113261	Homo sapiens skin-specific protein (xp33	6.64	6.08
	434525	W01370	Hs.46824	ESTs	6.61	6.92
	408063	8E086548	Hs.42346	calcineurin-binding protein calsarcin-1	6.60	7.29
	425280 411388	U31519 X72925	Hs.1872 Hs.69752	phosphoenolpyruvate carboxykinase 1 (sol desmocollin 1	6.55 6.55	6.79 3.44
15	413731	BE243845	Hs.75511	connective tissue growth factor	6.52	4.86
	455863	AA907305	Hs.36475	ES7s	6.50	4.24
	412247	AF022375	Hs.73793	vascular endothelial growth factor	6.49	4.56
	407102	AA007629		glycerol-3-phosphate dehydrogenase 1 (so	6.47	7.23
20	421407	TB2331	Hs.182278	ESTs, Weakly similar to CGHU6C collagen	6.47	6.55
20	406867 429504	AA157857 X99133	Hs.182265 Hs.204238	keratin 19 lipocatin 2 (oncogene 24p3) (NGAL)	6.44 6.43	6.23 6.79
	446945	A1193115	Hs.16611	tumor protein D52-like 1	6.43	5.66
	413172	M38180	Hs.38586	hydroxy-delta-5-steroid dehydrogenase, 3	6.39	7.09
25	407395	AF005082		gb:Homo sapiens skin-specific protein (x	6.39	4.76
25	450626	AW190989	Hs.1508	Insulin-degrading enzyme	6.37	6.22
	450713	AL133611	Hs.25362	Homo sapiens mRNA; cDNA OKFZp43401317 (f	6.37	4.91
	437596 430191	AA761490 Al149880	Hs.188809	ESTs, Moderately similar to S65657 alpha ESTs	6.35 6.34	5.31 6.15
	433713	AW976511	Hs.112592	ESTs	6.34	5.67
30	420107	AL043980	Hs.7886	pellino (Drosophila) homolog 1	6.33	6.39
	422069	AJ010063	Hs.343603	titin-cap (telethonin)	6.33	5.77
	437176	AW176909	Hs.42346	calcineurin-binding protein calsardin-1	6.30	5.45
	433412	AV653729	Hs.8185	CGI-44 protein; suffide dehydrogenase fi	6.29	6.68
35	447335 413063	BE617695 AL035737	Hs.286192 Hs.75184	hypothetical protein FLJ20940 chitinase 3-like 1 (cartilage glycoprote	6.28 6.21	10.35 5.98
33	440116	A1798851	13.73104	hemoglobin, gamma G	6.18	6.86
	454229	AW957744	Hs.278469	lacrimal proline rich protein	6.17	6.54
	441188	AW292830	Hs.255609	ESTs	6.12	6.68
40	451144	AW956103	Hs.61712	pyruvate dehydrogenase kinase, isoenzyme	6.12	5.79
40	431319 442498	AA873350	Hs.302232	ESTs	6.11	7.91
	414555	U54617 N98569	Hs.8364 Hs.76422	Homo sapiens pyruvate dehydrogenase kina phospholipase A2, group IIA (platelets,	6.10 6.08	5.63 6.96
	418321	D63477	Hs.84087	KIAA0143 protein	6.08	4.71
	443072	AI937532		gb:wp78d02.x1 NCI_CGAP_Bm25 Homo sapien	6.07	5.48
45	423712	W46802	Hs.81988	disabled (Drosophila) homolog 2 (mitogen	6.04	5.81
	442679	R53718		hypothetical protein FLJ 10659	6.03	5.67
	424824	AI217440	Hs.143873	ESTs	6.02	5.46
	413719 428358	BE439580 AA993222	Hs.75498 Hs.101915	small inducible cytokine subfamily A (Cy Stargardt disease 3 (autosomal dominant)	6.01 5.94	7.05 7.17
50	430821	AA487264	Hs.154974	Homo sapiens mRNA; cDNA DKFZp667N064 (fr	5.92	5.79
	424670	W61215	Hs.116651	epithelial V-like antigen 1	5.92	5.63
	424673	AA345051	Hs.294092	ESTs, Weakly similar to 138022 hypotheti	5.91	6.81
	418205	L21715	Hs.83760	troponin I, skeletal, fast	5.91	6.95
55	400440 444239	X83957 R57988	Hs.83870 Hs.10706	nebulin	5.89 5.89	7.01 5.49
23	419517	AF052107	Hs.90797	epithelial protein lost in neoplasm beta Homo sapiens clone 23620 mRNA sequence	5.86	5.88
	432626	AA471098	Hs.278544	acetyl-Coenzyme A acetyltransferase 2 (a	5.86	5.58
	407584	W25945	Hs.8173	hypothetical protein FLJ10803	5.81	5.09
60	449335	AW150717	Hs.345728	STAT induced STAT inhibitor 3	5.79	6.33
60	445607	AA488107	Hs.30156	ESTs, Weakly similar to unnamed protein	5.78	5.91
	424571 412630	BE379766 AA738437	Hs.26226	polymerase (RNA) II (DNA directed) polyp Homo sapiens cDNA: FLJ21286 fis, clone C	5.78 5.76	3.74 4.21
	408819	AW163483	Hs.48320	double ring-finger protein, Dorfin	5.71	4.59
	433027	AF191018	Hs.279923	putative nucleotide binding protein, est	5.70	4.71
65	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	5.68	6.12
	408515	AI289507	Hs.299883	hypothetical protein FLJ23399	5.67	4.81
	443827	A1087867	Hs.134667	ESTs	5.67	5.54
	429693 427373	8E254962 A8007972	Hs.211612 Hs.130760	SEC24 (S. cerevisiae) related gene famil myosin phosphatase, target subunit 2	5.67 5.66	4.12 4.27
70	428666	AL080190	Hs.189242	Homo sapiens mRNA; cDNA DKFZp434A202 (fr	5.65	5.16
	421834	BE543205	Hs.288771	DKFZP586A0522 protein	5.65	4.52
	427081	AI474533	Hs.170528	ESTs, Moderately similar to ALUC_HUMAN!	5.65	4.81
	419731	S47242	Hs.92909	SON DNA binding protein	5.64	3.77
75	420787	AA564248 A1380552	He goens	ESTs, Weakly similar to 138022 hypotheti	5.64	3.27
,,	420682 410541	AJ380552 AA065003	Hs.88602 Hs.64179	ESTs syntenin-2 protein	5.63 5.62	4.13 5.84
	431360	NM_000427		loricrin	5.62 5.61	5.14
	418127	BE243982	Hs.83532	membrane cofactor protein (CD46, trophob	5.61	4.28
00	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	5.60	5.76
80	427850		Hs.161051	ESTs, Moderately similar to ALU6_HUMAN A	5.51	16.04
	429679			tumor necrosis factor, alpha-induced pro hypothetical protein	5.49 5.40	5.28
	422082 419461		Hs.111244 Hs.288869	nuclear receptor subfamily 2, group F, m	5.49 5.49	5.23 4.40
	. 10401				4.75	7,70

						0.22
	430714	AA484757	Hs.287601	Homo sapiens cDNA FL113830 fis, clone TH	5.48	5.38
	407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	5.46 5.45	5.11 3.63
	400494		II. 40753	ENSP0000238970*:CIG30 (Fragment).	5.43 5.43	4.25
5	415062 449291	H45100 BE176893	Hs.49753 Hs.23440	uveal autoantigen with coiled coil domai KIAA1105 protein	5.41	3.82
-	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	5.41	2.62
	417035	AA192455	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	5.40	5.40
	434535	AI611729	Hs.167619	ESTs, Moderately similar to ALUC_HUMAN !	5.40	5.20
10	408085	N25929	Hs.342849	ADP-ribosytation factor-like 5	5.39 5.37	4.59 14.96
10	413778 435090	AA090235 AI640635	Hs.75535 Hs.332879	myosin, light polypeptide 2, regulatory, EST	5.37	5.33
	406805	A1686003	Hs.296031	ESTs	5.35	5.49
	426510	AW861225	Hs.251928	BANP homolog, SMAR1 homolog	5.35	6.83
	406706	X03740	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	5.34	7.50
15	456332	AA228357		gb:nc39d05.r1 NCI_CGAP_Pr2 Homo sapiens	5.34	4.88
	421999	U50535	Hs.110630	Human BRCA2 region, mRNA sequence CG006	5.34 5.34	4.75 3.59
	418479	AA829976	Hs.81071	mannosidase, afpha, class 1A, member 2 extracellular matrix protein 1	5.34	4.71
	417059 424008	AL037672 R02740	Hs.137555	putative chemokine receptor, GTP-binding	5.34	4.5
20	415694	AW194301	Hs.339283	Human DNA sequence from clone RP1-187J11	5.34	8.69
	452747	BE153855	Hs.61460	lg superfamily receptor LNIR	5.31	5.81
	449271	AW338067	Hs.7869	Homo sapiens cDNA FLJ11946 fis, clone HE	5.30	4.35
	437135	AL038624	Hs.208752	ESTs, Weakly similar to ALUS_HUMAN ALU S	5.29	4.92 5.02
25	419925	AA159850	Hs.93765	liporna HMGIC fusion partner aldo-keto reductase family 1, member C3	5.29 5.28	5.33
23	415192 453999	D17793 8E328153	Hs.78183 Hs.240087	ESTs	5.28	3.40
	408958	T99607	Hs.49346	signal recognition particle 54kD	5.28	2.84
	452496	AA114926	Hs.169531	ESTs	5.28	5.48
20	424058	AL121516	Hs.138617	thyroid hormone receptor interactor 12	5.27	3.72
30	443265	AI916207	Hs.9167	SH3 domain binding glutamic acid-rich pr	5.26 5.26	4.62 6.21
	407013	U35637	Hs.83870 Hs.76550	gb:Human nebulin mRNA, partial cds Horno sapiens mRNA; cDNA DKFZp564B1264 (f	5.26	4.21
	414602 410284	AW630088 U50939	Hs.61828	amyloid beta precursor protein-binding p	5.26	4.43
	445107	AJ208121	Hs.147313	ESTs, Weakly similar to 138022 hypotheti	5.25	5.61
35	446267	AW450103	Hs.151124	ESTs	5.24	4.44
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	5.23	3.14
	448585	AB020676	Hs.21543	KIAA0869 protein	5.23 5.22	6.21 6.84
	421993	R22497 AA147026	Hs.110571 Hs.76704	growth arrest and DNA-damage-inducible, ESTs	5.22	5.29
40	414407 423720	AA147026 AL044191	Hs.23388	hypothetical protein DKFZp434F0318	5.22	5.85
10	415997	NM_003590	Hs.78946	cuttin 3	5.21	3.66
	411531	AB014511	Hs.70604	ATPase, Class II, type 9A	5.21	3.95
	441619	NM_014056		DKFZP564K247 protein	5.20	4.38
45	435232	NM_001262		cyclin-dependent kinase inhibitor 2C (p1	5.19 5.19	4.52 3.13
45	415167	AA160784	Hs.26410 Hs.178604	ESTs ESTs	5.18	5.38
	431416 439995	AA532718 AL137480	Hs.6834	KIAA1014 protein	5.17	3.14
	416784	AA334592	Hs.79914	turnican	5.17	6.18
	446082	AJ274139	Hs.156452	ESTs	5.16	5.14
50	400196			Eos Control	5.16	5.05
	414525	C14904	Hs.45184	Homo sapiens cONA FLJ12284 fis, clone MA	5.16 5.15	4.31 4.89
	414242	AA74923D AW969847	Hs.26433 Hs.292718	dolichyl-phosphate (UDP-N-acetylghucosam ESTs, Wealdy similar to RET2_HUMAN RETIN	5.14	5.22
	430699 440383	AA884208	Hs.30484	ESTs	5.13	5.09
55	431628	AF146277	1.5.00 10 1	CD2-associated protein	5.13	5.03
	407047	X65965		gb:H.sapiens SOD-2 gene for manganese su	5.13	4.31
	433688	AA628467	Hs.112572	Homo sapiens cDNA FLJ14130 fis, clone MA	5.12	3.57
	437704	AA766142	Hs.131810	ESTs, Moderately similar to ALU1_HUMAN A	5.12 5.11	3.30 6.08
60	426101	AL049987 AA236291	Hs.183583	Homo sapiens mRNA; cDNA DKFZp564F112 (fr serine (or cysteine) proteinase inhibito	5.10	4.31
00	428297 416382	D86985	Hs.79276	KIAA0232 gene product	5.10	3.79
	437150	R51407	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	5.10	6.58
	454947	AW846590		gb:QV0-CT0180-011099-025-d07 CT0180 Homo	5.09	4.82
	434647	W74158	Hs.103189	lipopolysaccharide specific response-68	5.09	4.90
65	418730		Hs.325625	Homo sapiens done 23938 mRNA sequence	5.09 5.09	3.46 6.26
	449338		Hs.394	adrenomedutin gb:hn41c11.x1 NCI_CGAP_RDF2 umo sapiens	5.09 5.08	5.60
	438962 431693			serine (or cysteine) proteinase intribito	5.07	2.83
	420583		Hs.65450	reticulon 4	5.06	6.71
70	431048		Hs.249129	cell death-inducing DFFA-like effector a	5.06	6.06
	432125			Homo sapiens cDNA FLJ12300 fis, clone MA	5.05	6.32
	447945		Hs.9670	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.05 5.05	3.72 2.86
	442547		Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S EDG-2 (endothelial differentiation, lys	5.03	4.43
75	414176 445263		Hs.75794 Hs.42586	KIAA1560 protein	5.03	6.67
, ,	448490		Hs.271692	ESTs, Weakly similar to 138022 hypotheti	5.03	4.88
	450515			biphenyl hydrolase-like (seriné hydrolas	5.03	4.36
	440624	AF017987	Hs.7306	secreted frizzled-related protein 1	5.01	5.48
90	417165		Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	5.01 5.01	5.61 5.32
80	417640		Hs.82353	protein C receptor, endothelial (EPCR) ESTs	5.01 5.01	3.90
	413475			hypothetical protein FLJ23309	5.00	4.54
	424074		Hs.210761	ESTs, Weakly similar to 138022 hypotheti	5.00	3.19

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And the second

	424620	AA101043	Hs. 151254	kalākrein 7 (chymotryptic, stratum com	4.99	6.25
	439039	AI656707	Hs.48713	ESTs	4.99	6.60
	422305	AI928242	Hs.293438	ESTs, Highly similar to AF198488 1 trans	4.98	9.59
5	410579	AK001628	Hs.64691	KIAA0483 protein	4.98 4.98	4.52 3.84
,	449710 434230	AA002207 AA551569	Hs.17385	Homo sapiens clone IMAGE:119716, mRNA se hypothetical protein PRO2822	4.98	3.63
	426458	AA379306	Hs.117558	ESTs	4.98	3.56
	421690	AW162667	Hs.106857	calbindin 2, (29kO, calretinin)	4.96	6.41
10	448144	AW169230		ESTs, Moderately similar to PC4259 ferri	4.96 4.96	3.28 5.75
10	412129 450071	M21984 AA018283	Hs.73454 Hs.24359	troponin T3, skeletal, fast Homo sapiens cDNA FLJ11174 fis, clone PL	4.96	3.21
	433934	AW273261	Hs.216292	ESTs	4.95	4.39
	446320	AF126245	Hs.14791	acyl-Coenzyme A dehydrogenase family, me	4.95	4.01
16	446161	AA628206	Hs.14125	p53 regulated PA26 nuclear protein	4.94 4.94	4.54 4.49
15	453225 444476	BE258769 AF020038	Hs.11223	acetyl-Coenzyme A acyttransferase 2 (mit isocitrate dehydrogenase 1 (NADP), soluti	4.94	4.19
	445493	AI915771	15.11225	metallothionein 1E (functional)	4.93	5.68
	422292	Al815733	Hs.114360	transforming growth factor beta-stimulat	4.93	5.47
20	417054	AF017060		aldehyde oxidase 1	4.93 4.93	4.51 3.34
20	425917	W28517	Hs.117167 Hs.281462	Homo sapiens cDNA: FLJ23067 fis, clone L ESTs, Wealdy similar to 138022 hypotheti	4.93	5.61
	408681 451267	AW953853 Al033894	Hs.117865	solute carrier family 17 (anion/sugar tr	4.92	3.27
	447137	AW970192	Hs.171942	ras responsive element binding protein 1	4.91	4.26
25	427451	A1690916	Hs.178137	transducer of ERBB2, 1	4.90	6.00
25	432314	AA533447	Hs.312989	ESTs phosphotidytinositol transfer protein, b	4.90 4.89	3.79 3.71
	440692 428594	AL031591 BE387236	Hs.7370 Hs.75415	beta-2-microglobulin	4.89	3.27
	437802	AJ475995	Hs.122910	ESTs	4.87	4.06
	437974	T74445	Hs.5957	Homo sapiens clone 24416 mRNA sequence	4.86	6.54
30	427156	BE621719	Hs.173802	KIAA0603 gene product	4.86 4.86	5.15 5.50
	433179 428957	AW362945 NM_003881	Hs.162459 Hs.194679	ESTs WNT1 inducible signaling pathway protein	4.85	5.29
	453855	AA039576	Hs.37858	ESTs, Weakly similar to ALUB_HUMAN !!!!	4.85	3.59
	433143	BE552155	Hs.294035	ESTs, Weakly similar to ALUS_HUMAN ALU S	4.85	3.45
35	429279	AB018271	Hs.198689	KIAA0728 protein	4.83	3.80
	445773	H73456	Hs.13299	Homo sapiens mRNA; cDNA DKFZp761M0111 (f	4.82 4.82	4.20 4.01
	416349 408138	X69089 AA535740	Hs.79227	myomesin (M-protein) 2 (165kD) tumor protein p53-binding protein, 1	4.81	4.19
	432566	AW439330	Hs.256889	ESTs, Weakly similar to 2109260A B cell	4.80	3.99
40 ⁻	444677	AL110212	Hs.301005	purine-rich element binding protein B	4.80	3.50
	422658	AF231981	Hs.250175	homolog of yeast long chain polyunsatura	4.80	10.20
	431926	AW972724	Un 161FCE	gb:EST384816 MAGE resequences, MAGL Horno	4.79 4.79	4.39 2.98
	407839 421998	AA045144 R74441	Hs.161566	ESTs poly(A)-binding protein, nuclear 1	4.77	4.78
45	416987	D86957	Hs.80712	KIAA0202 protein	4.76	3.99
	448988	Y09763	Hs.22785	gamma aminobutync acid (GABA) A recepto	4.76	7.59
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha ESTs, Highly similar to T42626 secreted	4.75 4.75	4.38 3.92
	453180 413276	N46243 Z24725	Hs.110373 Hs.75260	mitogen inducible 2	4.75	5.68
50	437239	AW503395	Hs.5541	ATPase, Ca transporting, ubiquitous	4.74	5.57
	414622	A1752666	Hs.76669	nicotinamide N-methyltransferase	4.74	11.58 3.79
	429587	AA283969	Hs.334706	Homo saptens cDNA FLJ11801 fis, clone HE gb:Human nonspecific crossreacting antig	4.74 4.73	4.88
	407242 445229	M18728 BE276013	Hs.172364	Homo sapiens mRNA for FLJ00086 protein,	4.73	4.79
55	447429	AB007920	Hs.18586	KIAA0451 gene product	4.72	2.38
	444930	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	4.71	5.10
	414848	A1803447	Hs.77496	small nuclear ribonucleoprotein polypept ESTs, Wealdy similar to K1CJ_HUMAN KERAT	4.71 4.70	2.51 6.13
	439652 453145	W67826 R63438	Hs.55412 Hs.183454	Homo sapiens cDNA FLJ14883 fis, clone PL	4.70	3.06
60	421302	T34462	Hs.103291	neuritin	4.69	4.96
	425118	AU076611	Hs.154672	methylene tetrahydrofotate dehydrogenase	4.68	5.01
	448079	R76981	11- 20150	thyroid hormone receptor-associated prot	4.68 4.67	3.97 3.42
	434558 408239	AW264102 AA053401	Hs.39168	ESTs ESTs, Moderately similar to ALU7_HUMAN A	4.67	6.17
65	454416	AI912097	Hs.163208	ESTs	4.66	3.97
	427215	AW246148	Hs.268371	hypothetical protein FLJ20274	4.66	3.37
	451583		Hs.24133	ESTs	4.65	3.81 6.14
	446525		Hs.211556 Hs.54900	hypothetical protein MGC5487 serologically defined colon cancer antig	4.65 4.65	3.65
70	436176 450528			PRO0461 protein	4.64	2.99
	417259			chondroitin sulfate proteoglycan 2 (vers	4.64	4.72
	408741		Hs.646	carboxypeptidase A3 (mast cell)	4.63	5.55
	417733		Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	4.63 4.63	5.04 3.55
75	436280 428744		Hs.192853	Homo sapiens cDNA: FLJ22562 fis, clone H ubiquitin-conjugating enzyme E2G 2 (homo	4.63	2.85
, ,	427007			transforming, acidic coited-coit contain	4.63	3.00
	453767			extracellular matrix protein 2, female o	4.62	5.14
	449971	AA807346		Homo sapiens cDNA FLJ14296 fis, clone PL	4.62	4.49
80	409598			mitochondrial ribosomal protein S28	4.62 4.62	3.56 4.24
30	413305 412577		6 Hs.323511 Hs.74076	Homo sapiens cDNA: FLJ23176 fis, clone L CD163 antigen	4.61	8.03
	424046		Hs.138202	serine (or cysteine) proteinase inhibito	4.61	6.86
	452289			mitogen-activated protein kinase kinase	4.61	4.33
				C07		

	458971	AL119206	Hs.101874	ESTs, Weakly similar to ALUI_HUMAN ALU S	4.61	4.16
	433256	AW604447	Hs.339408	ESTs, Weakly similar to S26689 hypotheti	4.61 4.61	3.58 3.22
	440596	H13032	Hs.103378	hypothetical protein MGC11034 Homo sapiens mRNA; cDNA DKFZp564H1916 (I	4.60	4.74
5	427919	AA173942	Hs.326416	ESTs	4.60	4.11
,	424651 436701	AJ493206 AW959032	Hs.32425	ESTs, Moderately similar to 178885 serin	4.60	2.34
	413691	AB023173	Hs.75478	ATPase, Class VI, type 118	4.59	4.35
	448625	AW970786	Hs.178470	hypothetical protein FLJ22662	4.59	4.00
	436283	AI480319	Hs.120058	ESTs	4.59	3.76
10	451710	AW867467	Hs.278712	eukaryotic translation initiation factor	4.59	3.51
	436086	Z43133	Hs.9961	Homo sapiens cDNA: FLJ21954 fis, clone H	4.59	3.64
	434697	AL133033	Hs.4084	KIAA1025 protein	4.58	5.10
	402294			Target Exon	4.57	5.47
15	424098	AF077374	Hs.139322	small proline-rich protein 3	4.57 4.57	5.12 4.66
15	406648	AA563730 AU076517	Hs.277477	major histocompatibility complex, class sotute carrier family 9 (sodium/hydrogen	4.57	4.15
	428423 441566	AA604110	Hs.184276 Hs.151725	ESTs	4.57	3.21
	400109	AA004110	15.131123	Ecs Control	4.56	4.76
	419740	AB037835	Hs.92991	KIAA1414 protein	4.56	3.63
20	421481	AW391972	Hs.104696	KIAA1324 protein	4.55	7.16
	440266	AA088809	Hs.19525	hypothetical protein FLJ22794	4.55	4.44
	421979	AW062518	Hs.233150	hypothetical protein MGC5560	4.55	4.36
	408702	AW959893	Hs.27099	hypothetical protein FLJ23293 similar to	4.54	5.78
25	418021	M15881	Hs.1137	uromodulin (uromucoid, Tamm-Horsfall gly	4.54	4.61
25	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	4.54 4.54	4.32 2.59
	421986	AL137438	Hs.110454	SEC15 (S. cerevisiae)-like	4.53	6.18
	414798	AI286323	Hs.97411 Hs.300945	hypothetical protein MGC12335 Microfibril-associated glycoprotein-2	4.53	5.87
	410132 449843	NIM_003480 R85337	Hs.24030	solute carrier family 31 (copper transpo	4.53	4.87
30	424399	A1905687	113.24000	AJ905687:IL-BT095-190199-019 BT095 Homo	4.53	10.61
20	452924	AW580939	Hs.97199	complement component C1q receptor	4.51	6.07
	454000	AA040620	Hs.5672	hypothetical protein AF140225	4.51	4.59
	404730			Target Exon	4.51	4.30
	449943	AF104266	Hs.24212	latrophilin	4.51	3.40
35	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	4.50	2.97
	435992	AI033259	Hs.118317	Homo sapiens cDNA FLJ12088 fis, clone HE	4.50	4.77 3.30
	421311	N71848	Hs.283609	hypothetical protein PRO2032	4.50 4.49	5.06
	449785	AJ225235	Hs.288300	hypothetical protein FLJ23231 gb:am08a06.s1 Soares_NFL_T_GBC_S1 Homo s	4.49	4.24
40	437611 419612	AA897108 AI498267	Hs.110613	KIAA0421 protein	4.49	4.16
40	414496	W73853	113.110013	ESTs	4.49	3.15
	450306	AL080080	Hs.24766	thioredoxin domain-containing	4.48	3.38
	444895	AI674383	Hs.22891	solute carrier family 7 (cationic amino	4.47	4.45
	432559	AW452948	Hs.257631	ESTs	4.47	5.39
45	442554	AW467376	Hs.129640	ESTs	4.47	4.00
	421429	NM_014922		death effector filament-forming Ced-4-fi	4.46	4.47
	422313	AF045941	Hs.115166	sciellin	4.45 4.45	5.07 3.35
	435748	AA699756	Hs.117335	ESTs	4.45	3.28
50	453283 441925	AA694386 R83113	Hs.290914	ESTs protein kinase C substrate BOK-H	4.45	3.28
50	440030	AA932693		EST STANDSE C STANDARD CONTAIN	4.45	3.20
	446515	AL048875		hypothetical protein DKFZp5661133	4.44	3.66
	406707	S73840	Hs.931	myosin, heavy polypeptide 2, skeletal mu	4.44	5.90
	432341	AL137662	Hs.274401	Homo sapiens mRNA; cDNA DKFZp434P086 (fr	4.44	3.99
55	410453	AW749036		gb:RC2-BT0318-241199-011-f10 BT0318 Homo	4.44	3.49
	450196	AW956868	Hs.24608	DKFZP564D177 protein	4.43	4.13
	444147	A8002306	Hs.10351	KIAA0308 protein	4.43 4.42	3.95 3.88
	427809	M26380	Hs.180878	lipoprotein lipase hexokinase 2	4.42	5.46
60	428157 413299	A1738719 AA857487	Hs.198427 Hs.75275	ubiquitination factor E4A (homologous to	4.42	3.77
00	440245		Hs.7100	hypothetical protein	4.42	3.51
	442379			transglutaminase 2 (C polypeptide, prote	4.42	1.79
	408569		Hs.86412	chromosome 9 open reading frame 5	4.42	3.35
	430361		Hs.239926	sterol-C4-methyl oxidase-like	4.41	5.78
65	414489		Hs.73105	ESTs	4.41	5.43
	447731	AA373527	Hs.19385	CGI-58 protein	4,41	5.28
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	4.41	4.41
	448503		Hs.21332	BT8 (POZ) domain containing 1	4.41	3.68
70	432546		Hs.180638	hypothetical protein FLJ13081	4.41	3.55 3.44
70	445620		Hs.17441	ESTS	4.41 4.41	3.43
	454065		Hs.88500	gb:601311808F1 NIH_MGC_44 Homo sapiens c mitogen-activated protein kinase 8 inter	4.40	2.04
	418802		Hs. 190738	ESTs	4.39	4.26
	431816 429138		Hs.197298	NS1-binding protein	4.39	4.47
75	426643		Hs.171595	HIV TAT specific factor 1	4.39	3.09
. •	44894		Hs.193288	ESTs	4.39	2.63
	41400			FBJ murine osteosarcoma viral oncogene h	4.37	19.16
	403593	3		Target Exon	4.37	6.35
90	40810			ESTs	4.31	5.82
80	42962			ESTs, Weakly similar to 13131848 alpha1	4.31 4.25	4.14 6.61
	42953			small proline-rich protein 2A	4.23	5.28
	41450		Hs.23558 Hs.170673	ESTs, Weakly similar to A48042 lysosomal ESTs, Weakly similar to T24832 hypotheti	4.18	5.81
	43853	3 AI440266	113.110013	CS1S, Weakly Stithar to 124032 hypotheti		

	426143	8E379836		proteasome (prosome, macropain) subunit,	4.15	5.12
	414527	BE241739	Hs.76359	catalase	4.14	5.13
	422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	4.13	8.60
5	408199	AA132637	Hs.15396	Homo sapiens, clone IMAGE:3948909, mRNA,	4.12 4.10	5.94 10.00
,	412477 411558	AA150864 AA102670	Hs.70725	microsomal glutathione S-transferase 1	4.09	5.39
	444252	R21135	Hs.54985	gamma-aminobutyric acid (GABA) A recepto ESTs	4.07	6.01
	400295	W72838	16.51503	AI905687:IL-BT095-190199-019 BT095 Homo	4.06	13.32
	438746	A1885815	Hs.184727	Human melanoma-associated antigen p97 (m	4.06	7.57
10	429856	AA971576	Hs.225951	topoisomerase-related function protein 4	4.05	6.24
	422168	AA586894	Hs.112408	\$100 calcium-binding protein A7 (psorias	4.01	4.61
	403710			C4000160:gij12735793(ref)XP_011928.1(pr	4.00	4.06
	406643	N77976	Hs.347939	hemoglobin, alpha 2	3.97	1.22
1.5	436372	AW972301	Hs.310286	ESTs	3.96	5.41
15	428340	AF261088	Hs.154721	aconitase 1, sotuble	3.94	5.33
	424604	AW865388	Hs.151076	KIAA1243 protein	3.91	7.59
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	3.91	14.81
	410204 448520	AJ243425 AB002367	Hs.326035 Hs.21355	early growth response 1	3.87 3.87	9.96 5.09
20	443021	AA368546	Hs.8904	doublecartin and CaM kinase-like 1 lg superfamily protein	3.86	7.65
20	430418	R98852	Hs.36029	heart and neural crest derivatives expre	3.81	6.19
	447796	AW953622	Hs.223025	RAB31, member RAS oncogene family	3.76	5.10
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	3.76	5.12
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	3.75	5.46
25	426281	AK000987	Hs.169111	oxidation resistance 1	3.74	5.14
	423973	AF038461	Hs.136574	arachidonate 12-lipoxygenase, 12R type	3.74	6.30
	445234	AW137636	Hs.146059	ESTs	3.72	5.59
	457411	AW085961	Hs.130093	iroquois-class homeobox protein IRX2	3.71	4.85
20	456063	NM_006744	Hs.76461	retinol-binding protein 4, interstitial	3.71	6.72
30	413880	AI560842	Hs.110915	interleukin 22 receptor	3.71	4.01
	422640 452241	M37984 AL050204	Hs.118845 Hs.28540	troponin C, stow. Homo sapiens mRNA; cDNA DKFZp586F1223 (f	3.71 3.70	9.10 3.21
	453560	AA348626	Hs.5890	hypothetical protein FLJ23306	3.69	5.13
	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	3.69	7.69
35	413922	AI535895	Hs.221024	ESTs	3.68	4.80
	428698	AA852773	Hs.334838	KIAA1866 protein	3.64	5.22
	451951	AW082870	Hs.210954	ESTs	3.64	3.69
	452308	AI167560	Hs.61297	ESTs	3.64	4.35
40	441128	AA570256		ESTs, Weakly similar to 123273 hypotheti	3.63	2.91
40	421978	AJ243662	Hs.110196	NICE-1 protein	3.61	6.05
	418533	NM_004533	Hs.85937	myosin-binding protein C, fast-type	3.61	6.22
	452413	AW082633	Hs.215030	ESTs	3.58	3.03
	453003	AA808466	Hs.103395	hypothetical protein FLJ14146	3.55	6.39
45	408522 423503	AI541214 M92843	Hs.46320 Hs.343586	Small proline-rich protein SPRK (human,	3.54 3.53	10.68 15.11
43	419879	Z17805	Hs.93564	zinc finger protein homologous to Zfp-36 Homer, neuronal immediate early gene, 2	3.53	5.29
	428382	AF007132	Hs.184019	Homo sapiens clone 23551 mRNA sequence	3.51	4.46
	447165	AL042400	Hs.75668	Homo sapiens, Similar to RIKEN cDNA 1700	3.51	3.67
	418067	AI127958	Hs.83393	cystatin E/M	3.51	3.74
50	420202	AL036557	Hs.95910	putative lymphocyte G0/G1 switch gene	3.50	14.64
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	3.50	2.79
	442321	AF207664	Hs.8230	a disintegrin-like and metalloprotease (3.48	7.91
	450860	AA021007		integrin, beta 8	3.47	5.89
55	414665	AA160873	41. 75.400	serum amyloid A1	3.46	9.22
J	413663	BE247585	Hs.75462	BTG family, member 2	3.46	5.63
	427408	AA583206 AF086289	Hs.2156	RAR-related orphan receptor A	3.45	3.08
	430171 453655	AF085289 AW960427	Hs.234766 Hs.342874	skin-specific protein transforming growth factor, beta recepto	3.45 3.42	4,77 8.09
	450607	AL050373	Hs.25213	hypothetical protein	3.41	6.43
60	412596	AA161219	Hs.799	diphtheria toxin receptor (heparin-bindi	3.41	6.10
	427681	AB018263	Hs.180338	turnor necrosis factor receptor superfami	3.39	6.59
	440590	A1863446	Hs.266308	mosaic senne protease	3.34	3.09
	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	3,31	10.06
	422101	AW404176	Hs.111611	ribosomal protein L27	3.30	3.93
65	431986	AA536130	Hs.149018	Novel human gene mapping to chomosome 20	3.30	3.54
	412649	NM_002206		integrin, alpha 7	3.28	6.89
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	3.28	5.44
	425163 412061	D10040 AA833763	Hs.154890	fatty-acid-Coenzyme A ligase, long-chain ESTs	3.28	5.93 5.75
70	437592	NM_003851	Hs.330211 Hs.5710	cellular repressor of E1A-stimulated gen	3.27 3.27	5.73 5.83
, ,	452849		Hs.30792	hook2 protein	3.26	5.66
	421462		Hs.104624	aquaporin 9	3.25	4.98
	422083	NM_001141		arachidonate 15-lipoxygenase, second typ	3.24	6.56
	444935		Hs.223569	ESTs	3.24	5.96
75	422057	AI205785	Hs.30348	ESTs	3.22	5.72
	410017	AW952426	Hs.109438	Homo sapiens clone 24775 mRNA sequence	3.21	5.26
	407948		Hs.56279	ICEBERG caspase-1 inhibitor	3.21	4.61
	452089		Hs.271492	ESTs, Weakly similar to PC4211 hepatocel	3.19	4.42
90	448249		Hs.337124	ESTs	3.18	2.97
80	430869		Hs.37	acetyl-Coenzyme A acetyltransferase 1 (a	3.17	5.66
	443623		Hs.9641	complement component 1, q subcomponent,	3.16	12.00
	452865 452392		Hs.119567	ESTs, Weakly similar to A47582 B-cell gr	3.16	6.03 5.70
	452392	20013	Hs.507	comeodesmosin	3.15	5.70

						- 03
	410231		Hs.61153	proteasome (prosome, macropain) 26S subu	3.15	5.87 4.98
	420309		Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.15 3.13	17.37
	406791 419648	AI220684 173661	Hs.347939 Hs.91877	hamoglobin, alpha 2 thyroid hornone responsive SPOT14 (rat)	3.12	4.63
5	421485	AA243499	Hs.104800	hypothetical protein FLJ 10134	3.12	3.02
-	432375	BE536069	Hs.2962	S100 catcium-binding protein P	3.12	8.51
	417713	D42047	Hs.82432	KIAA0089 protein	3.12	5.82
	446948	BE409053	Hs.299629	peroxisomal long-chain acyl-coA thioeste	3.11	6.51
10	444195	AB002351	Hs.10587	KIAA0353 protein	3.11 3.11	5.44 6.61
10	415704	NM_001677	Hs.78629	ATPase, Na? transporting, beta 1 polypep	3.10	3.52
	401905 443071	AL080021	Hs.8986	ENSP00000252232*:Sterol regulatory eleme complement component 1, q subcomponent,	3.10	5.10
	427095	AA316080	Hs.173554	ubiquinol-cytochrome c reductase core pr	3.10	5.39
	413835	AI272727	Hs.249163	fatty acid hydroxytase	3.08	5.56
15	448106	AI800470	Hs.171941	ESTs	3.07	5.19
	432908	AI861896		ESTs	3.07	3.47 7.48
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.07 3.05	3.97
	429506	D49835 U58515	Hs.171942 Hs.154138	ras responsive element binding protein 1 chitinase 3-like 2	3.02	6.75
20	424998 419358	T78763	Hs.90063	neurocatcin delta	3.00	7.68
20	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member	2.99	5.44
	426402	BE387327	Hs.80475	polymerase (RNA) II (DNA directed) polyp	2.99	6.84
	450472	Al190071	Hs.55278	ESTs	2.98	5.06
25	421335	X99977	Hs.103505	ARS component B	2.97 2.96	9.31 4.30
25	431316	AA502663	Hs.145037	ESTs	2.96	2.97
	420996	AK001927	Hs.100895 Hs.60677	hypothetical protein FLJ10462 ESTs	295	6.59
	451176 444204	AA046457 AI129194	Hs.143040	ESTS	2.93	3.92
	436723	AW975895	Hs.307486	ESTs	2.93	6.64
30	436664	AW197887	Hs.253353	ESTs	2.93	3.82
	406962	M13485		gb:Human metallothionein I-B gene, exon	2.93	3.10
	453092	X64838	Hs.31638	restin (Reed-Steinberg cell-expressed in	2.93	5.35 9.84
	444734	NM_001360	Hs.11806	7-dehydrocholesterol reductase	2.91 2.91	7.02
35	430310	U60115 AA918425	Hs.239069	four and a half LIM domains 1 ESTs	291	5.41
35	420876 426050	AF017307	Hs.177744 Hs.166096	E74-like factor 3 (ets domain transcript	2.91	5.64
	428232	BE272452	Hs.183109	monoamine oxidase A	2.90	9.54
	413796	AW408094	Hs.75545	interleukin 4 receptor	2.89	5.37
40	413884	A1668892	Hs.239758	hypothetical protein FLJ 12389 similar to	2.88	5.34
40	411372	A1147861	Hs.213289	low density tipoprotein receptor (famili	2.86	6.31
	428500	AI815395	Hs.184641	fatty acid desaturase 2	2.86 2.86	3.93 6.05
	444135	AK000374	Hs.10346 Hs.284176	hypothetical protein FLJ20154 transferrin	2.85	6.11
	452689 403108	F33868	HS.204170	ENSP00000241415*:Hypothetical 67.7 kDa p	2.85	3.17
45	434433	AW629759		gb:hh70e05.y1 NCI_CGAP_GU1 Homo sapiens	2.84	3.35
	434952	T10269	Hs.4285	Homo sapiens cDNA: FLJ22505 fis, clone H	2.83	4.05
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	2.83	3.57
	406922	S70284	Hs.119597	gb:stearoyl-CoA desaturase (human, adipo	2.82 2.82	3.80 6.40
50	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065 Homo sapiens cDNA FLJ11276 fis, clone PL	2.82	2.97
50	429807 425180	AK002138 U00115	Hs.306227 Hs.155024	B-cell CLL/lymphoma 6 (zinc finger prote	2.81	5.15
	415409	AW993701	113.133024	NS1-associated protein 1	2.80	6.16
	433848	AF095719	Hs.93764	carboxypeptidase A4	2.80	2.88
	425750	AL050276	Hs.42400	zinc finger protein 288	2.79	5.99
55	433638	AW872507	Hs.3462	cytochrome c oxidase subunit VIIc	2.78 2.78	5.25 4.17
	429128	AA446869	Hs.119316	ESTs Dh. b. a. C. of manufair	2.77	7.37
	446292 430420	AF081497 AW140027	Hs.279682 Hs.26373	Rh type C glycoprotein Homo sapiens cDNA: FLJ23449 fis, clone H	2.76	6.09
	419923		Hs.120219	ESTs	2.76	4.31
60	407555			gb:H.sapiens XG mRNA (clone PEP11).	2.76	4.12
	425240		Hs.1869	phosphoglucomutase 1	2.74	5.92
	459317			Eos Control	2.74	19.85 5.72
	425819		Hs.93231	ESTs qb:xp61h09.x1 NCI_CGAP_Ov39 Homo sapiens	2.74 2.73	3.93
65	408839		Hs.283643	Homo sapiens cDNA FLJ11606 fis, clone HE	2.72	5.94
05	418253 409453		Hs.95612	ESTs	2.72	6.51
	406625		Hs.119597	stearoyl-CoA desaturase (delta-9-desatur	2.72	3.80
	420074		Hs.190074	ESTs	2.71	4.04
70	429547			FGENESH predicted novel secreted protein	2.71	2.84
70	444026		Hs.10119	hypothesical protein FLJ14957	2.71 2.70	6.17 5.23
	407112		Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S ATP-binding cassette, sub-family A (ABC1	2.69	5.33
	429615 419098		Hs.211562 Hs.87271	ESTs	2.69	3.22
	424206			amine oxidase, copper containing 3 (vasc	2.69	6.64
75	443102		Hs.132965	ESTs	2.68	5.85
	411939	Al365585	Hs.146246	ESTs	2.68	5.38
	453201		Hs.135098	ESTs	2.68	3.69
	420231		Hs.19813	ESTs Target Even	2.67 2.67	4.70 4.97
80	404996		LL 24120	Target Exon transmembrane 7 superfamily member 2	2.66	6.36
00	452955 447205			ESTs, Moderately similar to T17372 plasm	2.65	15.65
	417365		Hs.82028	transforming growth factor, beta recepto	2.65	7.74
	444169			ESTs	2.64	3.40

	431247	AL021578	Hs.278489	matritin 4	2.64	3.35
	423960	AA164516	Hs.136309	SH3-containing protein SH3GLB1	2.63	5.12
	432093	H28383	11- 20-40	gb:yl52c03.r1 Soares breast 3NbHBst Homo	2.63	4.08
5	408669 440924	A1493591 AF151872	Hs.78146 Hs.7527	platelet/endothelial cell adhesion motec	2.61 2.59	6.44 6.37
•	416232	AW502678	Hs.79090	small fragment nuclease exportin 1 (CRM1, yeast, homolog)	2.59	6.46
	425320	U29344	Hs.83190	fatty acid synthase	2.59	3.93
	402315			NM_003430:Homo sapiens zinc finger prote	2.58	6.09
10	449539	W80363	Hs.58446	ESTs	2.58	4.05
10	418271	NM_000919	Hs.83920	peptidylglycine alpha-amidating monocxyg	2.58	5.61
	449967 438752	R40978 AW238673	Hs.271498 Hs.146038	ESTs, Moderately similar to ALU1_HUMAN A ESTs	2.58 2.58	3.54 5.24
	424675	NM_005512	Hs.151641	glycoprotein A repetitions predominant	2.57	5.16
	438763	A1583207	Hs.99029	CCAAT/enhancer binding protein (C/EBP),	2.57	6.45
15	413630	AL036883	Hs.75450	delta steep inducing peptide, immunoreac	2.56	6.38
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	2.56	2.90
	427666 426403	AJ791495 NM_000361	Hs.180142 Hs.2030	calmodulin-like skin protein (CLSP) frombomodulin	2.56 2.56	2.67 5.19
	432906	BE265489	Hs.3123	. lethal giant larvae (Drosophila) homolog	2.55	5.62
20	420924	R01026	Hs.245321	ESTs	2.55	3.22
	427527	AI809057	Hs.153261	immunoglobulin heavy constant mu	2.55	5.45
	407083	Z48511		H.sapiens XG mRNA (clone PEP11)	2.55	4.50
	445437 425097	AI224165	Hs.148725	ESTs	2.54	4.72
25	420105	NM_014247 AW015571	Hs.32244	PDZ domain containing guanine nucleotide ESTs, Wealdy similar to FMOD_HUMAN FIBRO	2.54 2.53	5.28 6.55
	429554	NM_012275	Hs.207224	Interleukin 1, delta	2.53	2.84
	408896	AI610447	Hs.48778	niban protein	2.53	7.08
	409169	F00991	Hs.50889	(clone PWHLC2-24) myosin light chain 2	2.52	8.68
30	420235	AA256756	Hs.31178	ESTs	2.51	4.21
30	436314 440602	AI983409 AI743491	Hs.292692	ESTs ESTs	2.51 2.50	3.11 2.71
	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	2.48	2.86
	430235	BE268048	Hs.236494	RAB10, member RAS oncogene family	2.48	5.37
25	423929	M69136	Hs.135626	chymase 1, mast cell	2.48	3.21
35	426689	BE 245550	Hs.171825	basic helix-loop-helix domain containing	2.48	7.88
	421811 414420	AA022550 AA043424	Hs.108548 Hs.76095	PABP-interacting protein 2 Immediate early response 3	2.48 2.47	5.28 8.33
	420693	NM_001972	Hs.99863	elastase 2, neutrophil	2.47	2.78
••	420139	NM_005357	Hs.95351	lipase, hormone-sensitive	2.46	10.12
40	447179	AW015633	Hs.157299	ESTs	2.46	3.45
	451687	AL041260	Hs.26837	Homo sapiens mRNA; cDNA DKFZp586K1123 (f	2.46	5.47
	420322 421064	AB014555 AI245432	Hs.96731	huntingtin interacting protein-1-related	2.45	6.18
	421818	AW992976	Hs.101382 Hs.50098	tumor necrosis factor, alpha-induced pro NM_002489:Homo sapiens NADH dehydrogenas	2.45 2.45	5.75 6.73
45	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	2.44	10.55
	439639	AA370045	Hs.6607	AXIN1 up-regulated	2.44	5.22
	436009	H57130	Hs.120925	ESTs	2.44	2.94
	414814 434060	D14697	Hs.77393	famesyl diphosphate synthase (famesyl	2.43	5.17
50	425335	AA744902 BE394327	Hs.197922 Hs.296267	hypothetical protein PRO1489 follistatin-fike 1	2.43 2.43	5.56 10.52
	406997	U07807	115.250201	metaflothionein IV	2.42	4.35
	431545	AF095703	Hs.8110	L-3-hydroxyacyl-Coenzyme A dehydrogenase	2.42	6.72
	417029	AW952192	Hs.273385	guanine nucleotide binding protein (G pr	2.41	5.22
55	412825 445462	AW167439 AA378776	Hs.190651	Homo sapiens cDNA FLJ13625 fis, clone PL	2.41	5.56
33	448954	AB014564	Hs.288549 Hs.22616	hypothetical protein MGC3077 KIAA0664 protein	2.41 2.40	5.24 5.31
	447218	BE617762	Hs.10748	hypothetical protein DKFZp434B195	2.40	5.24
	423810	AL132665	Hs.132955	BCL2/adenovirus E18 19kD-interacting pro	2.39	5.55
60	450440	AB024334	Hs.25001	tyrosine 3-monooxygenase/tryptophan 5-mo	2.39	7.63
oo	430356 418355	N87990 L42563	Hs.239870 Hs.1165	Homo sapiens mRNA; cDNA DKFZp564H0764 (f	2.38	5.99
	415273	AW575691	Hs.79123	ATPase, H7 transporting, nongastric, atp KIAA0084 protein	2.38 2.38	3.84 5.22
	427272	NM_001096	Hs.174140	ATP citrate tyase	2.38	5.41
	437186	AA338305	Hs.5472	hypothetical protein FLJ20173	2.35	5.13
65	443679	AK001810	Hs.9670	hypothetical protein FLJ10948	2.33	5.81
	431179 418400	AI338644	Hs.195432	aldehyde dehydrogenase 2 family (rpiancho	2.33	7.89
	456876	BE243026 AL044870	Hs.301989 Hs.208780	KIAA0245 protein ESTs, Weakly similar to T29547 hypotheti	2.33	5.36 3.27
	407082	Z47055	113.200700	gb:Human partial cDNA sequence, famesyl	2.32 2.31	4.65
70	426508	W23184	Hs.170171	glutamate-ammonia ligase (glutamine synt	2.31	9.37
	408536	AW381532	Hs.135188	ESTs	2.31	2.60
	410552	X66945	Hs.748	fibroblast growth factor receptor 1 (fms	2.30	5.94
	437201 417314	F29279 N68168	Hs.171625	hypothetical protein MGC14697	2.30	5.75
75	433738	AI684802		gb:za11c01.s1 Soares fetal liver spteen ESTs	2.30 2.30	3.12 3.91
. •	410531	AW752953		gb:QV0-CT0224-261099-035-g02 CT0224 Homo	2.30	3.51
	422491	AA338548	Hs.117546	neuronatin	2.29	5.66
	434411	AA632649	Hs.201372	ESTs	2.28	4.40
80	451926	AW134519	Hs.96125	Homo sapiens, Similar to clone FLB3816,	2.28	5.14
-00	401131 401205			NM_001651*:Homo sapiens aquaporin 5 (AQP Target Exon	2.27 2.27	5.62 2.98
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.26	2.50 3.94
	456546	AJ243662	Hs.110196	NICE-1 protein	2.26	2.52

	*****		11- 420242	SCY-	2.25	3.13
	443049 440160	AI028613 BE560269	Hs.132343 Hs.7010	ESTs NPD002 protein	2.25	4.93
	438367	N79688	Hs.204354	ras homolog gene family, member B	2.25	9.58
	442987	AA075975	10.204001	Homo sapiens clone TCCCtA00427 mRNA sequ	2.24	6.19
5	421545	AA292810	Hs.90034	hypothetical protein FLJ21916	2.24	2.58
	447150	AI439011	Hs.86386	myeloid cell leukemia sequence 1 (BCL2-r	2.23	9.03
	450014	N41322	Hs.18441	ESTs	2.23	4.50
	426611	BE178050	Hs.171271	catenin (cadherin-associated protein), b	2.22	5.64
10	434039	L32977	Hs.3712	ubiquinol-cytochrome c reductase, Rieske	2.22	5.57
10	427569	BE299197	Hs.179665	cyclin-dependent kinase inhibitor 1A (p2	2.22 2.22	5.10 6.43
	444637	T19101	Hs.11494	fibulin 5	2.21	9.10
	406710	AJ708347	Hs.184014	ribosomal protein L31	2.20	6.13
	42490 9 407228	S78187 M25079	Hs.153752 Hs.155376	cell division cycle 258 hemoglobin, beta	2.20	11.34
15	450612	AL359946	Hs.14779	acetyl-CoA synthetase	2.20	7.03
13	458568	A1769067	Hs.127824	ESTs, Weakly similar to T28770 hypotheti	2.20	5.68
	407370	AA682384	Hs.182084	ESTs	2.20	7.00
	438942	AW875398	Hs.6451	PRO0659 protein	2.19	6.09
	400228			NM_021724*:Homo sapiens nuclear receptor	2.19	6.95
20	410185	BE294068	Hs.737	immediate early protein	2.18	11.72
	428150	AW950547	Hs.70312	cytochrome c oxidase subunit VII a polype	2.17	7.05
	400307	AF005081		Homo sapiens skin-specific protein (xp32	2.17	6.41
	424425	AB031480	Hs.146824	SPR1 protein	2.17	3.68
26	414459	Y11525	Hs.76171	CCAAT/enhancer binding protein (C/EBP),	2.17 2.16	3.11 8.40
25	400082		41. 4000	Eos Control	2.16	6.B3
	434702	AL039734	Hs.4099	nardilysin (N-arginine dibasic convertas	216	3.72
	439651	AF086480	Hs.56255	ESTs ESTs, Weakly similar to ALU1_HUMAN ALU S	2.15	3.34
	431838 420225	AI097229 AW243046	Hs.217484 Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	2.14	6.20
30	428848	NM_000230	Hs.194236	leptin (murine obesity homolog)	214	3.42
20	415213	NM_002933	Hs.78224	ribonuclease, RNase A family, 1 (pancrea	2.14	9.81
	434454	AF217798	Hs.3850	LIS1-interacting protein NUDEL; endoolig	2.14	6.75
	452467	AW500815		ESTs	2.13	4.66
	418226	AA424202	Hs.83834	cytochrome b-5	2.13	5.41
35	414815	AW292140	Hs.130286	ESTs	2.12	4.14
	430967	H16791	Hs.100895	ESTs	2.12	4.14
	426102	AF200496	Hs.166371	interleukin 1. zeta	2.12	3.77
	410223	S73775	Hs.60708	calsequestrin 1 (fast-twitch, skeletal m	2.11	5.30
40	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	2.11	4.01
40	427228	AA115770	Hs.174051	small nuclear ribonucleoprotein 70kD pol	2.10 2.10	5.13 3.33
•	436961	AW375974	Hs.156704	ESTs	2.10	8.13
	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	2.08	5.42
	445831 431593	NM_006055 NM_002108	Hs.13351 Hs.276590	LanC (bacterial lantibiotic synthetase c ESTs	2.08	4.43
45	423887	AL080207	Hs.134585	DKFZP434G232 protein	2.08	3.92
43	424389	AA339786	143.134303	lymphocyte-specific protein 1	2.07	5.52
	407394	AF005081		gb:Homo sapiens skin-specific protein (x	2.06	5.93
	400198	70 000001		Eos Control	2.05	10.48
	426335	AI054347	Hs.2017	ribosomal protein L38	2.04	5.57
50	443652	A1080692	Hs.134229	ESTs, Weakly similar to 154401 hypertens	2.04	3.36
	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	2.02	3.32
	443932	AW888222	Hs.9973	tensin	2.02	9.28
	421324	BE257515	Hs.103503	deoxyribonuclease Hike 2	2.02	5.71
55	426406	AI742501	Hs.169756	complement component 1, s subcomponent	2.01 2.01	5.49 3.05
23	410669	AW805749	110 444050	superoxide dismutase 2, mitochondrial	2.01	2.77
	445193 400078	A1279390	Hs.144658	ESTs, Weakly similar to T17257 hypotheti Eos Control	2.00	11,41
	456267	Al127958	Hs.83393	cystatin E/M	1.99	3.59
	413125	BE244589	Hs.75207	glyoxalase I	1.98	6.70
60	415433	W70067	Hs.58066	ESTs	1.98	5.59
• • •	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	1.98	3.52
	417553	L09190		trichohyalin	1.98	3.39
	403105			Target Exon	1.98	5.05
	414081	AW969976		matrix Gla protein	1.97	8.74
65	422639	AI929377	Hs.173724	creatine kinase, brain	1.97	5.51
	452208	AA024792	Hs.31895	hypothetical protein MGC4093	1.97	5.67
	436106	AI050715	Hs.2331	E2F transcription factor 5, p130-binding	1.97	5.75
	439265	AL134430	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R	1.96 1.96	5.09 5.49
70	430037	BE409649	Hs.227789 Hs.6891	mitogen-activated protein kinase-activat splicing factor, arginine/serine-rich 6	1.95	5.95
70	440054 417088		Hs.81170	pim-1 oncogene	1.95	8.19
	429451		Hs.202833	heme oxygenase (decycling) 1	1.95	5.19
	415274		Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.95	6.78
	452472			ESTs, Weakly similar to CS5663 oligodend	1.94	5.98
75	414860		Hs.77502	methionine adenosyltransferase II, alpha	1.94	5.13
	437220		Hs.334305	GS1999full	1.94	3.42
	450461	BE408081	Hs.46736	hypothetical protein FLI23476	1.94	5.66
	424924	AL039103	Hs. 153834	pumitio (Orosophila) homolog 1	1.93	5.28
00	413945			CD14 antigen	1.93	5.38
80	428193			Kruppel-like factor 4 (gut)	1.93	5.75
	415988			bleomycin hydrolase	1.92	4.65 9.79
	425783		Hs.1948	ribosomal protein S21	1.92 1.91	7.00
	431476	BE612705	Hs.256697	histidine triad nucleotide-binding prote	1.31	7.00

	456653	AI807519	He 104520	Homo sapiens cDNA FLJ13694 fis, clone PL	1.91	3.41
	401846	M001313	Hs.104520	NM_000988*:Homo sapiens ribosomal protei	1.91	5.62
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	1.90	4.00
•	400199			Eos Control	1.89	15.74
5	429367	AB007867	Hs.278311	plexin B1 Eos Control	1.88 1.68	5.58 9.07
	400083 433465	AV657778	Hs.3314	selenoprotein P. plasma, 1	1.88	5.16
	400079			Eos Control	1.87	8.57
10	411807	AK000290	Hs.44033	dipeptidyl peptidase 8	1.86	5.19
10	409178	BE393948	Hs.50915	kaffikrein 5 KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	1.85 1.85	2.75 5.33
	422624 443121	BE616678 Z19267	Hs.76152 Hs.9006	VAMP (vesicle-associated membrane protei	1.85	6.01
	451092	AI207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein,	1.84	2.82
1.5	430572	U33114	Hs.245188	tissue inhibitor of metalloproteinase 3	1.83	5.10
15	426812	AF105365	Hs. 172613	solute carrier family 12 (potassium/chto	1.83 1.82	6.48 3.63
	439927 415089	AA854650 N25117	Hs.124597 Hs.299465	ESTs ribosomal protein S26	1.82	6.69
	406400	NESTIT	16.233403	katilkrein 8 (neuropsin/ovasin) (KLK8)	1.82	2.95
	406467			Target Exon	1.79	2.65
20	426672	AW270555	Hs.171774	hypothetical protein	1.79	5.24
	414088 433271	AW797956 BE621697	Hs.75748 Hs.14317	proteasome (prosome, macropain) subunit, nucleolar protein family A, member 3 (H/	1.78 1.78	6.02 5.92
	429307	AU076592	Hs.198951	jun B proto-oncogene	1.77	5.44
	433640	AW390125	Hs.240443	Homo sapiens cDNA: FLJ23538 fis, clone L	1.77	5.79
25	425503	W92517	Hs.158203	actin binding LIM protein 1	1.77	9.27
	429191	AF065215	Hs.198161	phospholipase A2, group IVB (cytosolic)	1.77 1.77	5.44 6.97
	425875 431021	AU077333 A1869664	Hs.160483	erythrocyte membrane protein band 7.2 (s thiosulfate sulfurtransferase (rhodanese	1.77	5.23
	432891	AF161483	Hs.279761	HSPC134 protein	1.75	5.73
30	432872	AI908984	Hs.279623	selenoprotein X, 1	1.75	5.72
	451335	AB023192	Hs.26285	imidazoline receptor candidate	1.75 1,74	6.87 3.01
	428975 417824	NM_004672 AA084798	Hs.194694 Hs.82646	mitogen-activated protein kinase kinase DnaJ (Hsp40) homolog, subfamily B, membe	1.74	5.75
	439908	AI168031	Hs.155507	ESTs	1.74	2.63
35	427349	AA360154	Hs.177415	Finkel-Biskis-Reilly murine sarcoma viru	1.74	6.80
	445919	T53519	Hs.334692	hypothetical protein MGC14141	1.74 1.73	5.65 6.13
	427391 425299	W60675 AW505214	Hs.155560	hypothetical protein FLJ10350 catnexin	1.73	5.88
	430449	AA352723	Hs.241471	RNB6	1.72	5.14
40	456766	R87310	Hs.7740	oxysterol binding protein-like 1	1.71	4.35
	407694	U77594	Hs.37682	retinoic acid receptor responder (lazaro	1.71	6.16
	412374 417483	X01388 BE549343	Hs.73849 Hs.82208	apolipoprotein C-III acyt-Coenzyme A dehydrogenase, very long	1.70 1.70	5.1B 7.46
	410584	AB011112	Hs.64742	KIAA0540 protein	1.69	6.19
45	431882	NM_001426	Hs.271977	engrailed homotog 1	1.68	2.63
	441379	AW175787	Hs.334841	selenium binding protein 1	1.67	7.42
	422115	A1878953	Hs.111811	microsomal glutathione S-transferase 3	1.67 1.66	6.93 6.26
	406742 432191	Al458091 AA043193	Hs.279860 Hs.273186	tumor protein, translationally-controlle hypothetical protein, clone Telethon(Ita	1.65	5.83
50	452363	AJ582743	Hs.94953	Homo sapiens, Similar to complement comp	1.65	7.54
	446623	AF279865	Hs.15711	kinesin family member 138	1.65	5.36
	406712	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.65 1.64	12.30 5.70
	400202 401429			NM_002795*:Homo sapiens proteasome (pros C14001067:gi 4126465\dbj BAA36581.1 (AB	1.64	3.82
55	415166	NM_003652	Hs.78068	carboxypeptidase Z	1.62	5.95
	410169	AJ373741	Hs.59384	hypothetical protein MGC3047	1.61	6.60
	406713	U02629	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.60 1.60	11.13 10.97
	453027 416955	AI879341 AW889150	Hs.539 Hs.80595	ribosomal protein S29 NM_004552*:Homo sapiens NADH dehydrogena	1.60	5.90
60	439053	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b	1.57	5.60
	400201			NM_006156*:Homo sapiens neural precursor	1.57	5.32
	407049	X72632	U. 360006	NM_021724":Homo sapiens nuclear receptor	1.57 1.57	5.42 7.09
	430775 427380	AI879186 NM_005534	Hs.250895 Hs.177559	ribosomal protein L34 interferon gamma receptor 2 (interferon	1,56	5.37
65	407143	C14076	Hs.332329	EST	1.56	6.54
	436127	W94824	Hs.11565	RIKEN cDNA 2010100012 gene	1.56	6.35
	413659	BE155647	11- 30000	gb:PM2-HT0353-130100-002-e09 HT0353 Homo	1.55	5.96 4.09
	445624 435044			tivB (bacterial acetolactate synthase)-I proteasome (prosome, macropain) 26S subu	1.55 1.55	5.71
70	410397		Hs.63042	DKFZp564J157 protein	1.54	5.14
	429071	AW794126		ribosomal protein S27 (metallopanstimufi	1.54	8.70
	412915			NM_004541:Homo sapiens NADH dehydrogenas	1.54	6.57
	446429		Hs.201391	ESTs	1.53 1.53	2.87 6.07
75	414551 406801		Hs.76394 Hs.190813	enoyl Coenzyme A hydratase, short chain, ribosomal protein L9	1.52	5.63
, ,	437895		Hs.5898	KIAA0668 protein	1.51	5.74
	413929	BE501689	Hs.75617	collagen, type IV, atpha 2	1.51	6.40
	425456		Hs.157850	ribosomal protein L9	1.51	7.08 5.26
80	409635 404467		Hs.55296	HLA-B associated transcript-1 Target Exon	1.50 1.50	5.82
50	406743		Hs.279860	tumor protein, translationally-controlle	1.50	5.25
	454098	W27953	Hs.292911	Plakophilin	1.48	3.14
	429205	A1492393	Hs. 198248	UDP-Gal:betaGlcNAc beta 1,4- galactosyll	1.48	6.24



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	413825	BE299181	Hs.75564	CD151 antigen	1.47	5.64
	421143	AB024536	Hs.102171	immunoglobulin superfamily containing to	1.45	6.19
	440254	AI879332	Hs.7101	anaphase-promoting complex subunit 5	1.45	5.50
_	406711	N25514	Hs.77385	myosin, light polypeptide 6, alkati, smo	1.42	11.24
5	423513	AF035960	Hs.129719	transglutaminase 5	1.42 1.41	3.18 6.92
	406896	D00159	11. 2002	gloHomo sapiens gene for pancreatic elas	1.40	5.38
	433453	8E548307	Hs.3297	ribosomal protein S27a	1.37	5.51
	405800	AA505535	Hs.107809	gb:nh84h10.s1 NCI_CGAP_Br1.1 Homo sapien KIAA0726 gene product	1.37	5.46
10	421748 424372	NM_014718 AW952803	Hs.21732	Homo sapiens cDNA FLJ11780 fis, clone HE	1.36	4.06
10	408250	R92918	Hs.19597	KIAA 1694 protein	1.27	2.74
	431931	AB035302	Hs.272212	cadherin 9, type 2 (T1-cadherin)	1.15	2.65
	406587	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	14.272214	C15000544*:gif5454148freffNP_006368.1 U	1.06	3.11
	409574	AW419080	Hs.250645	ESTs .	1.00	3.60
15	404175			Target Exon	1.00	3.08
	452640	AA027115	Hs.100206	ESTs, Weatdy similar to A53856 aryl-acyl	1.00	2.82
	443564	A1921685	Hs.199713	ESTs	1.00	2.51
00	TABLE 65					
20	Pkey:		ie Eos probeset iden	ither number		
	CAT numi		cluster number			
	Accession	i: Gent	ant accession numb	Dens		
	Okan	CAT Number	Accorcion			
25	Pkey 407328	534268_1	A1673735 AA9780	66		
23	427890	1373988_1	AA417000 AA435	761 AAQ72Q17 AI66N397		
	444207	9172_3	RE730425 AAS14	221 AAR65491 AIR2R293 AA470456 AI276739 AA169357 RE	932464 AA5148	89 AW819039 AW819083 BE843048 AI432496 AI470335
			A1247243 RG5339	194 AAS1 37R3 AIRR7309 AAS28036 AW972006 AW873028 A	J924914 AUB188	10 AW 15Z378 AW(084945 A1521413 A1669583 BE932521
• •			AI581370 BE1802	38 AW089750 AW771461 AW089714 AJ590949 AJ819148 A	A731056 BF815	234 BF911506 AA235803 AA485373 AI735658
30			AW393133 AW07	3080 AI707637 BF353320 BE843111 AW819036 AW393135	BG697291 AVE	48670 AV654332 AV687530 BG500904 AI007430
			AI676072 AA8370	110 AI452482 AI625817 AW241750 BE048616 AI290928 AI66	50/14 AA46553	0 RE1/208/ W046213 WA120215 V1000220 VV025022
			BE674169 BF001	208 AA948166 BE175650 AA524664 AA490345 A1244948 A/ 004 AW819026 BE843092 AV686437 AV723049 BG616948 A	MOUZ930 MMO3	400 AIRD 1006 DERS7751 AIR62074 AAR40027 AW769317
			BG678060 Al5650	1112 BF876213 R82948 H26425 H82876 BE843095 BE84314	IN OCESSEAL D	C617830 AA216802 RE774985 RE006682 RE342375
35			AA3434// AA540	083 BF984258 AV657996 AI749532 BE758614 BE857252 B	F932516 RF768	573 AV657993 AV657777 AV752631 BE774974 T55847
33			DC006761 DE011	511 BE710793 BE180119 BG617338 H45942 T55897 AV657	7718 BG563497	
	407102	7177_2	AWGAST70 RED3	0005 E33652 RC057R18 AI36R018 AI4214R5 AI300352 AI378	3525 Al264177 /	A1276281 A1245302 A1281050 A1190036 AW451438
	407 102	1111_2	A14/2//2003 AA01	0970 C22200 E10647 E22275 AWA73816 RE445785 AA7745	28 F33447 CD1	177 AW772227 F17759 H42812 R09701 AA349096
			R48772 H42892 I	H42537 R47898 N28263 H25721 F32386 H43971 R48205 F2	21390 H45809 A	A007629 R47897 R83734 H45844 AW983653 H43970
40			H42536 H24496 1	R48875 H42961 H22079 R86018		
	437596	2875_1	BC022398 AV743	3635 AW976922 AW152652 AA910013 AA834629 BG536317	7 AW849807 AV	713062 AI684337 BE044081 AA761490
	440116	454673_1	R69942 BG65545	57 BF111453 A1149320 N23160 A1446431 A1758316 AV7417	81 B1791950 BN	A055014 A1798851 AA865357 A1417230 N67277 155592
			T52179	and the second second		
45	443072	449629_1	AV734838 AI937	532 AI032318 AW749500 AA091720		20072220 DE122112 DE095700 AA756029 D7023A
45	442679	31783_3	BG621493 BI056	706 BG496376 R53718 W65356 R79357 BG434247 AA3577 6754 BG434311 AW978683 AWZ73417 BM054662 A1799888	69 AW9/8086 1	MANU ALARTHA DEGES SE ALRESOS AWOSTO DE 7234
			BG494628 AA15	67 AA807170 AA837395 W61252 AA831085 AA287371 AW	750754 A 48005	ne atanaesa atanaesa ateaana atanaesa AW514069
			A A 2020CO A A 02	5452 AI371234 AA425696 AA453422 AA827697 R23653 D20	1240 AA772517	H13802 R66972 R79360 R27351 F03379 AA031952
		•	NEOSON D33143	R79358 R39136 R38800 R15089 R52937 R37502 H01021 R	33634 R46551	Z40404 BG291052 BG570357 AW391046 BG496872
50			H23558			
50	424571	9758_1	DC370766 AW16	52643 A1803450 A1564343 A1092711 A1140525 AW152156 AI	620740 A15546	89 AI161209 AI290242 AI339745 AI374611 AI347388
			A1859206 A11404	520 AI76612A AAAG3G12 AAAG6235 AAAG3RRG AIG571£G AW	<i>1</i> 022264 AU0972	77 A1144126 AKKKKUS1 AA983529 AA86USU/ NS3909
			AAR43767 NR11	63 N70629 AA <i>424</i> 577 AA983537 RF003004 AA626688 AA23	15977 AID57152	A1095366 A1095356 AA458646 AW 194479 AA 190459
			41375272 AW57	1777 AI359198 AA993793 RE614394 RE738239 AA127883 A	MD34344 T5950	4 D81608 AA908704 AW051665 AA382765 AA307206
55			N24639 Al37071	5 BE244980 AAS48596 AW449675 AI 191008 BF223749 N70	0752 N2ZZ66 AI	191012 AAU28001 AI419106 BF213661 BF391346
				4968 BE858217 BF793358 AV756758 BG483603 At093724 B	3F693395 BG54	5345 AI/44294 159549 AA611/73 BG49973/
	420787	55832_7	BE674920 AA56		ne .	
	456332	21353_10	BG/40024 AV/2	20262 BG198346 BG215119 AW841716 AA228357 AW84178 34455 BE672212 AI151416 AI566231 AI417585 AI378391 AA	236364 A13375	74 A1346166 AA406590 AA748618 AW771957 AA478626
60	418479	175360_1	AM232073 AIRS	9444 AIB 10315 BE503662 BG231886 AIB88230 AI289102 BI	F594638 AW07	4094 AW512456 AAB32229 AI056108 AI025868 AI245806
00			D61957 At09384	L1 AI721013 AI597594 AA993022 AI128620 AI285106 W3745	59 W35410 N90	037 AAB903Z3 R39943 AI468/41 AAB299/6 AA4/92U1
			AI539018 AA875	5875 AA448827 AW779493 Z39056 H84925 AA223923 AW5	17592 AI804400	AA911882 BM353143 D62885 AI457883 AI880626
			R31694 R42772	R68804 R44147 R71463 AV742540 BF966987		
	431628	30288_1	AE146227 NIA (012120 AE164377 AWQ76054 AW662923 AW770101 AI 597	184 AA713959	AA808021 AW444640 AI018159 AL050105 AW958324
65		_	DIRECTTS DIASE	2694 DE604426 AI620024 AA211487 RC617872 AW629675	AARRIO AWA	153668 RF171208 RF768429 BF326254 AW181992
			AW118462 AWS	572001 BG533184 AA768779 AA825697 AA808149 BF03642	24 AJ420469 AY	V175925 AA173981 AA557142 AW302163 AW088608
			AA847195 AI41	8480 BM353163 Al015673 Al357621 Al374592 Al245029 Al5	80659 AI37015	4 AA/6/503 AA643885 BMUSTSUT BU4S6655 AVV3045V4
			AW377222 AW	371202 BE 138896 R80586 BM090998 D25882 M85322 AI54	1363 BF6/5114	RP350253 WW051000 BC013551 BL234130 BL012114
70			BI086785 BG19	0411 BG217933 BG219447 BF886143 BG403278	12 44050552 4	ROLESPAA RESCENAA MASCERAA RESCENAA GODACO
70	426101	3211_1	AL049987 BG63	20667 BG571984 AW362842 BE150456 BE326465 AW8724 29448 N56349 AA460220 AW971193 AA453725 AI742087 A	12 AA000333 A	M70 A1017507 A1850141 RE045272 AW277065 A1921333
			AA442379 AA2	23448 N30349 AA40UZZU AW3/ 1133 AA433/ 23 AI/ 42U0/ A 6360 AI037003 AI006463 AA033647 AA663034 AA633R37 A	AR12876 AWN	0895 AAG00372 AAG63178 A1187977 AA229164 AW270324
			A A 2020CC T280	081 AAG330RG RG7884Q3 R31133 AI363QRG AI916737 TRA79	16 T84294 AW9	61515 A1459289 BF 109829 BI491853 A1084517 AW 103030
			RFR35233 A147	2712 AV741009 AA551512 N28268 AA436880 AA447794 BI	E835410 BEB35	385 BE818352 BE818350 R64648 BE646467 AA493776
75			AA437299 RF8	18343 R95914 R31089 BF576826 AU186065 BF802058 AI21	17018 AA24754	1 Al191725 BE766918
	454947	1083824_1	AW846590 AW	846615 AW846584 AW846592 AW846621 AW846610		
	438962		A1207343 RER1	3684 RE928775 AA828585		
	431693		ADDTERES AITE	1914/12 1916-2014 1917-1947 AW167132 AW264027 AL394192	BM272158 BM	272359 BG057287 BE464852 AI620722 BE046016
		_	A1758979 AWA	74705 AW474624 AW4405RB AI289435 AW002172 AI458169	9 A1634183 A11	25609 A1951377 A1631154 A1453490 A1857358 A1469750
80			DCCD2EA3 ALAS	21010 EDDE1E AWE19770 DESSEC77 AISSOISI AAQRSIG3 AI	R14417 AW798	184 RD9775 Al669379 AWZU/UZ6 AJ659678 AJ6Z6U/O
			BF940660 AA7	44971 C00469 A1672560 AL045697 BF847489 BF842860 T6	5400 AI853491	H24845 T54772 BE090906 BE090917 BE090877 AA152265
			BE244301 BIO	38346 B1038045 W94876 AA093121 B1523346 AW470130 N	32723 AA25887	1 K05731 RI257108



	450515	13638_2	BE299605 AIS89870 AA847598 AI470122 BF939896 AI304356 BE223045 BF435800 AI394207 AI708171 AW025415 AI079409 AW008420 AW304226 N34543 AW603578 AA526981 AA983631 N99134 AA626645 R45023 AA902417 AW672925 AA449985 AA953982 AW675471 AA010062 N80194 H14620 H28475 H26247 BF333581 AW842369 H06848 H05608 H81745 H15016 R51905 AA860423 AI860304 AA876023
	434230	41110_1	AC110000 NM 018539 AA702388 N530A3 RE351064 N70103 AI207469 AA551569 AW383189 W00906 W00935 N54252
5	448144	48653_1	projest jakojena alazizno awiegoto rostoros riosrost riosrost Biosrost Biosetta Bios
-	453225	12287_1	AKACKETA DIETOK NILI DAGI 11 DAGA 118 BITSRTER ALI125294 ALI121192 ALI118572 AL 517117 BE793962 BIB26721 AW149620 BG721751 BI916889
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			AA975721 AA985555 BC927U32 AA948389 AA451625 AA916141 AL57219 AV10726 ANTIBOT SI AA16045 A35163 A371635 A446143 BC429150 A1915306 Z30130 AA126929 BC926630 AA081013 AA553696 AA916094 BC924321 A1039722 A1964968 A1372839 A4101406 A1538215

	428193	430_1	AW074303 A AW874084 B	A620711 BF197792 AW008766 D25944 A1687397 IE720622 A1127241 AA236239 A1679709 A167913	10 AL040569 D44830 Bi011351 AL575805 Al290876 Al014784 Al3 7 AA621680 AV714408 BF446905 BM314505 BF514079 BM314191 5 AL572470 AA57343 Al568487 BE049325 AA687950 BG925989 1 ALGREE BOCKETS DERBOERD BLOSEGES	AA8452UI			
5	431021	10409_1	NM_003312 BG194276 B AA768558 A RE718621 A	024576 AA298805 H04001 H45668 BG682146 AL552388 BI462361 BG547513 BG696863 BI256661 4. 003312 BC010148 AK000862 D87292 BG709214 B7972765 BG740474 BI771592 BI1593659 BI820468 BI523933 AI859664 AA314620 BF724353 G194276 BG195282 BI524679 BF435589 AI300546 AA481682 AW780207 AI800832 AI380540 BE222877 AW300707 AA481445 AW7015893 AI381541 AT86558 AI138798 AA432063 AA948713 AI859485 AI307419 AI336589 AI301672 BT055581 AI312785 AI521208 AI927918 AI989759 M78015 F718621 AI327864 AI795909 AI335381 BF334524 AW007444 AA706797 AA975178 AA884739 AA443837 AA933897 AI826464 AI271737 AA053419					
10	427391	9048_3	AA053459 A	A446748 BG954446 BF760569 H150467 AH27583 RF735800 AH25772 AH37300) AM78232 AA603071 BE714413 AW078660 AW070418 R02364 B 9 AI215670 AI769136 AA586848 AW451158 N50799 AA936337 AI	355427 BE677905			
15			A1494204 AA T03896 BF9 BE447074 A	A953319 AA155753 A1052675 AAD44804 A128267 39430 AA974325 AW072996 AW005963 BG2524 W194649 A1915192 AL567164 RF691569 AL5659	755 BF448136 A365247 BF439175 BE207948 A1089272 B911455 8 BG741226 F25798 AA180204 AI682613 AU152530 AA420766 AI 71 A1192002 A318600 AA7516144 BIB34864 A1753954 BE908511 A 170 AW471137 AW276992 AL536717 BF591783 AI571746 BF9391	373,993 A1885767 \W628731 AA034958 72 BG745029			
	400202	11771_2	BG575588 6 H23835 BIO BER73890 6	2054960 H51485 AW799491 A1370437 H26413 A 35010 F22360 BF849322 15745945 AA155007 AA573157 AW874610 AA911	AS85334 AU151276 AA074274 AA936883 AW131643 AI221650 A1 6387 N75963 BMDR1306 AW044671 BCD13008 NM_002795 D2655	N 105476 AW952294 N BG118716 BI910891			
20			BF972860 E BE904726 E BG472870 I	IG119842 B1094093 AL538757 BE271653 B18565 B1871370 AV708990 BF971483 BE298241 B11970 BE3395697 N28533 AA316042 N42043 AW404464 BA370058 RG947618 D31230 AA308300 AA36031	38 BE909573 BG109826 BE784430 BE899255 BI835973 BMN1080 07 BE272092 BG120374 AW963509 BE540572 AV744947 BG9430 AW892094 AA379896 AW801110 AW406977 AA379791 BG94188 11 AA371733 AA732937 AA494241 W32225 BF745937 A1383690 B	9 BE671371 BG664956 141 AW327463 9 BE076254 AA360459 1G202360			
25	400201	24179_2	AW009362 RG9447R4	BE379126 B1198555 BF126026 N28289 BE38830 AA187402 RG283893 AV712007 W01301 BG7741	5 BG716628 BG707476 BG768814 BE312007 BF125930 BF037916 1 BG327102 A571450 BF038400 A18884699 A17189862 A174214 B 109 W77840 C15672 BI570016 A1752473 AA4884409 C14921 M417- 17 AW407023 AA337516 F36177 AA374444 AA402758 A1141545 B	NS C15220 F30164			
	413659 406800	1526081_1 0_0	BE155647 (AA505535						
30	TABLE 65	C:							
	Pkey: Ref:	Se	quence source.	rresponding to an Eos probeset The 7 digit numbers in this column are Genbank I In chromosome 22" Dunham, et al. (1999) <u>Nature</u> 4	identifier (GI) numbers. "Dunham, et al." refers to the publication en 102:489-495.	titled "The DNA			
35	Strand: Nt_positio			and from which exons were predicted. In positions of predicted exons.					
	_		Strand	NL position					
	Pkey 405121	Ref 8102330	Minus	35816-36004.36587-36684					
	401203	9743387	Minus	172961-173056,173868-173928					
40	400494	9714719	Plus	169845-170272					
	402294	2282012	Minus	2575-3000					
	404730	8389582	Plus	119832-120016,124110-124275					
	403593	6862650	Minus	62554-62712,69449-69602					
4.5	403710	6437516	Ptus	27413-28978					
45	401905	8671966	Plus	153965-154441,156599-156819					
	403108	8980955	Plus	93253-93667					
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055					
	402315	7381741	Minus	30728-32065					
60	401131	8699812	Minus	94802-94987,95804-95887,96323-96487,9759					
50	401205	9743388	Plus	167373-167433,167936-168031	,				
	403105	8980016	Minus	145287-145744	•				
	401846	7712190	Minus	82775-82823,82912-83022					
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077					
55	406467	9795551	Plus	182212-182958					
33	401429 404467	8217890 8077630	Minus Minus	86946-87579 24951-25853					
	406587	8189273	Minus	120577-120718					
	404175	9931117	Minus	107420-107547,109625-109796					

60									
	TABLE 6	6A. DISEASE	INDICATIONS	AND PREFERRED UTILITIES FOR SELECTED	GENES	avs.			
			ease indication	s and preferred utilities for about 439 selected gen	es. These genes were identified using Eos/Affymetrix Genechip arr	. ,,,,			
	Primeke		os probeset id						
65	ExAccn:		r Accession nu ID number	muer					
05	UgID:	Unigene							
	Disease	disease	indicated for s	elected nene as described in table 1 and abbrevial	ed as follows: AWPC (androgen independent prostate diseases), a	rth (arthritic diseases), bph			
	Oliocore	thenian	nmetatie hunom	uzzay hoold nione. (zazepsih rohheld) held. (eisely	ol diseases). FWS (bone diseases), quo (brain diseases), Dreasi (Dr	easi diseases), deiv			
		Inening	disappael min	reasih leanadansat dansa /saseasih letravdant a	tes), fibro (fibrofic diseases), headok (head & neck diseases), leid (i	elomyoma diseasas), icux			
70		(feukon	de diseasees) he	enC (fiver diseases), hung (lung diseases), ovar lov	arian diseases), endo (ovarian endometrició diseases), omuc (ovari	an mucinous diseases),			
		panc (pa	ancreatic diseas	es), pros (prostate diseases), renal (renal disease	s), mela (skin diseases), stom (stomach diseases), test (lesticular di	iseases), uter (uterine			
		dicasca	e1						
	Utility:				ed as follows: CTL (DNA vaccine target), diag (diagnostic or progno	stic largell, mad			
75				arget), s.m. (small molecule target)					
75			11.45	11- Ta-	Ciarana	Utility			
		y Ex Acon	UgID	Ug Title	Disease	mAb+diag+s.m.			
		X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	angio, blad, tung, cerv, ovar, headnk, esoph	mAb			
	400297		Hs.306201	hypothetical protein DKFZp564O1278	breast, blad, coton, pros breast, ovar, pros, stom, uter, blad, lung, headnk	mAb			
80	400303		Hs.79136	LIV-1 protein, estrogen regulated		s.m.			
OU	400843			NM_003105*:Homo sapiens sortilin-related	blad m blad tugo headok ceru mela escob	mAb+diag			
	402075			ENSP00000251056*:Plasma membrane calciu		CTL			
	402901			NM_025206*:Homo sapiens hypothetical pro	blad	mAb+s.m.			
	404287			FGENESH predicted novel CUB-domain conta	panc, lung, colon, uter, esoph	112 10 TO 1111			

	404682			ortholog of mouse polydomain protein	pane	diag
	404875				blad	CTL+s.m.
	404977				blad, ovar	mAb+diag
	405033				blad	s.m.
5	405547			NM_018833":Homo sapiens transporter 2, A	cerv, meta	mAb+s.m.
	406400			kallikrein 8 (neuropsin/ovasin) (KLK8)	ovar, uter	diag
		M21305		FGENES predicted novel secreted protein	angio, blad, fibro	diag
			Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	glio, blad	CTL
10			Hs.39384	putative secreted figand homologous to f	ovar, uter, cerv, panc	mAb+diag diag
10			Hs.40098	cysteine knot superfamily 1, BMP antagon	blad, panc, stom, uter, lung, esoph	CIL
			Hs.22575	B-cell CLUlymphoma 6, member B, zinc 6	angio	diag
		X89426 Y00787	Hs.41716 Hs.624	endothelial cell-specific molecule 1 interleukin 8	angio, renal blad, stom, headnk, cerv, lung, angio, esoph, panc	diag
			Hs.44424	Homo sapiens orphan neurotransmitter tra	mela	mAb+s.m.
15	408369		Hs.118747	SLC15A2 Solute carrier family 15 (H+/pep	pros, lung, fibro, uter, glio, cerv, ovar	mAb
13	408380	AF123050	Hs.44532	diubiquitin	lung, blad, headnk, panc, stom, fibro, esoph, mela	CTL
	408482	NM_000676		adenosine A2b receptor	tung, esoph, headnk	mAb+s.m.
	408562	Al436323	Hs.31141	roundabout (axon guidance receptor, Dros	uter, fibro	mAb+s.m.
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	tung	mAb+s.m.
20	408908	BE296227	Hs.250822	serine/threonine kinase 15	blad, lung, headnk, stom	s.m.
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	uter, ovar, lung, colon, storn, headnk, breast, panc	CTL+diag
	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	breast, pros	mAb+s.m.
	409103	AF251237	Hs.112208	XAGE-1 protein	tung	CTL
25	409178	BE393948	Hs.50915	kalfükrein 5	ovar, breast, mela	diag mAb+s.m.
25	409220	BE243323	Hs.51233	turnor necrosis factor receptor superfami	angio, renal, colon, stom	mAb+s.m.+CTL
	409348	AJ401535	Hs.146090	ESTS	renal, giio glio	mAb+diag
	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	lung, headnik, panc, storn, cerv, esoph, blad	diag
	409420 409632	Z15008 W74001	Hs.54451 Hs.55279	taminin, gamma 2 (nicein (100kD), kalini serine (or cysteine) proteinase inhibito	lung, blad, headrik	diag
30	409637	AA323948	Hs.55407	Homo sapiens mRNA; cONA DKFZp434K0621		mAb+s.m.+CTL
50	409663	A1743750	Hs.98306	KIAA1862 protein	renal	CTL
	409745	AA077391	10.5000	gb:7B14E12 Chromosome 7 Fetal Brain cDNA		mAb+s.m.+CTL
	409757	NM 001898	Hs.123114	cystatin SN	pane, stom, lung, blad,	diag
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	tung, cerv, blad, test, esoph	CTL+s.m.
35	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	breast, panc, ovar, colon, headnk, lung, blad, esoph	diag
	410001	AB041036	Hs.57771	kallikrein 11	ovar, pros, uter, cerv, tung	diag
	410055	AJ250839	Hs.58241	gene for serine/threonine protein kinase	renal	s.m.
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	renal, blad	CTL
40	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	lung, renal	CTL s.m.
40	410309	BE043077	Hs.278153	alpha-2,8-sialyltransferase III	panc	mAb+s.m.
	410407	X66839	Hs.63287	carbonic anhydrase IX	renal, lung, colon, storn, ovar, uter, blad	mAb+diag+s.m.
	410418	D31382	Hs.63325	transmembrane protease, serine 4	colon, blad, lung, ovar, panc, headnk colon, ovar, uter, cerv, headk, panc	diag
	411274 411411	NM_002776 AA345241		kallikrein 10 ESTs, Weakly similar to KIAA1330 protein	renal	mAb+s.m.
45	411773			professe, serine, 21 (testisin)	ovar	diag
43	412078		Hs.73149	paired box gene 8	ovar	CTĽ
	412140		Hs.73625	RAB6 interacting, kinesin-like (rabkines	tung, blad, headnk, breast, ovar, panc, angio, test, mela	s.m.
	412580		Hs.17901	similar to CABLES [Homo sapiens]	mela	mAb+s.m.+CTL
	412609		Hs.74124	ocular albinism 1 (Nettleship-Falls)	mela	s.m.
50	412628	A1972402	Hs.306051	hypothetical protein MGC2648	pros	diag
	412709		Hs.74518	KIAA0027 protein	glio	mAb+s.m.
	412719			ESTs	lung, headnk, blad, glio, cerv	s.m.
	412959		Hs.75090	KIAA0282 protein	glio	CTL+s.m. mAb+s.m.
5.5	412986		Hs.75110	cannabinoid receptor 1 (brain)	glio	mAb mAb
55	413048		Hs.75182	mannose receptor, C type 1	fibro, panc	diag
	413063		Hs.75184	chitinase 3-like 1 (cartilage glycoprote	glio, ovar, blad, hung panc, tung, blad, breast, cerv, ovar, headnk, esoph, mela, stom	CTL+s.m.
	413278		Hs.833 Hs.75294	interferon-stimulated protein, 15 kDa	blad	diag
	413324 413385		Hs.840	corticotropin releasing hormone indoleamine-pyrrola 2,3 dioxygenase	blad, lung, mela, fibro, uter	s.m.
60	413554		Hs.75426	secretogranin II (chromogranin C)	panc, glio	diag
00	413719		Hs.75498	small inducible cytokine subfamily A (Cy	panc, lung, headnk, cerv, colon, uter, stom, esoph	diag
	414577		Hs.72116	hypothetical protein FLJ20992 similar to	angio	CTL+diag
	414774		Hs.77274	plasminogen activator, urokinase	lung, blad, headnk, panc, stom, ovar, esoph	diag
		X72755	Hs.77367	monokine induced by gamma interferon	breast, blad, lung, fibro, panc, colon, headnk,	
65					cerv, stom, renal, ovar, test, mela, esoph	diag
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	glio, lung, renal, esoph, panc, headnk, arth	mad+s.m.+CTL
		AA926960		CDC28 protein kinase 1	tung, ovar, storn, colon, cerv, headnk, test	s.m.
	414907	X90725	Hs.77597	polo (Drosophia)-like kinase	blad, lung, ovar, test	s.m.
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	mela	mAb+s.m.
70		3 C18356	Hs.295944	tissue factor pathway inhibitor 2	angio, pane, stom, lung, uter	CTL+diag
		AI732617	Hs.182362	ESTs	blad, ovar, renat	mAb+s.m.+CTL
		AJ733881	Hs.72472	BMP-R1B	breast, uter, pros	mAb+s.m.
	41566		Hs.306814	Homo sepiens lysyl oxidase-like 4 (LOXL4	meta	diag mAb+diag+s.m.
75	415669		5 Hs.78589	serine (or cysteine) proteinase inhibito	lung	mAb+s.m. mAb+s.m.
75	41581		Hs.78867	protein tyrosine phosphatase, receptor-t	lung, glio, headnk, cerv, mela, esoph, fibro	mAb+s.m.
	415910		Hs.78913	chemokine (C-X3-C) receptor 1	glio	mAb
	41592			Homo sapiens mucolipin-3 (MCOLN3)	mela pros, ovar, blad, lung, headnk, panc, colon, stom	mAb+s.m.+CTL
		9 AJ267700 1 AF295370		ESTs defensin, beta 3	headnk, esoph, mela	CTL+diag
80		9 AA236776		MAD2 (mitotic arrest deficient, yeast, h	lung, headrik, colon, uter, stom	CTL+s.m.
		0 AASB1386		Kremen 2	esoph, fung, cerv, over	mAb+s.m.
	41635			phospholipase A2, group IID	test, mela, fibro	CTL
		0 U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	ovar, uter	diag

	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	breast, panc, uter, mela n	nAb+s.m.
			ns.42043 Hs.79432			iag
	416836		Hs.80247		pros, EWS, glio	iag
_			Hs.292453		g-0	nAb+s.m.
5	417034	NM_006183		neurotensin		liag
	417079	U65590	Hs.81134			liag
			Hs.42146			CTL PAbra =
	417355		Hs.82002	Choose Carrisophia type a		nAb+s.m. nAb+diag
10		BE260964	Hs.82045			nAb
10		BE270266 J04129	Hs.82128 Hs.82269			πAb+diag
		AA804698	Hs.82547			mAb aAm
		AW067903	Hs.82772			CTL
	417931		Hs.82961			diag
15	417933		Hs.82962	thymidylate synthetase		6.M.
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	spell storet transit hand and a second a second and a second and a second and a second and a second a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second	mAb+diag+s.m.
	418030	BE207573	Hs.83321	neuromedin B	Such bearing	diag diag
	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur		CTL+diag
20	418281	U09550 U38945	Hs.1154 Hs.1174	oviductal glycoprotein 1, 120kD (mucin 9 cyclin-dependent kinase inhibitor 2A (me		s.m.
20	418478 418506	AA084248	Hs.372651	Unknown protein for MGC:29643 (formerly		mAb+diag
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic		mAb+s.m.
	418558	AW082266	Hs.86131	Fas (TNFRSF6)-associated via death domai	esoph, headrik	s.m.
	418678	NM_001327		cancer/testis antigen (NY-ESO-1)		CTL
25	418830	BE513731	Hs.88959	hypothetical protein MGC4816		CTL
	418857	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	5-65	s.m. mAb+s.m.
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus		CTL
	419080	AW150835 AA374372	Hs.18878	hypothetical protein FLJ21620	torius auce, mily	diag
30	419171	NM_002846	Hs.89626	parathyroid hormone-like hormone protein tyrosine phosphatase, receptor t	ting, esopi, resona, and	mAb+s.m.
50	419172	AW338625		ESTs; similar to TRANSMEMBRANE 4 SUPER		mAb+s.m.
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	blad, lung, headnk, panc	CTL+s.m.
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	panc, lung, storn, cerv, pros, headnk, esoph	diag
	419235	AW470411	Hs.288433	neurotrimin	panc, fibro, headnk, tung	mAb+diag
35	419452		Hs.90572	PTK7 protein tyrosine kinase 7	ovar, pros, lung, breast, uter, lest, panc, stom	mAb+s.m. mAb+s.m.
		AW997938		ATP-binding cassette, sub-family C (CFTR	glio, omuc, stom, tung, panc, colon, renal, uter	mAb+diag
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	lung, fibro, test glio	CTL+s.m.
		AA429104 AL120193	Hs.45057 Hs.339810	ESTs longevity assurance (LAG1, S. cerevisiae	glio	mAb+diag
40		NM_007019		ubiquitin carrier protein E2-C	blad, lung, colon, ovar, test, esoph, mela	CTL+s.m.
40	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	blad, stom	mAb
		BE378432	Hs.95577	cyclin-dependent kinase 4	lung, mela	s.m.
	420208		Hs.95972	silver (mouse homolog) like	mela	CTL
4.5		Y13645	Hs.97234	uroplakin 2	blad	mAb
45		NM_00240		mammaglobin 2	ovar, uter, cerv	diag CTL+s.m.
		AF050877	Hs.99236	regulator of G-protein signalling 20	headnk, glio, cerv, mela	CTL
		AI683183	Hs.99348	distal-less homeo box 5	uter, endo, tung renal	mAb+s.m.
	420737 420789		Hs.99899 Hs.199882	CD70; tumor necrosis factor (ligand) s ESTs	renal	mAb+s.m.+CTL
50		AA918425	Hs.177744	FGENES predicted novel protein containin	panc, blad	s.m.
		AU076725	Hs.101408	branched chain aminotransferase 2, mitoc	blad, lung	CTL+s.m.
		AJ250717	Hs.1355	cathepsin E	blad, panc, storn, lung, fibro, ovar, esoph	sm+diag
		F07783	Hs.1369	decay accelerating factor for complement	angio, pane, stom	diag
66		Y15221	Hs. 103982	small inducible cytokine subfamily B (Cy	breast, panc, headnk, lung, storn, blad, cerv, colon, fibro, lest, mela, esoph	n diag mAb+s.m.
55		U90545	Hs.327179	solute carrier family 17 (sodium phospha	renal lung	mAb+s.m.
	421508	U76362	Hs.104637 3 Hs.105115	solute carrier family 1 (glutamate trans absent in metanoma 2	blad, esoph, lung, mela	mAb+s.m.+CTL
	421524			GDNF family receptor alpha 1	breast	mAb+s.m.
		AF026692		secreted frizzled-related protein 4	breast, ovar, panc, cerv, uter, pros, lung, stom, headnk	diag
60		AJ000152		defensin, beta 2	headrik, tung	CTL+diag
		AI910275	Hs.350470	trefoil factor 1 (breast cancer, estroge	breast, panc, lung, omuc	diag
		AL035250		endothelin 3	mela	mAb+diag mAb+s.m.
		BE314828		ATP-binding cassette, sub-family B (MDR/	tung	mAb+s.m.
65		AF145074		ATP-binding cassette, sub-family C (CFTR	lung, cerv, headrik, blad glio	mAb+s.m.
05	422033		Hs.110903 Hs.288126	claudin 5 (transmembrane protein deleted spondin 2, extracellular matrix protein .	panc, pros	diag
	422109		Hs.1473	gastrin-releasing peptide	panc, tung, colon, fibro	diag
		L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	headnik, blad, bung, cerv, storn, esoph	diag
	422163			prominin (mouse)-like 1	colon, breast, fibro	mAb+s.m.
70	422192			fts485	meta	s.m.
	422260			regenerating gene type IV	colon, ornuc, storn, panc	mAb+diag
		AF019225		apolipoprotein L	blad, lung, headnk, renal	diag s.m.
	42228			CDC45 (cell division cycle 45. S. cerevis	lung, blad, test, cerv, headnk, esoph	mAb+s.m.+CTL
75	42230		Hs.114924	solute carrier family 16 (monocarboxylic epiregulin	mela panc, colon, blad	mAb+diag
15	42233 42239		Hs.115263 Hs.116051	MYEOV Myeloma overexpressed gene (in a s		CTL+s.m.
	42242			prostate differentiation factor	blad, panc, pros, angio, colon, stom, lung, mela	diag
	42262			transforming growth factor, bela-induced	colon, renal	mAb+diag
	42276	5 AW40970	1 Hs.1578	bacutoviral IAP repeat-containing 5 (sur	lung, blad	s.m.
80	42280	9 AK001379		hypothetical protein FLJ10549	blad, cer, lung, uter, angio, storn, test	s.m.
	42266		Hs.1584	cartilage oligomeric matrix protein (pse	breast, ovar, pros. panc, lung, colon, uter	diag CTL+s.m.
	42295			ECT2 protein (Epithelial cell transformi downstream of cadherin 6 (by 3.3kb)	ovar, blad, panc , lung, headnk, colon, stom renal, ovar, blad	mAb+s.m.
	42316	1 AL049227	Hs.124776	Compagant Caman (I) stant	terral and	

			11- 4004	ephrin-A1	pros, panc, renal	mAb+s.m.
		NM_004428 NL039402			breast, renal, ovar, pros, colon	CTL
			Hs.128425		gio	mAb
			Hs.129711		renzi, colon	mAb
5			Hs.129836		pros	s.m.
•			Hs.1690	henarin-binding growth factor binding or	lung, blad, headnk, panc	diag
			Hs.1695	matrix metalloproteinase 12 (macrophage	blad, tung, headnk, ovar, panc, colon, storn, utar, cerv, esoph, test	mAb+diag+s.m.
		U77629	Hs.135639		colon, stom, ovar	CIL
		D13666	Hs.136348	,	breast, colon, blad, lung, fibro, panc, headnk, ovar, mela	mAb+diag
10	424008	R02740	Hs.137555	putative chemokine receptor, GTP-binding	blad, headrik, storn, cerv, esoph	mAb+s.m.
		AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	headnk, lung, cerv	diag mAb+s.m.+CTL
		AK000520	Hs.143811	hypothetical protein FLJ20513	colon, stom	5.M.
		W74048	Hs.1765	tymphocyte-specific protein tyrosine kin	mela, fibro	s.m.
1.5		AA285249	Hs.146329	protein kinase Chk2 (CHEK2)	lung, coton, test panc	s.m.
15		NM_005209		crystallin, beta A2	lung	s.m.
		AF242388	Hs.149585	lengsin integrin, alpha 5 (fibronectin receptor.	panc, pros, angio, blad, lung	mAb+s.m.
		NM_002205 AA101043	Hs.151254	kalikrein 7 (chymotryptic, stratum com	ovar	diag
	424620	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	headnik, panc, tung, blad, uter, cerv, colon, storn, test, mela	diag
20		U31875	Hs.272499	short-chain alcohol dehydrogenase family	blad, breast	CTL+s.m.
20	424825	AF207069	Hs.153357	procollagen-lysine, 2-oxoglutarate 5-dio	mela	CTL+s.m.
	424905	NM_002497		NIMA (never in mitosis gene a)-related k	ovar, blad, tung, headnk, panc, stom	s.m.
	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	renal, fibro	mAb+s.m.
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	pros, colon, storn, uter, cerv, headnk, esoph, panc	diag
25	425088	AA663372	Hs. 169395	hypothetical protein FLJ12015	glio, mela	mAb+s.m.+CTL
	425115	R44664	Hs.123956	downstream of: G protein-coupled recept	glio	mAb+s.m. mAb+diag+s.m.
	425247	NM_005940		matrix metalloproteinase 11 (stromelysin	breast, over, lung, colon, panc, headnk, stom, uter, cerv, blad, esoph	5.M.
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	tung, headrik	mAb+s.m.
20	425535	AB007937	Hs.158287	syndecan 3	mela, glio lung, headnk, cerv, esoph, blad	mAb
30	425650	NM_001944		desmoglein 3 (pemphigus vulgaris antigen	blad	mAb
	425721	AC002115	Hs.159309	uroplakin 1A dickkopf (Xenopus laevis) homolog 4	endo, uter, colon	CTL+diag
	425723 425734	AF056209	Hs.159311 Hs.159396	peptidylglycine alpha-amidating monooxyg	lung	s.m.
	425776		Hs.159499	parathyroid hormone receptor 2	ovar, uter, tung	mAb+diag
35	425842	AI587490	Hs.159623	NK-2 (Orosophila) homolog B	panc, glio	s.m.
55	425852		Hs.159651	death receptor 6, TNF superfamily member	blad, lung, headnk	mAb+s.m.
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322	(f blad, panc	mAb
	425921		Hs.162211	solute carrier family 6 (neurotransmitte	storn, panc	mAb+s.m.
	425998	AU076629	Hs.165950	fibroblast growth factor receptor 4	renal	mAb+s.m.
40	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	tiad	mAb+diag
	426215	AW963419		stanniocalcin 2	breast, lung, renal, colon, ovar, uter	mAb+diag mAb+s.m.
	426227		Hs.154299	Human proteinase activated receptor-2 mR	panc, lung, colon, esoph, stom	diag
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	panc, blad, storn	CTL+s.m.
45	426344	H41821	Hs.322469	transcriptional activator of the c-fos p	glio ovar, tung, headrik, cerv, colon, uter, storn, test	CTL+s.m.
45	426427	M86699	Hs.169840	TTK protein kinase	blad, breast	s.m.
	426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor bone morphogenetic protein 7 (osteogenic	ovar, colon, blad, lung, cerv	mAb+diag
	426514 426600	BE616633	Hs.170195 8 Hs.171014	VGF nerve growth factor inducible	mela	diag
	426761	AI015709	Hs.172089	PORIMIN Pro-oncosis receptor inducing me	lung, esoph, pros, uter, panc, colon, ovar, headnk	mAb+s.m.
50	426812			solute carrier family 12 (potassium/chlo	renal ,	mAb+s.m.
50	426890			ESTs	renal, colon, ovar, uter, storn	CTL
	427239			ubiquitin carrier protein	tung, blad, test, mela	CTL+s.m.
	427335			G antigen 7B	lung, headnk, blad, mela, esoph	CTL
	427343		Hs.176977	protein kinase C binding protein 2	glio	CTL+s.m.
55	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	colon, stom, panc	CTL
	427747	AW411425		serine/threonine kinase 12	blad, lung, ovar, storn, test, esoph	s.m. mAb
	427923	AW274357	7 Hs.301406	FGENESH predicted 11 TM protein	mela	mAb+diag
	427969		3 Hs.2230	epidermal growth factor (beta-urogastron	panc	CTL
60	428093			ESTs	ovar, panc	mAb+s.m.
60	428141		Hs.182611	solute carrier family 11 (proton-coupled	glio	s.m.
	428179		Hs.279696	serum/glucocorticoid regulated kinase-li	breast ovar, uter, colon, stom	mAb+s.m.
	428187		Hs.285529	G protein-coupled receptor 49	ovar, panc, , tung	diag
	428242		Hs.2250 58 Hs.183572	leukemia inhibitory factor (cholinergic solute carrier family 22 (organic cation	renal	mAb+s.m.
65	428296 428330		Hs.2256	matrix metalloproteinase 7 (matrilysin,	uter, ovar, fibro, pros, panc, lung, blad, headnk, esoph, mela, stom	mAb+diag+s.m.
05	428368			matrix metalloproteinase 3 (stromelysin	headnk, storn, esoph, coton	diag
	428392		Hs.2265	secretory granuta, neuroendocrine protei	panc	diag
	428450		91 Hs.184339	KIAA0175 gene product	ovar, cerv, panc, lung, blad, mela	s.m.
		Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	lung, blad, colon, uter, ovar	s.m.
70		AF10403		solute carrier family 7 (cationic amino	lung, blad, headnk, cerv, esoph, glio, uter, stom, colon, mela	mAb+s.m.
		AW58349		pancreatic polypeptide	panc	diag
	42850	5 AL035461	Hs.2281	chromogranin 8 (secretogranin 1)	panc, tung	diag
		3 BE22080			mela, panc, stom, headnk	mAb mAb+s.m.
7.0			56 Hs.184942		ovar, EWS, uter	CTL+s.m.
75		4 AK00166			blad, ovar, pros, tung, stom, test	mAb
		8 AA85277			breast, colon, lung, panc, storn, headnk, ovar, EWS	diag
		8 AW59320		Ksp37 protein	tung ovar, cerv, lung, panc, stom, renal	diag
		8 AA43398		CA125 antigen; mucin 16		mAb+s.m.
80		8 AK00053			ovar glio, mela	mAb+s.m.
οU		4 Y12851 1 Al418430	Hs.193470 Hs.104935		gio, meia renal	mAb+s.m.+CTL
		3 AA30661			cerv, panc, colon, stom, headrik, renal	mAb+diag
		9 AF12027			lung, cerv	diag
	42030	2 W.14021	- 113.134U03		g,	•

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			Hs.194591		the state of the s	mAb+s.m. mAb+s.m.
			Hs.197962			mAb+s.m.
		AF052693	Hs.198249			mAb+s.m.
5		AAD19004 AF056085	Hs.198396 Hs.198612			mAb+s.m.
,		AL117405	Hs.335891			mAb+s.m.
		AW009166	Hs.99376			diag
		AB024937	Hs.211092			mAb+diag
		AL134197	Hs.93597		lung, mela	S.M.
10		NM_000867	Hs.2507	5-hydroxytryptamine (serotonin) receptor	leio	mAb+s.m.
	430147	R60704	Hs.234434		glio	s.m.
		AA361258	Hs.237868		mela, tung, panc, stom, esoph, headnk	mAb+s.m.+CTL CTL
	430377	NM_001922			mela	mAb+s.m.
15	430486	BE062109	Hs.241551		hing, blad, headnk, cerv, esoph mela	s.m.
13	430822	AJ005371 X54232	Hs.248017	g,	glio, hung, cerv, blad, esoph	mAb+s.m.
	430890 431053		Hs.2699 Hs.249141		gio	mAb
	431130	NM_006103			ourse vides	diag
		AW583672			panc, tung, glio, test	diag
20				EDG-7 (endothetial differentiation, lys	ovar, pros, lung, blad	mAb+s.m.
	431620	AA126109	Hs.264981	2-5-oligoadenylate synthetase 2 (69-71	esoph, cerv	CTL+s.m.
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (do	panc, uter, cerv, stom, esoph, mela	mAb+diag
		NM_002204		integrin, alpha 3 (antigen CD49C, alpha	ovar, panc, blad, headnk, mela, renal	mAb+s.m. CTL
25		AA534908	Hs.2860	POU domain, class 5, transcription facto	test, renal, blad	mAb+diag
25		8E019924	Hs.271580	uroplakin 1B	lung, blad, headnk, uter, cerv, storn, ovar renat	mAb+s.m.+CTL
	431870 431939	AW449902 AW008061	Hs.105500 Hs.231994	ESTs ESTs	renal, colon	mAb+s.m.+CTL
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	lung, blad, cerv, headnik, ovar, colon, pros, panc, breast, esoph, test, mela	
	432196	AW300888	Hs.273230	hypothetical protein FLJ 10830	renal	CTL
30	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	breast, colon, ovar, stom, panc, uter, cerv, fung	mAb+diag+s.m.
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	renal	CTL
	432596	AJ224741	Hs.278461	matrilin 3	panc, breast	diag
	432606			granzyme K (serine protease, granzyme 3;	renal, breast, lung, storn, hepC, fibro	CTL
25	432800	BE391046	Hs.278962	AIM-1 protein	mela, pros	mAb+s.m. CTL+s.m.
35	432829	W60377	Hs.57772	ESTs	blad	mAb+s.m.+CTL
	432867		Hs.233364 Hs.279651	ESTs melanoma inhibitory activity	storn, colon panc, storn, mela	diag
	432974	W94322 AL036071	Hs.279899	tumor necrosis factor receptor superfami	pros, renal	mAb+s.m.
		AF217513	Hs.279905	clone HQ0310 PR00310p1	colon, breast, lung, blad, cerv, uter, test, mela	s.m.
40		U29195	Hs.3281	neuronal pentraxin II	mela, esoph, colon, renal	diag
		AF095719	Hs.93764	carboxypeptidase A4	headnk, esoph, lung	s.m.
		AK000596	Hs.3618	hippocalcin-like 1	renal	CTL
		AW136973	Hs.362915	ESTs, Weakly similar to S69890 mitogen i	storn, colon	CTL+s.m.
		AF123659	Hs.93505	leucine zipper, putative tumor suppresso	mela	s.m. CTL
45		H91923	Hs.110024	NM_020142:Homo sapiens NADH:ubiquinone o		mAb
			Hs.283022	triggering receptor expressed on myeloid	glio	diag
		AF200492		interleukin-1 homolog 1 junctional adhesion molecule 2	tung, headnk angio, glio	mAb
		AF255910 AW292677		melanin-concentrating hormone receptor (mela, glio	mAb+s.m.
50		AJ271643	Hs.87469	putative acid-sensing ion channel	glio	mAb+s.m.
•	435481		Hs.5199	HSPC150 protein similar to ubiquitin-con	lung, blad, colon, ovar, uter, headnk, test	s.m.
		AI458213	Hs.77542	ESTs	renal, panc, headnk, lung	mAb+s.m.
	436608	AA628980		down syndrome critical region protein DS	blad, lung	CTL+s.m.
66		AF037335		carbonic anhydrase XII	breast, renal, ovar, glio	mAb+s.m. CTL
55	436961			ESTs	tung, panc, renal, uter, colon	diag
		AB018305		spondin 1, (f-spondin) extracellular mat	over, fibro	s.m.
		AU076916		guanine monphosphate synthetase	tung, blad, cerv, esoph, headnk headnk, cerv, tung, blad, breast, pros, ovar, stom, esoph	CTL
	437044 437100		Hs.14535	differentially expressed in Fanconi's an Homo sapiens cDNA: FLJ22314 fis, clone H	panc, renal	mAb+s.m.+CTL
60		A1765021	Hs.210775	ESTs	renal, uter, ovar	mAb+s.m.+CTL
		AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	tung	CTL
	437852	BE001838	Hs.256897	putative GPCR	blad, fung	mAb+s.m.
	437938		Hs.369628	gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapie		mAb+s.m.+CTL
65	438380		Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	glio, mela	diag CTL+diag
65	438549			trinucleotide repeat containing 3	mela	mAb+s.m.+CTL
	438859			Homo sapiens mRNA for KIAA1647 protein		mAb+s.m.+CTL
	438929 438966			ESTs gb:EST391184 MAGE resequences, MAGP H	renal	mAb+s.m.+CTL
	43901			membrane-spanning 4-domains, subfamily A	uter, stom, pros, fibro	mAb
70	43922			UL16 binding protein 2	lung, headnk, cerv, esoph, blad, colon	mAb
. •	43947		Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	lung	mAb+s.m.
	43956			CEGP1 protein	breast, AWPC, pros, blad	diag
	43960	6 W79123	Hs.58561	G protein-coupled receptor 87	lung, blad, headnk, cerv, esoph	mAb+s.m.
75	43973			sema domain, immunoglobulin domain (lg).	blad, lung, cerv, renal	mAb+s.m. mAb+s.m.+CTL
75	43975			Homo sapiens mRNA full length insert cDN	colon, storn, panc, lung	mAb
	43997			hypothetical protein FLJ10430	renal, cerv, pros, headrik, colon, test blad, ovar, lung, headrik, test	s.m.
	44000		7 Hs.6844 Hs.266331	NALP2 protein; PYRIN-Containing APAF1-li Horno sapiens Fc receptor homolog express	nela ovar, iung, neautik, test	diag
	44006 44022			tumor necrosis factor receptor superfami	glio	mAb
80	44030				renal, colon, blad	mAb+s.m.
	44031				renal	mAb+s.m.+CTL
	44051	6 S42303	Hs.161	cadherin 2, type 1, N-cadherin (neuronal	glio, ovar, uter, renal, hepC	mAb+diag
	44067	2 AF08381	1 Hs.7345	MAD1 (mitotic arrest deficient, yeast, h	mela	s.m.
					(01	

	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	tung, blad, headrik, test, mela, esoph	s.m.
			Hs.222119	ESTs, Weakly similar to S30433 keratin 1	renal	mAb+s.m.+CTL
			Hs.372210	ESTs, Wealthy similar to S72482 hypotheti	fibro, angio	mAb
_		AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	breast, tung, blad, panc, headnk, storn, ovar, pros	mAb+s.m.
5		AW874138	Hs.129017	ESTs; type la transmembrane protein	ovar, uter	mAb mAb+s.m.+CTL
		AA995998		gb:os26b03.s1 NCI_CGAP_Kd5 Homo sapiens	uter, ovar, renal	mAb+diag
	443105		Hs.9004	chondroitin sulfate proteoglycan 4 (mela ESTs	mela btad, ovar, tung, headnk, stom	mAb+s.m.+CTL
		A1128388 BE614387	Hs.143655 Hs.333893	c-Myc target JPO1	coton, tung, blad, panc	CTL
10		AF098158	Hs.9329	chromosome 20 open reading frame 1	colon, lung, blad, storn, test, mela	CTL
		AF169312	Hs.9613	PPAR(gamma) angiopoietin related protein	renal	diag
		AI085198	Hs.164226	Thrombospondin 1	angio, panc, uter	diag
		AW449952	Hs.190125	basic-helix-loop-helix-PAS protein	glio, uter, ovar	mAb+s.m.+CTL
16		NM_013409		follistation	tung, cerv, headnik, blad, esoph	diag mAb+s.m.
15	444006	AW163123	Hs.10071 Hs.10086	seven transmembrane protein TM7SF3 type I transmembrane protein Fn14	renal panc, colon, tung, ovar, renal, esoph, mela, blad, storn, cerv	mAb
	444371	BE395085 BE540274	Hs.239	forthead box M1	tung, headnk, blad, glio, test, mela	s.m.
	444381	BE387335	Hs.283713	hypothetical protein BC014245	breast, colon, blad, lung, panc, headnk, ovar, storn, uter,	
		0000.000		77	renal, angio, test, mela, esoph	diag
20	444488	AW192879	Hs.355660	ancient conserved domain protein 4	renal	mAb+s.m.
	444527	NM_005408		small inducible cytokine subfamily A (Cy	fibro, esoph	diag mAb+diag
	444781	NM_014400		GPI-anchored metastasis-associated prote	tung, blad, headrik, cerv ovar, tung, blad, headrik, panc, cerv, storn, utar, coton, esoph	CTL+s.m.
	444783 444809	AK001468 BE207568	Hs.62180 Hs.208219	anillin (Drosophila Scraps homotog), act oculospanin	mela	mAb+s.m.
25	445070	NM_000677		adenosine A3 receptor	gfio, renal	mAb+s.m.
	445417	AK001058	Hs.12680	a disintegrin-like and metalloprotease w	panc, headnk, stom, lung, esoph	diag
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	ovar, blad, uter, breast, lung, headrik, renal, fibro, panc, cerv	mAb+diag
	445891			DPCR1 protein	stom, panc, esoph, omuc, esoph	mAb CTI
20	445895	D29954	Hs.13421	KIAA0056 protein	pros	CTL mAb+diag
30	445051	BE048061	Hs.37054	ephún-A3	colon, breast breast, cerv, uter	mAb+s.m.
	446163	AA026880 AI281848	Hs.25252 Hs.194691	protactin receptor retinoic acid induced 3	storn, panc, colon, ovar	mAb+s.m.
	446341	AL040763	Hs.310735	FGENESH prediction similar to multidrug	mela	mAb+s.m.
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	ovar, fibro, panc, headnk, lung, colon, blad, mela, esoph, uter	diag
35	446650	AB016625	Hs.15813	solute carrier family 22 (organic cation	renal	mAb+s.m.
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	breast, panc, headnk, lung, fibro, mela	diag mAb+diag
	447004			FGENESH predicted secreted protein	glio colon, pros, fibro, breast, ovar, lung, panc	CTL+diag
	447033 447072		Hs.157601 Hs.17279	Predicted gene: Eos cloned; secreted w/V tyrosylprotein sulfotransferase 1	glio, panc	CTL+s.m.
40	447131		5 Hs.17466	retinoic acid receptor responder (tazaro	renal, breast, stom, tung, mela, ovar	mAb+s.m.
40	447208	BE315291	Hs.237971	hypothetical protein MGC5627	esoph, stom, colon	CTL+diag
	447269		1 Hs.17958	cerebroside (3-phosphoadenylylsulfate:g	renal	CTL
	447342		Hs.19322	Homo sapiens, Similar to RIKEN cONA 2010	colon, blad, pres, fung, stem, AWPC, ovar	· CTL
45	447400		Hs.18457	hypothetical protein FLI20315	colon, pros, stom, uter	CTL s.m.
45	447674			cyclin-dependent kinase 2	mela	mAb+s.m.+CTL
	447835			ESTs, Weakly similar to 138022 hypotheti Homo sapiens mRNA full length insert cDN	renal, ovar, uter mela	mAb+s.m.
	447937 448105			Transmembrane protease, serine 3	breast, panc, colon, lung, over, stom	mAb+s.m,+CTL
	448243			integrin, beta 8	ovar, uter, lung, stom, headnk, glio, panc	mAb+s.m.
50	448321		3 Hs.20912	adenomatous polyposis coli like	glio	mAb+s.m.+CTL
	448499		Hs.77550	p53-regulated DOA3	glio	
	448595			KIAA0644 gene product	breast, glio	mAb+s.m. diag
	448610		7 Hs.21602	nel (chicken)-like 1	meta tung, renal	mAb+s.m.
55	448733 448844		9 Hs.187958 Hs.177164	solute carrier family 6 (neurotransmitte FGENESH predicted novel cell surface pr	pane, lung, storn, omuc	mAb+s.m.
33	449048		Hs.22920	similar to S68401 (cattle) glucose induc	panc, ovar, uter, glio, headnk, lung	mAb
	449444			solute carrier family 16 (monocarboxylic	renal, panc	mAb+s.m.
	449523		79 Hs.54443	chemokine (C-C motif) receptor 5	tung, panc, renal, stom, hepC, fibro, mela	mAb+s.m.
	449720			hypothetical protein FLJ21562	colon	CTL
60	449722			cyclin 81	headrik, blad, lung, panc, angio, test, meta, esoph	ş.m. mAb+s.m.
	450001		14 Hs.406	solute carrier family 6 (neurotransmitte	renal breast, ovar, headnik, panc, tung, esoph, colon	mAb+diag+s.m.
	450375 450531			a disintegrin and metalloproteinase doma (BC017500) Similar to hypothetical prote	colon	CTL
	45070		Hs.288467	hypothetical protein XP_098151 (leucine-	lung, headnk, panc, breast, storn, ovar, esoph, colon	mAb+diag
65	450720			HUMPSPBA Human pulmonary surfactant-as		s.m.
	45093	N25156	Hs.25648	tumor necrosis factor receptor superfami	tung, renat	mAb+s.m.
	450983			ERO1 (S. cerevisiae)-like	blad, lung, ovar, panc	atag mAb+s.m.
	45109		Hs.25954	interleukin 13 receptor, alpha 2	glio, fibro, mela	CTL
70		0 AW25065		Human DNA sequence from clone RP3-447F transmembrane 4 superfamily member 7	3 colon, panc renal	mAb
70	45153	7 AF022813 7 R56631	3 Hs.26518 Hs.26550	retinoid X receptor, gamma	mela	CTL+s.m.
		8 Z43948	Hs.326444	cartilage acidic protein 1	blad, ovar, tung	mAb+diag
		9 U80456	Hs.27311	single-minded (Drosophila) homolog 2	pros	CIL
		9 F06972	Hs.27372	endothelial tyrosine kinase (Etk) (BMX).	angio	CTL+s.m.
75	45198	8 AF26392		papillomavirus regulatory factor PRF-1	renat	CTL mAbre median
	45209			a disintegrin-like and metalloprotease (ovar	mAb+s.m.+diag mAb
		0 H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRN	A breast, stom, panc stom, panc, renal, colon, mela, fibro	mAb+s.m.
		4 A1694413 3 X57522	Hs.373599 Hs.352018		cerv, esoph, blad, stom, mela, renal	mAb+s.m.
80		1 T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL		diag
		5 N54926	Hs.29202	G protein-coupled receptor 34	glio, libro, panc	mAb+s.m.
	45240	1 NM_007	115 Hs.29352	turnor necrosis factor, alpha-induced pro	blad, breast, panc, headnk, stom, lung, arth, renal, esoph	diag
		1 U88879	Hs.29499	toll-like receptor 3	renal, hepC	mAb

		BE153855	Hs.61460	lg superfamily re		breast, blad, lung, headn		mAb mAb+s.m.+CTL
		AW392555	Hs.18878	hypothetical prot		renal, headnk, colon, lung tung, ovar, breast, mela,		CTL
	452838 452862	AW378065	Hs.30743 Hs.8687		ressed antigen in mela sintegrin-like and metallo		th, lung, blad, esoph, storn	mAb+diag
5		BE241876	Hs.32352		ein DKFZp434K1210	renal		CTL
		AA442103	Hs.33084		nity 2 (facilitated glu	renal, pros		mAb+s.m. mAb+s.m.
	453642	Al370936 Al138387	Hs.34074	dipeptidytpeptida	ise VI epeat-containing 7 (liv	glio renat, mela		S.M.
		AL080235	Hs.256126 Hs.35861		rescence 1 (RIS1)	glio, lung, uter, headnk,	cerv, panc, pros	mAb+s.m.
10		AA847843	Hs.62711		oup (nonhistone chromoso	lung, uter, blad, test		CTL+s.m.
		AI590321	Hs.203845		ium channel, subfamily K, m	ovar		mAb+s.m. CTL
		NM_002448) homeo box homolog 1 (fo	uter, ovar glio, tung		mAb+s.m.
	456759	BE259150 M54968	Hs.127792 Hs.351221	delta (Drosophil v-Ki-ras 2 Kirster	n rat sarooma 2 viral on	bauc And mild		s.m.
15		Al693815	Hs.127179	cryptic gene		panc, pros, tung		diag
		AA331517	Hs.286055	chimerin (chima		glio		mAb+s.m. mAb
	458079	AI796870 AI418718	Hs.54277 Hs.144121		imilar to RIKEN cDNA 28100 imilar to T46916 hypotheti	mela, fibro glio		mAb+s.m.+CTL
		AW088642			mining region Y)-box 17 (S	ovar, uter, test		CTL
20								
	TABLE 6				• .			
	Pkey: CAT num		Inique Los prot Sene cluster nur	eset identifier num wher	ber .			
	Accession		Senbank access		·			
25								
	Pkey		CAT Nun	ber Accession	0000 DIGGGGG A1343640 A136	44E2 A10007E4 AUA/207404	AA077391 BG012775 BG997382 AA286	8933 AA150722 RI007625
	409745	MH1944_	5 B1030997	/ AA9218/4 AW18 ! DINNO INN DINNS?	8822 BIU27862 AL347618 AL36 75 BIOGESTO BIO31000 RIBSSR	1453 A10887 54 AVV <i>2</i> 0749 1 SA R1006277 R1007627 B10	06266 Bi006991 Bi006990 Bi007763 Bi0	07762 BG997377
			AA15078	0 BI033518 BI027	818 BG015789 BI033807 AA34	11445	•	
30	438966	1242593	1 AW9790	74 AAR34841 AAR	28650			200 05047265 41761052
	442438	24590_1	AK02217	5 AU147222 AI12	4945 AU121400 F07756 AW97	9025 AA828595 AA828577	7 BE935573 AA829588 A1743616 BE315 507647 T77777 AA807461 A1829714 A13	76820 AIRO9991
			AW1689 AW6618		79419 851/10/1 82034300 8	F134231 NO1101 F001431	F07647 T77332 AA897461 A1829714 A13	,0000,1120000
			ATTOOLO	•				
35	TABLE 6			121				
•	Pkey: Ref:		Unique number	corresponding to a	an Eos probesel abore in this column are Genha	ok Identifier (GI) numbers	"Dunham, et al." refers to the publication	entitled The DNA
	Rei.		sequence of hu	man chromosome	22" Dunham, et al. (1999) Natu	re 402:489-495.		
40	Strand:		Indicates DNA	strand from which	exons were predicted.			
40	NL_posit	ion:	Indicates nucleo	atide positions of p	redicted exons.			
	Pkey	Ref	Strand	Nt_position				
	400843				653-7784,8892-9023,9673-980	17,		
4.5	402075	8117407	Plus	121907-1220	335,122804-122921,124019-12			
45	402901	8894222		175426-1750				
	404287 404682	2326514 9797231		53134-5328 40977-4115				
	404875	9801324	Ptus		2,97722-97831			
50	404977			43081-4322				
50	405033 405547			142358-142	545 520,124914-125050			
	406400				1878-2140,4252-4385,5922-60	77		•
	100.00	010010						
55								
23	TABLE Pkey:	67:	Linious Foe no	obeset identifier nu	mher			
	ExAcco	:			nbank accession number			
	Unigen		Unigene numb	er				
60	Unigen		Unigene gene		linking the information in Table	67 to the commerces in Tal	No FR	
00	Seq ID	NO.	Sequence roa	IONCARON MUNICIPES	many ore mornation at raise	or to the acqueroos in re-	~ ~	
	Pkey	ExAccn		UnigeneID	Unigene Title		Seq ID No	
	418007			Hs.83169	matrix metalloproteinase 1 (i		Seq ID No 1 & 199 Seq ID No 2 & 200	
65	418007 428368			Hs.83169 Hs.83326	matrix metalloproteinase 1 (i matrix metalloproteinase 3 (:		Seq ID No 3 & 201	
05	417856			Hs.82772	collagen, type XI, atpha 1	au on nory on n	Seq ID No 4 & 202	
	444381	BE3873	335	Hs.283713	hypothetical protein BC0142		Seq ID No 5 & 203	
	452281			Hs.28792	Homo sapiens cDNA FLJ11	041 fis, clone PL	Seq ID No 6 Seq ID No 7 & 204	
70	428698 452863			Hs.334838 Hs.8687	KIAA 1866 protein ADAMTS2 (a disintegrin-lik	e and metallo	Seq ID No 8 & 205	
, 0	43220			Hs.298241	Transmembrane protease, s		Seq ID No 9 & 205	
	43420	6 AW136	973	Hs.362915	ESTs, Weakly similar to S69	3890 mitogen i	Seq ID No 10 & 207	
	42226			Hs.105484	regenerating gene type IV	1050 /6/14 4110	Seq ID No 11 & 208 Seq ID No 12 & 209	
75	40904 44342			Hs.50081 Hs.9329	Hypothetical protein, XP_05 chromosome 20 open readi		Seq ID No 13 & 210	
, ,	44321			Hs.143655	ESTs	•	Seq ID No 14	
	42866	4 AK001	666	Hs.189095	similar to SALL1 (sal (Droso		Seq ID No 15 & 211	
	41327			Hs.833 Hs.29352	interferon-stimulated protein turnor necrosis factor, alpha		Seq ID No 16 & 212 Seq ID No 17 & 213	
80	45240 45240			Hs.29352 Hs.29352	tumor necrosis factor, alpha tumor necrosis factor, alpha		Seq ID No 18 & 214	
	40838	Q AF123		Hs.44532	diubiquitin		Seq ID No 19 & 215	
	41620			Hs.79078	MAD2 (mitotic arrest deficie	ent, yeast, h	Seq ID No 20 & 216 Sep ID No 21 & 217	
	40975	7 NM_O	71979	Hs.123114	cystatin SN		Seq ID No 21 & 217	

	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	Seq ID No 22 & 218
	452194	AI694413	Hs.373599	olfactory receptor, family 2, subfamily	Seq ID No 23 & 219
	452194	AI694413	Hs.373599	olfactory receptor, family 2, subfamily	Seq ID No 24 & 220
5	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	Seq ID No 25 & 221 Sea ID No 26 & 222
)	422956 424905	BE545072	Hs.122579 Hs.153704	ECT2 protein (Epithelial cell transformi NIMA (never in mitosis gene a)-related k	Seq ID No 27 & 223
	415989	NM_002497 AJ267700	Hs.351201	ESTs	Seq ID No 28
	415989	A1267700	Hs.351201	ESTs	Seq ID No 29
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	Seq ID No 30 & 224
10	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	Seq ID No 31 & 225
	432857	AW016936	Hs. 233364	ESTs	Seq ID No 32
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	Seq ID No 33
	428970	BE276891	Hs.194691	retinoic acid induced 3 (RAIG1); metabo	Seq ID No 34 & 226
1.5	428953	AA306610	Hs.348183	tumor necrosis factor receptor superfami	Seq ID No 35 & 227
15	428953	AA306610	Hs.348183	tumor necrosis factor receptor superfami	Seq ID No 36 & 228
	428953	AA306610	Hs.348183	tumor necrosis factor receptor superfami	Seq ID No 37 & 229 Seq ID No 38 & 230
	428953 428953	AA306610 AA306610	Hs.348183 Hs.348183	tumor necrosis factor receptor superfami tumor necrosis factor receptor superfami	Seq ID No 39 & 231
	452203	X57522	Hs.352018	transporter 1. ATP-binding cassette, sub	Seq ID No 40 & 232
20	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	Seq ID No 41 & 233
20	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	Seq ID No 42 & 234
	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	Seq ID No 43 & 235
	425115	R44664	Hs.123956	downstream of: G protein-coupled recept	Seq ID No 44 & 235
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	Seq ID No 45 & 237
25	418870	AF147204	Hs.89414	chemoldine (C-X-C motif), receptor 4 (fus	Seq ID No 46 & 238
	415511	A1732617	Hs.182362	ESTs	Seq ID No 47
	440304	BE159984	Hs.125395	hepatitis A virus cellular receptor 1	Seq ID No 48 & 239 Seq ID No 49 & 240
	423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	Seq ID No 50
30	423161 410153	AL049227 BE311926	Hs.124776 Hs.15830	downstream of cadherin 6 (by 3.3kb) hypothetical protein FLJ12691	Seq ID No 51 & 241
50	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	Seq ID No 52 & 242
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	Seq ID No 53 & 243
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	Seq ID No 54 & 244
	436895	AF037335	Hs.5338	carbonic anhydrase XII	Seq 1D No 55 & 245
35	436895	AF037335	Hs.5338	carbonic anhydrase XII	Seq ID No 56 & 246
	421471	U90545	Hs.327179	solute carrier family 17 (sodium phospha	Seq ID No 57 & 247
	428296	NM_003058	Hs.183572	solute carrier family 22 (organic cation	Seq ID No 58 & 248
	426890	AA393167	Hs.41294	ESTs	Seq ID No 59 & 249 Seq ID No 60
40	437212	A1765021	Hs.210775	ESTs gb:EST391184 MAGE resequences, MAGP Homo	Seq ID No 61
40	438966 440311	AW979074 AI733079	Hs.125407	ESTs, Moderately similar to ALUE_HUMAN!	Seq ID No 62
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	Seq ID No 63
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	Seq ID No 64
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	Seq ID No 65 & 250
45	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	Seq ID No 56 & 251
	443595	AF169312	Hs.9613	PPAR(gamma) angiopoletin related protein	Seq ID No 67 & 252
	443595	AF169312	Hs.9613	PPAR(gamma) angiopoietin related protein	Seq ID No 68
	410407	X66839	Hs.63287	carbonic anhydrase IX	Seq ID No 69 & 253
50	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	Seq ID No 70 & 254 Seq ID No 71 & 255
30	420737	L08096	Hs.99899	CD70; tumor necrosis factor (figand) s hypothetical protein FLJ10430	Seq ID No 72 & 256
	439979 420789	AW600291 Al670057	Hs.6823 Hs.199882	ESTs	Seq ID No 73
	420789	A1670057	Hs.199882	ESTs	Seq ID No 74
	441392	AW451831	Hs.222119	ESTs, Weakly similar to S30433 keratin 1	Seq ID No 75 & 257
55	452431	U88879	Hs.29499	totl-like receptor 3	Seq ID No 76 & 258
	431870	AW449902	Hs.105500	ESTs	Seq ID No 77
	431870	AW449902	Hs.105500	ESTs	Seq ID No 78
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	Seq ID No 79 & 259
60	409745	AA077391	Hs.93522	gb:7814E12 Chromosome 7 Fetal Brain cDNA	Seq ID No 80 Seq ID No 81
UU	438859 409637	AI559626 AA323948	Hs.55407	Homo sapiens mRNA for KIAA1647 protein, Homo sapiens mRNA; cDNA DKFZp434K0621 (f	Seq ID No 82 & 260
	409637	AA323948	Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (f	Seq ID No 83
	409348	Al401535	Hs.146090	ESTs	Seq ID No 84
	447269	NM_004861	Hs.17958	cerebroside (3'-phosphoadenylylsulfate:g	Seq ID No 85 & 261
65	453195	BE241876	Hs.32352	hypothetical protein DKFZp434K1210	Seq ID No 86 & 262
	428841	AJ418430	Hs. 104935	ESTs	Seq ID No 87
	428841	AI418430	Hs.104935	ESTs	Seq ID No 88
	428841	Al418430	Hs.104935	ESTs	Seq ID No 89 Seg ID No 90 & 263
70	409663		Hs.98306	KIAA1862 protein KIAA1862 protein	Seq ID No 91 & 264
70	409663		Hs.98306 Hs.231994	ESTs	Seq ID No 92 & 265
	431939 432606		Hs.3066	granzyme K (serine protease, granzyme 3;	Seq ID No 93 & 266
	411411		Hs.55950	ESTs, Weakly similar to KIAA1330 protein	Seq ID No 94 & 267
	433867		Hs.3618	hippocalcin-like 1	Seq ID No 95 & 268
75	433867		Hs.3618	hippocalcin-like 1	Seq ID No 96 & 269
	437938		Hs.369628	gb:wq05c02.x1 NCI_CGAP_Kd12 Homo sapien	Seq ID No 97
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	Seq ID No 98 & 270
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	Seq ID No 99 & 271
90	432196		Hs.273230	hypothetical protein FLJ10830	Seq ID No 100 & 272
80	432198		Hs.273230	hypothetical protein FLJ 10830	Seq ID No 101 & 273 Seq ID No 102
	438929		Hs.253177	ESTs gene for serine/threonine protein kinase	Seq ID No 103 & 274
	410055 446650		Hs.58241 Hs.15813	solute carrier family 22 (organic cation	Seq ID No 104 & 275
	********		16,15010	and a control to the land and and and and and and and and and	•



	426812	AF105365	Hs.172613	solute carrier family 12 (potassium/chto	Seq ID No 105 & 276
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	Seq ID No 106 & 277
	449444	AW818436	Hs.351306	solute carrier family 16 (monocarboxylic	Seq ID No 107 & 278 Seq ID No 108 & 279
5	422627 444488	BE336857 AW192879	Hs.118787 Hs.355660	transforming growth factor, beta-induced ancient conserved domain protein 4	Seq ID No 109 & 280
,	450931	N25156	Hs.25648	tumor necrosis factor receptor superfami	Seq ID No 110 & 281
	409220	BE243323	Hs.51233	tumor necrosis factor receptor superfami	Seq ID No 111 & 282
	409220	BE243323	Hs.51233	tumor necrosis factor receptor superfami	Seq ID No 112 & 283 Seq ID No 113 & 284
10	425998 425998	AU076629 AU076629	Hs.165950 Hs.165950	fibroblast growth factor receptor 4 fibroblast growth factor receptor 4	Seq ID No 114 & 285
10	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	Seq ID No 115 & 286
	443987	AW163123	Hs.10071	seven transmembrane protein TM7SF3	Seq ID No 116 & 287
	432990	AL036071	Hs.279899	tumor necrosis factor receptor superfami	Seq ID No 117 & 288 Seq ID No 118 & 289
15	436576 451527	AI458213 AF022813	Hs.77542 Hs.26518	ESTs transmembrane 4 superfamily member 7	Seq ID No 119 & 290
1.5	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	Seq ID No 120 & 291
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	Seq ID No 121 & 292
	125218	H91923	Hs.110024	Empirically selected from AFFX single pr	Seq ID No 122 & 293 Seq ID No 123
20	436961 431630	AW375974 NM_002204	Hs.156704 Hs.265829	ESTs integrin, alpha 3 (antigen CD49C, alpha	Seq ID No 124 & 294
20	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	Seq ID No 125 & 295
	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	Seq ID No 126 & 296
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	Seq ID No 127 & 297
25	442438 447835	AA995998 AW591623	Hs.164129	gb:os26b03.s1 NCI_CGAP_Kid5 Homo sapiens ESTs, Weakly similar to 138022 hypotheti	Seq ID No 128 Seq ID No 129
LJ	429276	AF056085	Hs.198612	G protein-coupled receptor 51	Seq 1D No 130 & 298
	448595	AB014544	Hs.21572	KIAA0644 gene product	Seq ID No 131 & 299
	440516	\$42303	Hs.161	cadherin 2, type 1, N-cadherin (neuronal	Seq ID No 132 & 300
30	456759 447004	8E259150 AW296968	Hs.127792 Hs.157539	detta (Drosophila)-like 3 FGENESH predicted secreted protein	Seq ID No 133 & 301 - Seq ID No 134 & 302
50	425088	AA663372	Hs.169395	hypothetical protein FLJ12015	Seq ID No 135 & 303
	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	Seq ID No 136 & 304
	448321	NM_005883	Hs.20912	adenomatous polyposis coli like	Seq ID No 137 & 305
35	426344 419704	H41821	Hs.322469 Hs.45057	transcriptional activator of the c-fos p ESTs	Seq ID No 138 & 306 Seq ID No 139 & 307
33	412959	AA429104 D87458	Hs.75090	KIAA0282 protein	Seq ID No 140 & 308
	448499	BE613280	Hs.77550	p53-regulated DDA3	Seq ID No 141 & 309
	458435	AJ418718	Hs.144121	ESTs, Wealdy similar to T46916 hypotheti	Seq ID No 142 & 310
40	443785 427343	AW449952 AI880044	Hs.190125 Hs.176977	basic-hefix-loop-hefix-PAS protein protein kinase C binding protein 2	Seq ID No 143 & 311 Seq ID No 144 & 312
70	416857	AA188775	Hs.292453	FGENESH predicted TM containing protein	Seq ID No 145 & 313
	429149	AW193360	Hs.197962	Homotog of mouse ADP-ribosylation factor	Seq ID No 146 & 314
	418030	BE207573	Hs.83321	neuromedin B	Seq ID No 147 & 315
45	457561 457561	AA331517 AA331517	Hs.286055 Hs.286055	chimerin (chimaerin) 2 chimerin (chimaerin) 2	Seq ID No 148 & 316 Seq ID No 149 & 317
43	430147	R60704	Hs.234434	hairy/enhancer-of-split related with YRP	Seq ID No 150 & 318
	453642	Al370936	Hs.34074	dipeptidylpeptidase VI	Seq ID No 151 & 319
	453857	AL080235	Hs.35861	Ras-induced senescence 1 (RIS1)	Seq ID No 152 & 320
50	449048 418506	Z45051 AA084248	Hs.22920 Hs.37 2 651	simitar to \$68401 (cattle) glucose induc Unknown protein for MGC:29643 (formerly	Seq ID No 153 & 321 Seq ID No 154 & 322
50	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	Seq ID No 155 & 323
	421508	NM_004833	Hs.105115	absent in metanoma 2	Seq ID No 156 & 324
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	Seq ID No 157 & 325 Seq ID No 158 & 326
55	428784 431958	Y12851 X63629	Hs.193470 Hs.2877	purinergic receptor P2X, ligand-gated io cadherin 3, type 1, P-cadherin (placenta	Seq ID No 159 & 327
7,5	417542	J04129	Hs.82269	progestagen-associated endometrial prote	Seq ID No 160 & 328
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	Seq ID No 161 & 329
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	Seq ID No 162 & 330 Seq ID No 163 & 331
60	420208 430377	BE276055 NM_001922	Hs.95972 Hs.301865	silver (mouse homolog) like dopachrome tautomerase (dopachrome delta	Seq ID No 164 & 332
•	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	Seq ID No 165 & 333
	412580	AA113262	Hs.17901	similar to CABLES (Homo sapiens)	Seq ID No 165 & 334
	417166	AA431323 BE220806	Hs.42146 Hs.184697	Paired box protein Pax-3 plexin C1	Seq ID No 167 & 335 Seq ID No 168 & 336
65	428513 447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	Seq ID No 169 & 337
•••	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	Seq ID No 170 & 338
	446341	AL040763	Hs.310735	FGENESH prediction similar to multidrug	Seq ID No 171 & 339
	446341 458079	AL040763 A1796870	Hs.310735 Hs.54277	FGENESH prediction similar to multidrug Homo sapiens similar to RIKEN cDNA 28100	Seq ID No 172 & 340 Seq ID No 173 & 341
70	415668		Hs.306814	Homo sapiens lysyl oxidase-like 4 (LOXL4	Seq ID No 174 & 342
. •	447674		Hs.19192	cyclin-dependent kinase 2	Seq ID No 175 & 343
	447674		Hs.19192	cyclin-dependent kinase 2	Seq ID No 176 & 344
	440065		Hs.266331 Hs.77667	Homo sapiens Fc receptor homolog express lymphocyte antigen 6 complex, locus E	Seq ID No 177 & 345 Seq ID No 178 & 346
75	414945 440672		Hs.7345	MAD1 (mitotic arrest deficient, yeast, h	Seq ID No 179 & 347
	412609		Hs.74124	ocular albinism 1 (Nettleship-Falls)	Seq ID No 180 & 348
	453837	AL138387	Hs.256126	baculoviral IAP repeat containing 7 (liv	Seq ID No 181 & 349
	453837 434276		Hs.256126 Hs.93605	baculoviral IAP repeat-containing 7 (liv leucine zipper, putative tumor suppresso	Seq ID No 182 & 350 Seq ID No 183 & 351
80	408367		Hs.44424	Homo sapiens orphan neurobansmitter tra	Seq ID No 184 & 352
	444809	BE207568	Hs.208219	oculospanin	Seq ID No 185 & 353
	415929		Hs.304950	Homo sapiens mucolipin-3 (MCOLN3)	Seq ID No 186 & 354 Seq ID No 187 & 355
	421666	AL035250	Hs.1408	endothelin 3	200 IOI G 333

								C (D.N 4)	00 0 2CE
		W74048 AB007937			lymphocyte-speci syndecan 3	fic protein tyrosina	kun	Seq ID No 18 Seq ID No 18	
		R56631			retinoid X recepto	r. gamma		Seq ID No 15	
_		AA361258			intertaukin 7 rece			Seq ID No 19	91 & 359
5		BE387287		83384		ding protein, beta	(neur	Seq ID No 19	
		NM_0061		21602 278962	nel (chicken)-like AIM-1 protein	1		Seq ID No 1: Seq ID No 1:	
	432800 416350	BE391046 AF188625		189507	phospholipase A	2. group ND		Seq ID No 1	
	405545	74 10000			Tamel Evon	-		Seq ID No 1	96 & 364
10	414812	X72755		.77367	monokine induce	d by gamma interf	eron	Seq ID No 1	
	432874	W94322	HS.	279651	metanoma inhibit	ory acovity		Seq ID No 1	30 & 300
16	Table 68 lis	ts sequenc	ces as described	in Table 67					
15	Sec ID	NO. 1 1	DNA sequen	ce					
				8: NM_00242	1.2				
	Coding	sequen	ce: 1140	9					Ð,
20	1	11				41 	51 I		
20	ATGCACA	GCT TT	CCTCCACT G			STGTGGTGTC	ACACAGCTTC	60	
	CCAGCGA	CTC TA	GAAACACA A	GAGCAAGAT (TGGACTTAG	TCCAGAAATA	CCTGGAAAAA	120	
						GGAGAAATAG		180 240	
25						AAGTGACTGG TGCCTGATGT		300	
	GTCCTCA	CTG AG	GGGAACCC T	CGCTGGGAG	CAAACACATC	TGACCTACAG	GATTGAAAAT	360	
	TACACGO	CAG AT	TTGCCAAG A	GCAGATGTG (GACCATGCCA	TTGAGAAAGC	CTTCCAACTC	420	
	TGGAGTA	WIG TO	ACACCTCT G	CATCCCCAC	AAGGTCTCTG	AGGGTCAAGC TTGATGGACC	TOGROGRADAT	480 540	
30	CTTGCTC	ATG CT	TITCAACC A	GGCCCAGGT	ATTGGAGGG	ATGCTCATTT	TGATGAAGAT	600	
						GTGTTGCGGC		660	
	GGCCATT	CTC TI	CONTENTS OF	CATTCTACT	GATATCGGGG	CTTTGATGTA ATGGCATCCA	CCCTAGCTAC ACCCATATAT	720 780	
	GGACGTT	CCC AA	VAATCCTGT C	CAGCCCATC	GGCCCACAAA	CCCCAAAAGC	ATGTGACAGT	840	
35	AAGCTA	ACCT TI	GATGCTAT A	VACTACGATT	CGGGGAGAAG	TGATGTTCTT	TAAAGACAGA	900	
						TCAATTTCAT		960 1020	
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	CCCAAG	GACA TO	TACAGCTC (TTTGGCTTC	CCTAGAACTG	TGAAGCATAT	CGATGCTGCT	1140	
40	CTTTCTC	GAGG AF	AAACACTGG A	DATESARAR	TTCTTTGTTG	CTAACAAATA	CTGGAGGTAT	1200	
	GATGAA	TATA A	ACGATCTAT C	GATCCAGGT	TATCCCAAAA	TGATAGCACA GATTTTTCTA	TGACTTTCCT	1260 1320	
	GGAACA	AGAC A	ATACAAATT 1	IGATCCTAAA	ACGAAGAGAA	TTTTGACTCT	CCAGAAAGCT	1380	
4.5			CAACTGCAG						
45	C 10	NO. 3	DV2						
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50	1	11	1 :	21	31 	41	51 !		
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						TCCAGAAATA		120	
							TGGCCCAGTG GAAACCAGAT	180 240	
55	GCTGAA	ACCC TO	GAAGGTGAT	GAAGCAGCCC	AGATGTGGAG	TGCCTGATGT	GGCTCAGTTT	300	
	GTCCTC	ACTG A	GGGGAACCC	TCGCTGGGAG	CAAACACATC	TGACCTACAG	GATTGAAAAT	360	
							CTTCCAACTC	420 480	
							AGACATCATG TGGAGGAAAT	540	
60	CTTGCT	CATG C	TTTTCAACC	AGGCCCAGGT	ATTGGAGGGG	ATGCTCATTT	TGATGAAGAT	600	
	GAAAGG	TGGA C	CAACAATTT	CAGAGAGTAC	AACTTACATC	GTGTTGCCGC	TCATGCCCTC	660	
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							ATGTGACAGT	840	
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	TTCTAC	CATGC G	CACAAATCC	CTTCTACCCG	GAAGTTGAGC	TCAATTTCAT	TTCTGTTTTC AGATGAAGTC	960 1020	
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70	CCCAAC	GGACA T	CTACAGCTC	CTTTGGCTTC	CCTAGAACTG	TGAAGCATAT	CGATGCTGCT	1140	
70							CTGGAGGTAT TGACTTTCCT	1200 1260	
							TTTCTTTCAT	1320	
							CCAGAAAGCT	1380	
75	AATAG	CTGGT 7	TCAACTGCAG	GAAAAATTAG					
13	Can *1	D NO.	3 DNA sequ	100CC					
				n #: NM_002	422.2				
		g seque	ence: 64	1497					
80	1	1	11	21	31	41	51		
00	I ACAAG	GAGGC 4	I AGGCAAGACA	 GCAAGGCATA	GAGACAACAT	AGAGCTAAGT	AAAGCCAGTG	60	
	GAAAT	GAAGA (GTCTTCCAAT	CCTACTGTTC	CTGTGCGTGC	CAGTTTGCT	AGCCTATCCA	120	
							ATATCTAGAA	180 240	
	AACTA	CTACG	WCC1 CAAAAA	MONIGIUMAA	CAGITIGITA	. GUAGAAAGG	CAGTGGTCCT	240	

						2000110000	300
	GACTCCGACA CT	ATCCGAGA I	AATGCAGAAG	TTCCTTGGAT T	GGAGGTGAC (CCCCAACCIG	360
	TTCAGAACCT TI	CIGOROGIO.	CCCCAACTCC	AGGARARACOC A	ACCITACATA	CAGGATTGTG	420
	AATTATACAC CA	GATTTGCC	AAAAGATGCT	GTTGATTCTG (TGTTGAGAA	AGCTCTGAAA	480
5	GTCTGGGAAG AC	GTGACTCC	ACTCACATTC	TCCAGGCTGT A	ATGAAGGAGA	GGCTGATATA	540
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	GTTTTGGCCC AT	GCCTATGC	CCCTGGGCCA	GGGATTAATG (GAGATGCCCA	CTTIGATGAT	660 720
	GATGAACAAT GO	CONCERCT	CTTTCACTCA	COCABCACTO	ACCTTTGAT	GTACCCACTC	780
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	CAGTCCCTCT AT	TGGACCTCC	CCCTGACTCC	CCTGAGACCC (CCCTGGTACC	CACGGAACCT	900
	GTCCCTCCAG AL	ACCTGGGAC	GCCAGCCAAC	TGTGATCCTG	CTTTGTCCTT	TGATGCTGTC	960
	AGCACTCTGA G	GGGAGAAAT	CCTGATCTTT	AAAGACAGGC	ACTITIGGCG	CAAATCCCTC	1020
15	AGGAAGCTTG A	ACCTGAATT	GCATTTGATC	CACTCATTTT	COCCATCTCT	ACCABATCAS	1080 1140
13	GTGGATGCCG C	CACACCAAGT	TACTAGGAAG	CCTCCATACC	CARCACTCAT	CCACACCCTA	1200
	GGTTTCCCTC C	AACCGTGAG	GAAAATCGAT	GCAGCCATTT	CTGATAAGGA	AAAGAACAAA	1260
	ACATATTTCT T	TGTAGAGGA	CAAATACTGG	AGATTTGATG .	AGAAGAGAAA	TTCCATGGAG	1320
	CCAGGCTTTC C	CAAGCAAAT	AGCTGAAGAC	TTTCCAGGGA	TTGACTCAAA	GATTGATGCT	1380
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	CCAAATGCAA A	GAAAGTGAC	ACACACTITU	AAGAGTAACA	CONGCTIAA	TOTTOMAG	1500 1560
	CTCTGTGAAT T	AGGCACAAT	CTTTTCTCCT	COTTTCTCCTG	TGACTCGAGT	CACACTCAAG	1620
	GGAACTTGAG C	GTGAATCTG	TATCTTGCCG	GTCATTTTTA	TGTTATTACA	GGGCATTCAA	1680
25	ATGGGCTGCT G	CTTAGCTTG	CACCTTGTCA	CATAGAGTGA	TCTTTCCCAA	GAGAAGGGGA	1740
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30	Nucleic Acid			954			
	Coding seque	nce: 162.	.5582				
	1 1	1	21	31	41	51	
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55	TTCGTGGGTT C						180
	GGTGGAAAAC C	GAAACGGTGG	CTCTGGGATT	TCACCGTAAC	AACCCTCGCA	TTGACCTTCC	240
	TCTTCCAAGC 7	PAGAGAGGTC	AGAGGAGCTG	CTCCAGTTGA	TGTACTAAAA	GCACTAGATT	300
40	TTCACAATTC T	rccagaggga	ATATCAAAAA	CAACGGGATT	TTGCACAAAC	AGAAAGAATT	360
40	CTAAAGGCTC /	AGATACTGCT	TACAGAGTTT	CAAAGCAAGC	ACAACTCAGT	GCCCCAACAA	420
	AACAGTTATT 1	rccaggigga AATTCAGTCT	TTCCTTTAT	CTATATATA	TCACCATCCT	ATTCAGCAAA	540
	TTCCTCTTCA (COTTOGGAGA	TCACCTGTTT	TTCTGTTTGA	AGACCACACT	GGAAAACCTG	600
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	CGAAACCACT 1	TGATAGAAGT	GAGAGAGCAA	TTGTTGATAC	CAATGGAATC	ACGGTTTTTG	780
	GAACAAGGAT C	ITTGGATGAA	GAAGTTTTTC	AGGGGGACAT	TCAGCAGTTT	CACTCTTCAG	840 900
	CACCCAAGGC	TECTCAAGCT	CACIACIGIC	AGENTIATAG	GTATGCACCA	GAGGATATAA	960
50	TOGANTATGA	CTATGAGTAT	GGGGAAGCAG	AGTATAAAGA	GCCTGAAAGT	GTAACAGAGG	
• •	GACCCACTGT	AACTGAGGAG	ACAATAGCAG	: AGACGGAGGC	AAACATCGTT	GATGATTTTC	1080
	AAGAATACAA	CTATGGAACA	ATGGAAAGTT	ACCAGACAGA	AGCTCCTAGG	CATGTTTCTG	1140
	GGACAAATGA	GCCAAATCC	GTTGAAGAA	TATTTACTGA	AGAATATCTA	ACGGGAGAGG	1200
55	ATTATGATTC	CCAGAGGAAA	AATTCTGAGG	ATACACTATA	TGAAAACAA	GAAATAGACG TATGAATATA	1260 1320
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	AGAAAGGAGA	ACCAGCAGTO	GTTGAGCCT	GTATGCTTGT	CGAAGGACC	A CCAGGACCAG	1500
40	CAGGACCTGC	AGGTATTATO	GGTCCTCCA	GTCTACAAGG	CCCCACTGG	CCCCCTGGTG	1560
60	ACCCTGGCGA	TAGGGGCCCC	CCAGGACGT	CTGGCTTACC	AGGGGCTGA	F GGTCTACCTG F TCCAAAGGAC	1620 1680
	CAACCATCTC	TECTCAGGA	ATGTTACCG	AAGCTATTCT	TCAGCAGGC	CGGATTGCTC	1740
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	GTTCATCTGG	GGCCAAAGG*	T GAGAGTGGT	G ATCCAGGTC	TCAGGGCCC	T CGAGGCGTCC	1860
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	CACCCNAACG	TGGCCCTCA	A GGACCCAA	G GTCCAGCAG	G CCCAACTGG	A GACCCAGGTC	
	CTTCAGGTCA	AGCAGGAGA	A AAGGGAAA	C TTGGAGTTC	C AGGATTACC	A GGATATCCAG	
	GAAGACAAGG	TCCAAAGGG	T TCCACTGG	T TCCCTGGGT	T TCCAGGTGC	C AATGGAGAGA	2760
80	AAGGTGCACG	GGGAGTAGC	T GGCAAACC	& CCCCTCGGG	G TCAGCGTGG	T CCAACGGGTC	2820
	CTCGAGGTTC	AAGAGGTGC	A AGAGGTCCC	A CTGGGAAAC	C TGGGCCAAA	G GGCACTTCAC	2880
	GTGGCGATGG	CCCTCCTGC	C CCTCCAGGT	G AAAGAGGTC	C TCAAGGACG	T CAGGGTCCAC	3000
	ACCOMMON	ACCTCCCC	IG ACTODATE	C BACCACCAG	O CCCCCCTC	SC TGCCCAGGAC T GGGCCAGGGC	
	ACCTOOCK		- NCIOCNIII	- modernum			

	GAGTGGTTGG	ACCACAGGGA	CCAACCGGTG	AGACTGGTCC	TGCTGCAGGA	AAGAAGGTG	3120 3180
					TGGACCAGCA		3240
_	GTTTCCCAGG	GGAAAGAGGT	CTTCCTGGAG	CTCAGGGTGC	ACCTGGACTG .	AAAGGAGGGG	3300
5					AGAACGTGGG		3360
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					GCAAAAAGGT		3720
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					TGATGATGGC		4080
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	ATGGGGGAAT	TCCTGGTCCT	GCTGGTCCCT	TAGGTCCACC	TGGTCCTCCA	GGCTTACCAG	4680
	GTCCTCAAGG	CCCAAAGGGT	AACAAAGGCT	CTACTGGACC	CGCTGGCCAG	AAAGGTGACA	4740
30					TGAAGTCATT CATGCAAGCA		4800 4860
50					TGGTTCCCTC		4920
					GACCAATCCA		4980
					TGAATATTGG		5040
35					TITCACATCT		5100
33	AACCAGGAAG	TCCAGACAAA	CARTCIGAGG	GGGGAAAACT	TTCATCATGG GCTTTCATAC	TTAGATGTTG	5160 5220
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	THETHIGH	TAATGATGA	Affecting	GIGIGITI			
	Seq ID NO:	5 DNA sequ	ience				
55			on #: XM_057	014			
		quence: 143					
	1	11	21 1	31 	41	51 (
	GGGAGGGAG	A GAGGCGCGC	GCTGAAAGG		AGCCTGCGGC	GCCTCGGAG	60
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						CGCAGCGGCT	
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						GGGCCAATGG	
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80		T GTAAATGTT A AAAAAAAA		TTATATCTG	TAAATAAAA	A TTATTTCCAP	1260
50	CANCCITAN						
	Seq ID NO	: 6 DNA Seq	pence				
	Nucleic A		on #: Eos s				
	1	11	21	31	41	51	

	CAGGCCGGAC	i CACTTGCTAT	I ATGTAGGCNN:	I NNNNNNNNNN	NNNNAAATAC	I ACTTACTGTG	60
	TTCTAGAGGC	AGCCCTTTCT '	TATGCAGAAA	ATACAATACG	CACTGCATGA	GAAGCTTGAG	120
•	AGTGGATTCT .						180
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	GAAATTAAGT						360
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		CCATATTATC					1260
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		TGCATTGACA					1620
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50		GTTTGTTTCT ATACTACATG					1800
						TTTATTGTGT	1860
		GTAATTTTTT					1920
35		TATAGCAGAA TGCAGTCAAT				ATTTTGGTGT	1980 2040
33						AAAAAAAAA	2100
						AAGAGCAACA	2160
						AAGCAAGCAG	2220
40						GGCCGCGGG	2280 2340
70		AACGAAGCGA			COGGCAGGAA	GGGCCGCGGA	2373
45	Nucleic Ac	7 DNA sequid Accessionuence: 15	n #: Eos se	quence	41	51	
45	Nucleic Ac Coding seq 1	id Accessionuence: 15	л #: Еов ве 001 21 	31	1	1	
45	Nucleic Ac Coding seq 1 ATGCCAGGCA	id Accessionence: 15	n #: Eos se 001 21 CCGAACAGGC	31 GCCCCAGCAG	ACTACAGAGT	 GATATTGAAG	60
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45 50	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC	id Accessionence: 15 11	n #: EOS SC 001 21 CCGAACAGGC GGATGTACCT GGTGGATCCT	31 GCCCCAGCAG GACGACATCA GTTCTGGAAA	ACTACAGAGT GCGTCCGGGT AACAGAAGAA	 GATATTGAAG	
	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAGGCA CCAGTCTGTGC TCAAGACAGT CAGATCGCTA	id Accession uence: 15 11	m #: EOS BEG	31 GCCCCAGCAG GACGACATCA GTTCTGGAAA AAGGGGGAAT AACCTGATTC	ACTACAGAGT GCGTCCGGGT AACAGAAGAA TGGCCAGGTG CAGACACTGT	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGAATTT	120 180 240 300
	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC TCAAGACAGT CAGATCGCTA GCAGTCCGTA	id Accession uence: 15 11	m #: EOS BC: 001 21	31 GCCCCAGCAG GACGACATCA GTTCTGGAAA AAGGGGGAAT AACCTGATTC	ACTACAGAGT GCGTCCGGGT AACAGAAGAA TGGCCAGGTG CAGACACTGT GTACGTCAGT	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGAATTT CTTCCAAAGA	120 180 240 300 360
	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC TCAAGACAGT CAGATCGCTA ACACCAGAAT	id Accession uence: 15 11	m #: E08 Ber 001 21	31 	ACTACAGAGT GCGTCCGGGT AACAGAAGAA TGGCCAGGTG CAGACACTGT GTACGTCAGT	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGAATT CTTCCAAAGA AGTCAATGC	120 180 240 300
50	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC TCAAGACAGT CAGATCGCTA ACACCAGAAT AAACCTACAG GTCTGTCTGC	id Accession uence: 15 11	n #: EOB BC	31	ACTACAGAGT GCGTCCGGGT AACAGAAGAA TGGCCAGGTC CAGACACTGT ACGTCTCGCC AGACTGACCCTCGCC TCCAACCATC	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGAATTT CTTCCAAAGA AGTCAATGGC GAAAGTGAAA TGCCAAATCA	120 180 240 300 360 420 480 540
50	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC CAGATCGCTA GCAGTCCGTA ACACCAGAAT AAACCTACAG TTTCAGAATA	id Accession uence: 15 11	m #: EOS Bei 001 21	31	ACTACAGAGT GCGTCCGGGT AACAGAAGAA TGGCCAGGTC CAGACACTGT ACGTCTGGT ACGTCTGGGCC AGACTGAGCC TCCAACCATT	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGAATTT CTTCCAAAGA AGTCAATGAC GAAAGTGAAA AAGTCCCTCA	120 180 240 300 360 420 480 540
50 55	Nucleic Ac Coding seq 1 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGG TCAAGACAGT CAGATCGCTA GCAGTCCGTA ACACCAGAAT AAACCTACAG GTCTGTCTGG TTTCAGAATA CCTATCCTGG	id Accessio uence: 15 11 	n #: EOS SCI 001 21 CCGAACAGGC GGATGTACCT GGTGGATCCT CTATCGAGAG GCTGATTGAGAG TGAAAGAGAT ATCTTGGGAT ACTGTTTCA TACGCCCCGG TCTGCCCCTGG TCTGCCCCTGG	31	ACTACAGAGT ACTACAGAGT AACAGAAGAA TGGCCAGGTC CAGACACTGT GTACGTCAGT ACGTCAGGC AGACTGAGGC TCCAACCATC ATTTGGAGGC GCAGCCTGGC	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGATTT CTTCCAAAGA AGTCAATGCC GAAAGTGAAA TGCCAAATCA AAGTCCCTCA GAACGCTATC	120 180 240 300 360 420 480 540 600 660
50	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC CAGATCGCTA GCAGTCCGTA ACACCAGAAT AAACCTACAG TTTCAGAATA CCTATCCTGG TTTTCAGAATT TCGCTATGCCTA	id Accessio uence: 15 11 	n #: EOS SCI 021 	31	ACTACAGAGT ACTACAGAGA ACGACAGGT GGCCAGGT GTACGTCAGT ACGTCTAGCC ACGTCTAGCC ACGTCTAGCC ACGTCTAGCC ACGTCTAGCC ACGTCTAGCC ACGTCTAGCC ACGTCTAGCC ACTCCAAA TCCAGTCTAGCC TCCACTCCAAA TCCAGTCTGCC	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGATTT CTTCCAAAGA AGTCCAATCA GAAAGTGAAT AAGTCCTCA GAACGCTATC GCCTTCATTG AGCTTACTTG AGCTTACCTG	120 180 240 300 360 420 480 540
50 55	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTAG CAGTCGCTA GCAGTCCGTA ACACCAGATA AAACCTACAG GTCTGTCTGC TTTCAGAAT TTTTCAGAAT TGGCTATGCCAT ATGGTATGCC ATGGATATCC	id Accessio uence: 15 11 	M #: EOS BCO 21	31 GCCCCAGCAG GACGACATCA GTTCTGGAAA AAGGGGGAAT AACCTGATTC GCCAAACTTGA GCCTACCAG GTTTCCTCCT CTCTCAAACC TGGATGGTCT GCCTGGAACGAT	ACTACAGAGT ACTACAGAGT ACGCCAGGTC CAGACACTGT CAGACACTGT ACGCCAGGTC ACGCCAGGCC ACGCCCAGCC ACGCCCAGCC ACGCCCAGCC ACGCCCAGCC ACGCCCAGCC ACGCCCAGCC ACGCCCAGCC TCCACCATC TCACCCACC TCACCCACC TCACCCAAC TCAGCCTGCC TCACCCACC TCACCCAAC TCAGCGGAGCCTGCC TCAGCAGGGACC TCAGCAGGACC TCAGCAGGGACC TCAGCAGGACC TCAGCAGCACC TCAGCACC TCAGCAGCACC TCAGCACC TCACCACC	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATTAG GTATGATTT CTTCCAAAGA AGTCCATCAATGC GAAAGTGAAA AGGTCCCTCA GAAAGCTATC AGCCTTACTG GAAGCTATC AGCTTACCTG TAGCTTACCTG	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC TCAAGACAGT CAGATCCGTA ACACCAGAAT AAACCTACAG TTTTCAGAATA CCTATCCTGG TTTTCAGAATA TCGGTATGCG ATCGATATCCC CCATGTTTTC	id Accessio uence: 15 11 CANANCTANC AGGAGGATT TTGTCCTG ACACGTGCG ACAGGGTGT TTTCACAGGG CTGCCCCTAC TTGTACCTAC TTGTACACAGG CATTCTTTCA AGACACAGG AGACACATACT CCGGGCCACA AAACCANACA TTTTCTACT	m #: EOB Bei 001 21	31	ACTACAGAGT ACTACAGAGA ACAGAAGA TGGCCAGGT CAGACACTG GTACGTCAGT ACGTCAGC TCCAACCATC ACTTGGAGC TCCAACCATC TCAACCATC TCAACCATC TCACCAGC TCACCCGAC TCACTCCAA TCAGTTGTC TGCAAGGAGAA	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GATCAATGCC GAAAGTGAAATCA TGCCAAATCA AAGTCCCTCA AAGTCCCTCA GGACTTCATTG AGCTTACCTG AGCTTACCTG AGCTTACCTG AGCTTACTTG AGCTTACTTG AGCTTACTTG AGTTACCTG TGTTTTTTGGA	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55 60	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC CAGATCGCTA GCAGTCCGTA ACACCAGAAT ACACCAGAAT ACACCAGAAT ACACTACAGA CTTTCAGAATA CCTATCCTGG TTTTCAAAAT TCGCTATGC ATGGATATCC CATGTTTTC ATGGATATC	id Accessio uence: 15 11 	m #: EOS Ber 21	31	ACTACAGAGT GCGTCCGGGT AACACAGAA TGGCCAGGTC CAGACACTGT GTACGTCAGT ACGTCTGGCC AGACTGAGCC TCCAACCATG ACTTGGGCG GCAGCCTGC TCACTCCAAC TCACTCCAAC TCACTCCAAC TCAGTGGCC TCACTCCAAC TCAGTGGCC TCACTCCAAC TCAGTGGCC TCACTCCAAC TCAGTGGCC	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATTAG GTATGATTT CTTCCAAAGA AGTCCATCAATGC GAAAGTGAAA AGGTCCCTCA GAAAGCTATC AGCCTTACTG GAAGCTATC AGCTTACCTG TAGCTTACCTG	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC CAGATCGCTA ACACCAGAAT ACACCAGAAT ACACCAGAAT ACACCAGAAT ACACCAGAAT ACACCAGAAT ACACCAGAAT ACACCAGAAT ACACCAGAAT ACCTATCCTGG ATTGCAAAAT TCGCTATGCC ATGGTTTTC ATGGCTATGC CCATGTTTTC ATGGCTATAGC CCTTCCTCAC	id Accessio uence: 15 11	n #: EOB Ber 001 21	31	ACTACAGAGT ACTACAGAGA ACAGAAGA TGGCCAGGT CAGACACTG GTACGTCAGT ACGTCAGC TCCAACCATC ACTTGAGCC TCCAACCATC TCAGTCTCAG TCAGTCTCAACCATC TCAGTGTGTC TCACCCAA TTCAGTGGGA TTGAGGGA TTGAGGGA ATTGTTAAA ATTCTTTAAA	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GGATCATTGCC GAAATGAC GAAATCCCTCA AAATCCCTCA GGACTTACCTC GGCTTCATTG AGCTTACCTG TGCTTCATTG ATCTGTTCATT ATCTGTTGCA AAAAACCTGAG GCCTGCTTCT	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50 55 60	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC CAGATCGCTA ACACCAGAT AAACCTACAG GTCTGTGCTG TTTCAGAAT CCTATCCTGG TTTTCAGAAT TCGCTATCGC ATCGATATGC ATCGATATGC CCATGTTTTC ACATGTCCCCATGTTTTCCACAC CCATGTTTTCCACAC CCATGTTTTCCACAC CCATGTTTTCCACAC CCCAAGGGCCCCCCAAGGGCCCCCCCAAGGGCCCCCCAAGGGCCCCCC	id Accessio uence: 15 11	m #: EOS Ber 21	31	ACTACAGAGT GCGTCCGGGT AACACAGAA TGGCCAGGTC CAGACACTGT GTACGTCAGT ACGTCTGGCC AGACTGAGC TCCAACCATT ACTTGGAGGC GCAGCCTGCC TCATCCAAA TCAGTTGTC TGGAGGGAG TCAGTGGCC TGGAGGGAC TCAGTTTTAA GGAACCCGA ATTCTTTAA	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGAATT CTTCCAAAGA AGTCCTCA GAAGTGAAA TGCCAAATCA GAAGCCTATC GACCTTACCT AGCTTACCTG TGTTTTTGGA ATTCCTTCATT ATCTGTTGCA AAAACCTGAG GCCTGCTTCT TATTGGCTAAT	120 180 240 300 360 420 480 600 660 720 840 900 960 1020 1080
50 55 60	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC TCAAGACAGT GCAGTCCGTA ACACCAGATA ACACCAGAT TTTCAGATA TTTTCAGATT TCGTATGC ATGGTATGC ATGGTATGC CCAGGTTTT ATGCCTATGC CCCAAGGGG CCCCAAGGGG GGTGGGGCCC	id Accessio uence: 15 11 CANAACTAAC AGGAGGATT TIGTICCIG ACACCGTCCG CTGCCCCTAC TIGTICGCTGC TIGTICGCTGC TIGTICGCTGC CATTCTTCA AGACACTACT CAGGGCCACA AAACCAACAC TITICTACTT AAACCAACAC TITICTACTT AAGACACCAN CGGATGTCCAC CCGGATGCCAC	m #: EOS Ber 001 21	31	ACTACAGAGT ACTACAGAGT ACGAGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATTAGC GGATTATAGC GAAGGGAAATCA AGCCTCATCG GAAGGCTATC AGCCTTCATTG TATCCTTCATTG TATCCTTCATTG TATCCTTCATTG TATCCTTCATTG TATCCTTCATTG TATCCTTCATTG TATCCTTCATT AACCTGAG AAAACCTGAG CCCTCCTCATT ATCGTTACCT TATCGCTAAT AGCTTACTT ATCGTTACAT TATCGTTACAT TATCGCTAAT	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080 1140
50 55 60 65	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC CAGATCGCTA GCAGTCCGTA AAACCTACAGAT AAACCTACAG TTTTCAGAATA CCTATCCTGG TTTTCAGAATA CCTATCCTGG ATGGCTATGGC ATGGATATGC CCATGTTTTC ATGGCTATGC CCTATCTCTCAG GCCAGTAAGG GCTTCCTCAAC CCCCAAGGGG GCTGCGGCGC TCGACAGAAA	id Accessio uence: 15 11	n #: EOS SCI 21	31	ACTACAGAGT ACTACAGAGT ACGAGGAGA ACAGAAGAA TGGCCAGGTC GTACGTCAGT GTACGTCAGT GTACGTCAGT ACGATCAGCC TCCAACCATC TCAACCATC TCAACCATC TCAGTGGCG TCACTCAA TTCATTCAACA TTCAGTGGCG TGGAAGGGAG TTGGCGGCT ACTCTTTAA ACCCTCTG AACCAGGAGAGC CACAGGAACAAAAAA	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGAATT CTTCCAAAGA AGTCCTCA GAAGTGAAA TGCCAAATCA GAAGCCTATC GACCTTACCT AGCTTACCTG TGTTTTTGGA ATTCCTTCATT ATCTGTTGCA AAAACCTGAG GCCTGCTTCT TATTGGCTAAT	120 180 240 300 360 420 600 660 720 780 840 900 1020 1080 1140 1200
50 55 60	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTAG CAGTCGGTA GCAGTCCGTA ACACCAGATA ACACCAGATA TTTCAGAATA TCGTATCCTGG TTTTCAGAAT TCGCTATGCC ATGGATATCC CCAGGTTATC ATGTGCTATG GCCAGGAAGG CCTCCTCAC CCCCAAGGGG GGTGGGGCCG TCGACAGAAA TCAGACACCC GTTGCTCCCC	id Accessionence: 15 11 CANANCTANC AGGAGGATT TIGGECTG ACACCGTCCG ACACCGTCCG TIGGCGCAC TIGGCGCCAC AGGACAGG CATTCTTCA AGACCAGG AACACAACA AACAACAAC TITTCTACTT AAGACCAAAC TITTCTCCCAC AGGAAACCCAAA CCCCGGAAACC CCCCGAAAACC ATCACTGGGG AGAACCAGA	m #: EOB Ber 21 CCGAACAGGC GGATTACCT GGTGGATCCT GGTGGATCCT GGTGGATCCT GGTGGATTGAGAG GTGATTGAGAG TGAAGAGATCCT ATCTTGGGAT ACAGCTCCT AACAGCTCCT AACAGCTCCT AACAGCTGTACC AACAGTACAC AGTAATAAA CCCCAGCTGTACC AGCTGACCT TGTCTCTCT AGCAGACACC AGGAACACC AGGAACACC AGGACCTTCCT CCCAGGTTCCC CCAGGTTCCC CCAGGTTCCC CCAGGTTCCC CCAGGTTCCC CCAGGTTCCC CCAGGTTCCC CCAGGTTCCC CCAGGTTCCC CCAGGTTCCC CCAGCTTCCC CAGGTCCACCTT CCCAGGCTCCC CAGGCACCTC CCAGGCTCCC CAGCTTCCC CAGGCACCCT CCCAGGCTCCC CAGCTTCCC CAGGCACCCT CCCAGGCTCCC CAGCTTCCC CAGGCACCCT CCCAGCTTCCC CAGCTTCCC CAGCTTCCC CAGGCACCCT CCCAGCTCCC CAGCTTCCC CAGCTTCCC CAGCTTCCC CAGCTTCCC CAGCTTCCC CAGCTTCCC CAGCTCCC AGCTCC CAGCTCC CAGCTCC CAGCTCC CAGCTCC CAGCTCC CAGCTCC CAGCTCC CAGCTCC CAGCTCC CAGCTCC CAGCTCC CAGCTCC CAGCTCC CAGCTCC CAGCTCC CAGCTCC CAGCTC CAGCTC CAGCT CAG	31	ACTACAGAGT ACTACAGAGT ACGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATTAGG GTATGATGT CTTCCAAAGA AAGTCCATCA GAAGGCTATC GAAGGCTATC GAAGGCTATCA GCTTCATTG TATCCTTCATTG TATCCTTCATTG TATCCTTCATT ATCCTTCATT AAAAACCTGAG CCTGCTTCT ATTGGCTAAT ATGGCTAAT ATGGCTAAT ATGGCTAAT ATGGCTAACC CCACTCGGTG AAGGGAAGGC	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1140 1200 1260 1320
50 55 60 65	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC CAGTCGTGTG CAGATCGCTA ACACCAGAAT ACACCAGAAT AAACCTACAG GTTTTCAGAATA CCTATCCTGG TTTTCAGAATA CCTATCCTGG ATGGATATGC ATGGATATGC CATGTTTC CAGTTTTC CAGTTTTC CAGTTATGC GCAGTAAGG GTTGGCCGC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTAGATAACC GTAGATAACC GTAGATAACC GTAGATAACC GTAGATAACC GTAGATAACC GTAGATAACC	id Accessio uence: 15 11	n #: EOS SCI 01 101 101 101 101 101 101 101 101 101	31	ACTACAGAGT GCGTCCGGGT AACAGAGAA TGGCCAGGTC CAGACACTGT GTACGTCAGT ACGTCTGGCC AGACTGAGC TCCAACCATG ACGTCTGGCC ATTTGGAGG TCCAACCATG TCAGTCAGT TCAGTCTGAGC TCAACCATG TCAGTCTGAGC TCAACCATG TCAGTCTGAC TTCAGTCTGAGC ATTCGTCTT ATTGGTGTT ATTGGTGTT ATTGGTGTT AGAACAGAGC AGCAGCAGC AGCAGGAGC GCAGGAGGAGC CGCGCCCC CCAGGGGGGC	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGAATT CTTCCAAAGA AGTCCCTCA GAAGTGAAT GCCTAATCA GAAGTGAAT AGCCTTACTG AGCTTACTG AGCTTACTG ATTTTTGGA AAAACCTGAG GCCTGCTTCAT ATTGGCTAAT ATTGGCTAAT GGATCTTCAG CATGTCACC CCCTCGGCT CACGGGGAAGGCC CCCCTCGGCT	120 180 240 300 360 420 480 540 660 720 780 960 1020 1080 1140 1260 1380 1380
50 55 60 65	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC CAGATCGCTA ACACCAGAAT ACACCAGAAT ACACCAGAAT ACACCAGAAT TTCAGAATAC CCTATCCTGG ATGGTATGC ATGGATAGC CCTATCCTCAC GCAGGATAGC CCTTCCTCAC GTTGCTAGC GTTGGTATGC GTTGCTAGC GTTGCTAGC GTTGCTAGC GTTGCTAGC GTTGCTAGC GTTGCTAGC GTTGCTCAC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCCCCCC GTTGCTCCC GTTCCCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTGCTCCC GTTCCCC GTTGCTCCC GTTGCTCC GTTCCCC GTTCCCCC GTTGCTCC GTTCCCC GTTGCTCC GTTCCCC GTTCCCC GTTCCCC GTTCCCC GTTCCCC GTTCCCC GTTCCCC GTTCCCC GTTCCCC GTTCCCC GTTCCCC GTTCCCC GTTCCC GTTCCC GTTCCC GTTCCC GTTCCC GTTCCC GTTCCC GTTCCC GTTCCC GTTCCC GTTCC	id Accessio uence: 15 11	m #: EOS Ber 21	31	ACTACAGAGT GGGTCCGGGT AACAGAGAA TGGCCAGGTC CAGACACTGT GTACGTCAGGC ACAGCTCGGCC AGACACTGGCC AGACACTGGCC ACAGCACTGGCC TCCAACCATG CTCAACCATG TCAGGCCTGGC TCCAACCATG TCAGGCTGGC TCAGCCTGGCC TCACCACGCCC TCACCACGCCC TCACCACGCCCC TCACCACGCCCCCCCC TCACCACGCCCCCCCCCC	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGATTT CTTCCAAAGA AGTCCATCATCG GAAAGTGAATCA AAGTCCCTCA GCACTCATTC AGCCTTCATTC TACTTTCATCG TACTTTCCATCG TACTTTCCATCG TACTTTCCATCG TACTTTCCATCG TACTTTCCATCG TACTTTCCATCG TACTTTCCATCG TATTCCTTCATT TATCTTTTTGA TATCTTTTTGA TATCTTTTGCA TATCGCTAAT GGATCTTCACC CCCTCCGCT CCCCTCGCT CCCCTCGCT TTCCCTCCC	120 180 240 300 420 480 540 660 720 840 960 1020 1080 1140 1200 1320 1340 1440 1500
50 55 60 65 70	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG ACGTCTGTGC TCAAGACAGT GCAGTCCGTA ACACCAGATA ACACCAGATA TTTCAGATAT TCGTATCCTGG TTTTCAGATAT CCTATCCTGG CCAGGTTTTC ATGGCTATGCC ATGGATATCC CCCAAGGGT CCCCAAGGGT CCCCAAGGGT TCGACAGAAAT TCAGACACCC GTTGGTCCCCC GTAGATACG CTGCCCCC GTAGATACG CCCCAAGGGT TCGACAGCAC TCGACAGAAT TCAGACACCC GTTGGTCTCCC GTAGATACG TCGGCCTTCG GCAGCTTGG	id Accessio uence: 15 11	n #: EOB Ber 001 21	31	ACTACAGAGT ACTACAGAGT ACGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGAATT CTTCCAAAGA AGTCCCTCA GAAGTGAAT GCCTAATCA GAAGTGAAT AGCCTTACTG AGCTTACTG AGCTTACTG ATTTTTGGA AAAACCTGAG GCCTGCTTCAT ATTGGCTAAT ATTGGCTAAT GGATCTTCAG CATGTCACC CCCTCGGCT CACGGGGAAGGCC CCCCTCGGCT	120 180 240 300 360 420 480 540 660 720 780 960 1020 1080 1140 1260 1380 1380
50 55 60 65	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGG CAGTCGTGTG CAGATCGCTA ACACCAGAAT ACACCAGAAT ACACCAGAT TTTCAAAATCG TTTTCAAAAT CCTATCCTGG ATGGTATGC ATGGATAGC ATGGATAGC GTGGTTGTTGC CCATGTTTTC GCCAGGAT GCCAGTAGGC GTGGCAGCG GGTGGGCCG TCACACGAC GTTGCTCACC GTAGATAAGC CCCCAAGGGGCC CCCCAGCCTTCGCCCCCCCCCC	id Accessio uence: 15 11	m #: EOS Ber 21	31	ACTACAGAGT GGGTCCGGGT AAAGAAGAA TGGCCAGGTC CAGACACTGT GTACGTCAGGC ACGCTCGGCC ACGCTCGGCC ACGCCTCGGCC ACGCCTCGGCC CTCACCATC TCGCACCATC TCGCACCATC TCGCACCATC TCGCACCATC TCGCACCATC TCGCAGCTGGCC TCGCACGCCCCCCCC ACGCCCCCCCCCC	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGATTT CTTCCAAAGA AGTCCATCA GAAGTGAAA AAGTCCATCA GAACGCTATC GTATGATCA AAGTCCTCATTG TATCTTCATTG TATCTTCATTA AACACTGAG TACCTTCATT ATCTGTTGCA AAAACCTGAG GCTGCTTCT ATTGGCTAAT AATCTGTTGCA AAAACCTGAG GCCTGCTTCC TATTCACCC CCACTCGGTG AAGGGAAGGC CCACTCGGTC TTCCCTGCCT TTTGGGGTCC CTGTGGGCTCC CTGTGGGCTCC CTGTGGGCTCC CTGTGGGCTCC CCCCCCGCCCCC CCCCCCCC	120 180 240 300 420 480 540 660 720 840 900 1020 1140 1200 1320 1380 1440 1560 1560 1680
50 55 60 65 70	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC CAGTCGTAG CAGATCGCTA ACACCAGAAT ACACCAGAAT ACACCAGAAT ACACCAGAAT ACACCAGAAT TCGCTATCCTGG ATGGATATCCTGG CCTATCTTCAAAAT TCGCTATGCC ATGGATAACG CCCTAGGGG GGTGGGGGCC GTTGCTCACC CCCCAAGGGAAT TCAGACACCC GTAGATAACG CCTCCACCCG GTAGATAACG CCTCCACCCC GTAGATAACG CCTCCACCCCC CCTCCACCCCC CCTCCACCCCC CCCCCACGGGCCC CCCCCCCCCC	id Accessio uence: 15 11	n #: EOS Ber 001 21	31	ACTACAGAGT ACTACAGAGT ACTACAGAGT ACGGCCCGGGT AACAGAAGAA TGGCCAGGCC CAGACACTGGCC TCCACCAT ACTTGAGCC TCCACCAT TCAGCCTGGC TCCACCAT TCAGCGGCT TCAGCAGAACACAG TCAGCAGAACACAG ATTGCGGGCT ACCCCTCTG ACCCCTCTG AGAACACAG GCAGACCCGC CAGGGGCGC CAGGGGCGC CAGGGGCGC CTCCCCCAG GATGGCCCCCCCC CAGGGGCGC TTCCCCCCAG GCCCACAGGCCCC CAGGGGCGC TCTCCCCCCAG GCCAAAGCC CCCCCCCCCC	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATTAGC GGATTATAGC GGATGTAATGC GGAAGTGAAA AGGTCCTCA GGAAGCCATCA GGACTTACTATG TATGCTAATGA AAGTCCTCA GGACCTTACTG TATTCCTTCATTG TATTCCTTCATTG TATTCCTTCATT TATCCTTCATT TATCCTTCATT TATCCTTCATT TATTCGTTACT TATTCGCTAAT TATTCGCTAAT TATTCGCTAAT TATTCGCTAAT TATTCGCTGGCT TTCCCTGCCT TTCCCTGCCT TTCCCTGCCT CTGCCCAGCCC CAGCCCCACCC CAGCCCCCCC	120 180 240 300 420 480 540 600 660 780 900 960 1020 1260 1260 1380 1440 1560 1620 1620
50 55 60 65 70	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGGC CAGTCGTGTG CAGATCGCTA ACACCAGAT AAACCTACAG GTTGTGTGC TTTCAGAAT CCTATCCTGG TTTTCAGAAT CCTATCCTGG TTTTCAGATA CCTATCCTGG TTTCAGATA CCCAAGTTTTC ATGGCTATGGC ATGGCTATGGC ATGGCTATGGC GTGGGGGCGC GTGGAGAAA TCAGACACC GTTGCTCCCC GTAGATAAGG TCGGCCTCTC GCCAGCAGAA TCGGCCCC CCGTCCACCCC CCGTCCACCCC CCGTCCACCCC CCGTCCAGGG GCCGGAGGT TCAAGACTT	id Accessio uence: 15 11	n #: EOS Ber 21 21 21 21 21 21 21 21 21 21 22 23 24 25 26 26 27 27 27 27 27 27 27 27 27 27 27 27 27	31 GCCCCAGCAG GCAGACATCA GTTCTGGAAA AAGGGGGAAT AAGGGGGAAT GGCAAACTGA GTTCTCCAAAC GTTTCTCCAA GTTCCTCAAAC GTTCCTCAAAC GTTCCTCAAAC GTTCCTCAAAC GTCCAGACG GGCGCACAC GGCCCACAGAGG TTCCTCCAAC CCAGAAGGAT TTCCTCCAAC CCAGAAGGAT TTCCTCCAAC CCAGAAGGAC CCAGAGACC CGGCCACC CCAGAGAC CCAGAGACC CCAGAGACC CCAGAGACC CCAGAGACC CCAGAGACC CCAGACCC CCAGAGACC CCAGACCC CCAGACCC CCAGACCC CCAGACCC CCAGACC CCAGACC CCAGCCAC CCACC CCACCAC CCACC	ACTACAGAGT GCGTCCGGGT AACAGAGAA TGGCCAGGT CAGACACTGT GTACGTCGGGT ACGTCGGGCT GGAGCTGGC AGACTGGGC AGACTGGGC ACTGGCCG AGACTGGGC TCCAACCATT TCGGGGGT TCGAAGGGGC ACTCTTAA GGAAGGAGG AGACTGGG AGACCGG AGACCGG AGACCGG CCAGGGGGG TCTCATCGTC AGAGGAGG TCCATGGCGGCT TCATGGCGGGT TCTGCCCCAGGGGGGG TCTCATCGTC AGAGGAGGGGG TCTCATCGTC AGGCGTGCCCC TGCCCCCCCCCC	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GGATTATAAG GGATTATAG GGAAGTGAAA TGCCAAATCA GGAAGTGAAA TGCCTCATTG GGCTTCATTG TATTTTCGATC TATTTTTGA TATCTTCATT TATTTTGCA TATTTTTGCA TATTTTTGCA TATTTTGCA TATTTTGCA TATTTTGCA TATTTCATT TATTTGCTATT TATTTGCTATT TATTGGTAAT TGGCTAAT GGATCTTCAG CATGTTCAC CCCCTCGGCT TTCCCTGCCT TTTCCTGCCT TTTCCCTGCCT CCCCCCGGCT CCCCCCGGCT CCCCCCGGCT CCCCCCCGGCT CCCCCCCC	120 180 240 300 420 480 540 600 600 720 780 840 960 1020 1140 1260 1320 1440 1500 1520 1680 1680 1740
50 55 60 65 70	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGG CAGTCGTGTG CAGATCGCTA ACACCAGAAT AAACCTACAG GTCTGTGTGTG TTTCAAGATAC TTTCAAGAT TTGCTATGGATAT CCCTATGCTAG GCAGTATCCGG ATGGATAGC CCTACAGGG GGTGGGGCG GTGAGATAAGC CTCCACAGGG GGTGGGCGC GTAGATAAGC CTCACAGGG GGTGGGCGC GTAGATAAGC CCCCAAGGGT CCCCAAGGGT CCCCAAGGGT CCCCAAGGGT CCCCAAGGGT CCCCACGGT CCCCACGGT CCCCACGGT CCCCCAGGCT CCCCCACGGT CCCCCCCCCC	id Accessio uence: 15 11	n #: E08 Ber 21	31	ACTACAGAGT GGGTCCGGGT AACAGAGAA TGGCCAGGTC CAGACACTGT GTACGTCAGGC ACAGCTCTGGCC ACAGCACTGT CTGCCACCATT TCGCGCTT TCGCAGCTT TCGCAGCTT TCGAGGGG ACTCTGCCAA GGAACCCGC ACAGCAAAGA GGAACCCGC CAGCACACTT AGACCAGGGGGCC CAGCAGCAGCCGC CAGCAGCAGCCGCCCCCGGGCGCC CAGCCAAGCCGGGGGCGC CAGCCAAGCCGGGGGCGC CAGCCAAGCCGGGGGGCCC CAGCCAAGCCGGGGGGCCCCCCCC	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATTAGC GGATTATAGC GGATGTAATGC GGAAGTGAAA AGGTCCTCA GGAAGCCATCA GGACTTACTATG TATGCTAATGA AAGTCCTCA GGACCTTACTG TATTCCTTCATTG TATTCCTTCATTG TATTCCTTCATT TATCCTTCATT TATCCTTCATT TATCCTTCATT TATTCGTTACT TATTCGCTAAT TATTCGCTAAT TATTCGCTAAT TATTCGCTAAT TATTCGCTGGCT TTCCCTGCCT TTCCCTGCCT TTCCCTGCCT CTGCCCAGCCC CAGCCCCACCC CAGCCCCCCC	120 180 240 300 420 480 540 660 720 840 900 1020 1140 1200 1320 1380 1440 1500 1560 1680 1740 1860
50 55 60 65 70	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGGC CAGTCGTGTG CAGATCGCTA ACACCAGAT AAACCTACAG GTCTGTGTGC GTTTTCAAAAT TCGCTATGCAGAT ATGCATATGCCATATGCCATATGCCATATGCCATATGCCATATGCCATATGCCATATGCCATATGCCATATGCCATATGCCATATGCCTACCCCCCAAGGGGCCCCTCAAGGGGCCCGTAGATAAGGCTCCCCAAGGGGCCCGTAGATAAGGTTGGCAGAATTCAGACACCCGTAGATAAGGTTGGCAGGAGATTCAGACACCCGTAGATAAGGTTCGCCCCCCGCAGGGGGCCAGGAGGATGAGACTTCAGACACCCCGCAGCAGAAATAAGGTCCACCCCGCAGCAGAATAAGGTTCAGACACACAC	id Accessio uence: 15 11	n #: EOS Ber 21 21 21 21 21 21 21 21 21 21 21 22 23 24 25 26 26 27 27 27 27 27 27 27 27 27 27 27 27 27	31 GCCCCAGCAG GCAGACATCA GTCTGGAAA AAGGGGAAT AAGGGGGAT GCCAAATGGA GTTCTCCAAAC GTTTCTCAAACC GCCTGGACCA GTTCCTCAAACC GCCAGACAGAC GTCCACAAC GTCCACAAC GTCCACAAC GTCCACAAC GTCCACAAC CCAGAACATC GCCAGACCAC GCCAGACC GCGATCCCAA CCTCACAAC CCGCCACCC CCGAGACCCA CCGGATCCCA CCGGCCACC CCGAGCACCC CCGGATCCCA CCGGCCACC CCGGCCACC CCGGCCACC CCGGCCACC CCGGCCACC CCGCCAGC CCGCCAGC CCGCCAGCC CCGC	ACTACAGAGT GCGTCCGGGT AACACAGAGA TGGCCAGGT CAGACACTGT GTACGTCGG AGACTGGGC AGACTGGGC AGACTGGGC AGACTGGGC CTCACCATG TCGGCGGT TCGAAGGGG TCGAAGGGGG ATTGGGGGCT ATTGGGGGCT ATTGGGGGCT ATTGGGGGCT CTCACGTGGGGGGGGGG	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GGATTATAAG GGATTATAG GGAAGTGAAA GGACCTATC GGACTTATCA GCCTAATCA GGACCTATC GTATTGATCA GCTATCATTG TAGCTTACCTC TATTTGCAA AAAACCTGAG GCCTCCTTC TATTGGCAA AAAACCTGAG GCCTCCTCT TATTGGCAAAT CAGGACGCCAC CCCCTCGGCT CTTCCTGCT CTTCCTGGCT CTTCCCTGCCT CTTGCGCTCC CTGCCTCCCCC CCCCCCGGCTCC CTGCCCCCCCC	120 180 240 300 420 480 540 600 600 720 780 840 960 1020 1140 1260 1320 1440 1500 1620 1680 1740 1860 1980
50 55 60 65 70	Nucleic Ac Coding seq 1 1 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGG CAGTCTGTGG CAGTCGTAGA CAGATCGCTA ACACAGAAT AAACCTACAG GTCTGTGTGGC TTTCAGAATA CCTATCCTGG TTTTCAAAAT TCGCTATGGCATA GCAGTATCC CATGTTTTCAAAAT CCTATCCTGG GTGGTATCC GTAGATAAG CCTTCCTCAC GTTGCTGGGCGG GTGGGGGGGGGG	id Accessio uence: 15 11	n #: E08 Ber 21	31	ACTACAGAGT ACTACAGAGT GGGTCCGGGT AAAGAAGAA TGGCCAGGTC CAGACACTGT GTACGTCAGGC ACGACGCTGGCC ACGACGCTGGCC ACGACGCTGGCC ACGACGCTGGCC CAGACGAGGAGC TCCAACAGT TCAGTGGCGCT TCAGGGGGCT CAGAGGAGCCGGCC ACGAGCAGCCGGGCGCC CAGGGGGGCC CAGGCAAGCC CATCTCTCGT GGGGGGGCG CAGGGGGGGC CAGGGGGGGC CAGGGGGGGC CAGGGGGGGC CAGGGGGGGC CAGGGGGGGC CAGGGGGGGC CAGGGGGGGC CAGGGGGGGC CAGGGGGGGG	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGATTT CTTCCAAAGA AGTCCATCA GAAGTCAATCA AGAGCCTATC GGAAGCTATCA GCCTTCATTG TATCCTTCATTG TATCCTTCATT ATCCTTCATT ATCCTTCATT ATCCTTCATT ATCCTTCATT TATCCTTCATT TATTGCACC CCACTCGCTC CCACTCGCTC CCACCTCGCCC CCCCCCGCCCT CCCCCCCCCC	120 180 240 300 420 480 540 660 720 1020 1020 1140 1200 1140 1320 1340 1560 1660 1740 1860 1740 1860 1920
50 55 60 65 70	Nucleic Ac Coding seq 1 ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC CAGTCGTGTGC CAGATCGCTA ACACCAGAAT AAACCTACAG GTTTTCAGAATA CCTATCTGG TTTTCAGAATA CCTATCTGG ATGGATATCC ATGGATATCC CATGTTTC ATGGATATCC CCTAGGATA CCCAAGGGG GGTGGGGCG GTTGCTCCC GTAGATATCC GTAGATATCC CCCCAAGGGG GGTGGGCC TCCACCC CCTCCACCC CCGTCCAGCC GCCCCATCAG GCCCATCAG GCCCATCAG GCCCATCAG GCCCATCAG GTCCCATCC GTCCATCC GTCCACCC CTCCACCC CCTCCACCC CTCCACCC CCTCCACC CCCACC CCTCCCC CCTCCACC CCTCCCC CCTCCCC CCTCCCC CCTCCCC CCTCCCC CCTCCCC CCTCCCC CCTCCACC CCTCCC CCTCCC CCTCCC CCTCCC CCTCCC CCTCCC CCTCCC CCTCCC CCTCCC CCTCCC CCTCCC CCTCCC CCTCCC CCTCCC CCTCCC CCTCCC CCTCCC CCTCCC CCTCC CCTCCC CCTCC CCC CCTC CCTCC CCTC CCTC CCTC CCTC CCTC CCTC CCTC CCTC CCTC CC	id Accessio uence: 15 11	IN #1: EOB Ber 21 21 21 COGARCAGOC GGATUTACCT GGTGGATCCT GGTGGATCTCT CATAGGAGGAC GCTGATTGAG GCTGATTGAG GCTGATTGAG TGAAAGAGAT ACTGTGTTTCC ACTGTGTTTCC ACAGGTCCT ACAGGACAC ACAGGACAC ACAGGACAC AGAGCTCCT CCTCAGCTCGA AGAGCTCCT CCTCAGCTCGA AGAGCAC CCTGGCCAGC CAGGGCCGA AGAGCTCCT CCTGGCTCGA CGGAAGGAC CCCGGCCGA AGGGCGCGC ACAGGACCT CCCGGAAGGAC CCCGGCAGGAC ACGGAAGCTC CCCGGGAGGAC CCCGGGCGCC CTGGCCAC CCGGGCCGC CCGGGCCGCC CCGGGCCGCC CCGGGCCGCC	31	ACTACAGAGT ACTACAGAGT GCGTCCGGGT AACAGAGAA TGGCCAGGTC CAGACACTGT GTACGTCAGT ACGTCGGCG AGACTGGCC AGACTGGCC AGACTGGCC TCCAACCATG TCAGCTCGCC ATTGGGGGA TCCAACCATT ATTGGGGGA TCCAACATT ATTGGTGTCT ATTGGGGGA AGAACCGG AGAACCGG CCCAGCGAGAGC CCCAGCGAGAGC CCCCCCCC	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATATAAG GGATATAAG GGATATGATT CTTCCAAAGA AAGTCCCTCA GGAAGTGAAA TGCCAAATCA GAAGGCTATC TGCCAATCA AAGTCCTCA GAAGGCTATC TATTGCATTGC	120 180 240 300 360 420 480 540 660 780 840 960 1020 1080 1140 1260 1380 1440 1560 1620 1680 1740 1800 1800 1800 1800 1800 1800 1800 18
50 55 60 65 70	Nucleic Ac Coding seq 1 ATGCCAGGA ACCTCTCAAG CAGTCTGTGG CAGTCGTGTG CAGATCGCTA ACACCAGAT ACACCAGAT ACACCAGAT ACACCAGAT ACACCAGAT ACACCAGAT TTTCAGAATA CCTATCCTGG TTTTCAAAT TCGGTATGG ATGGATAG GCAGTAGGG GCAGTAGGG GCTGGACGG GTGGACCC GTAGATAGC GTTGCTCCC GTAGATAGC GTTGCTCCC GTAGATAGGG GCGGGGGGG GTGGTCCC GTAGATAGG TCGGCCTTC GCCAGCTTGG CCCCCC GGCGGAGGG TCAGACAT TCGGCCTCC GCGCGGAGGG TCAGCCT GCGCGGGGGGG GCGCGAGGG TCAGCCC GTCATCTCAC GCGCCATCAC GCTCTCTCAC GCGCGCACGC ATTCGGCGG TTCCATTTGCACC GCGCGCACGC ATTCGGCGGG TTCCATTTGCACCGC GCGCGCACGC TTCCATTTGCACCC GCGCGCACGC TTCCATTTGCACCC GCGCGCACGC TTCCATTTGCGCGGG	id Accessio uence: 15 11	n #: EOS Ber 21 21 21 21 21 21 21 21 21 21 21 22 23 24 25 26 26 26 27 27 27 27 27 27 27 27 27 27 27 27 27	31	ACTACAGAGT GGGTCCGGGT AACACAGAGA TOGCCAGGT CAGACACTGT GTACGTCGG ACACTGGGC ACACTGGGC ACACTGGGC ACACTGGGC CTCACCATG TCGGCGGT TCGACCATG TCGGAGGGGGGGGGG	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGATTT CTTCCAAAGA AGTCCATCA GAAGTCAATCA AGAGCCTATC GGAAGCTATCA GCCTTCATTG TATCCTTCATTG TATCCTTCATT ATCCTTCATT ATCCTTCATT ATCCTTCATT ATCCTTCATT TATCCTTCATT TATTGCACC CCACTCGCTC CCACTCGCTC CCACCTCGCCC CCCCCCGCCCT CCCCCCCCCC	120 180 240 300 420 480 540 660 660 780 840 960 1020 1140 1200 1320 1440 1500 1520 1680 1740 1860 1980 1980 2040 2040 2160

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	TCCTCCAGGC AGCCCATCTC	CCGGGGCTGG	GAGGACTTAA (GAGAAGCCC	GCAGAGAGGG	2340
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	CONTROCCICC GGTACACCAC	GCGCGCCCCV	CCTGGCCACT	TCTCCACCAC	CCCGATGCTG	3480
	TCCTTGCGCC AGAGGATGAT	GCATGCCAGA	TTCCGTAACC	CTCTCTCCCCG	ACAGCCTGCC	3540
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25	CTTCTCCACC TTGATCGTGC	GTTAGTATTG	AATGCAGAAG	GAAGGTACCT	CCAAGATTCA	3720
	CATGGAAATC CTCTTCGGAT	TAAACTAGGA	GGAGATGGTC	GAACCATTGT	AGATCTGGAA	3780
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	ACCACTACTA CGACGCCCCC	GCCTACCACT	ACACCGAGGC	CCACCACTGC	CACCACCCGC	4080
	CGCACGACCA CCAGGCGTC	: AACAACCACA	GTCCGAACCA	CTACGCGGAC	AACCACCACC	4140
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					630	

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		1020
5		1080 1140
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10		1440 1500
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	CTAGTITICC TGTTGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAC	1080 1140
	AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACTTCCCC	1200
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	GACAGCTGCC AGGGGGGACAG CGGGGGGCCC CTGGTGTGC AAGAGAGGAG GCTGTGGAAG TTAGTGGGAG CGACCAGCTT TGGCATCGGC TGCGCAGAGG TGAACAAGCC TGGGGTGTAC	1440 1500
	ACCOGTGTCA CCTCCTTCCT GGACTGGATC CACGAGCAGA TGGAGAGAGA CCTAAAAACC	1560
80	TGAAGAGGAA GGGGACAAGT AGCCACCTGA GTTCCTGAGG TGATGAAGAC AGCCCGATCC	1620
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	CGGCACCACT AGCAGGCCCG AAAGAGGCAC CCTTCCATCT GATTCCAGCA CAACCTTCAA	1740
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	CAAATGATGT	CCCCCCTTCA	CCCTCCCACA	CTCCTCCCAT	TACAGGCATG	CCCCACCACC	2040
	COMMICATOR	SCCIOCITCA	OCCICCOACA .	0100100011	1404000410	A CONTRACTOR A CC	
_	CCTAGCCTCA						2100
5	GCGGCCTTTC						2160
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	AACCCACCCT						2340
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						A GGAGTTTCAA	
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65						C ACGACCCACA	
						T CCTGGTCTGG	
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GTRACTAGGG GRICGECTT TOCTICACITY TRACEACHA GAGATITGE SECURIOCIC CATAGGGGGA GEARATGGG TITTOCTICTT TATAGCACHA GAGATATCA COCCUAGGCA GEACTAGGCCA TITTOCTICTT TATAGCACHA GAGATATCAG TECCAGAGAC CATATCAC CATAGGGGCA GAGATACCA TATAGCACHA GAGATACCA CAGATAGGACA CAGATAGCAC CAGATAGGACA CAGATAGGACA CAGATAGGACA CAGATAGGACA CAGATAGGACA CAGATAGGACA CAGATAGGACA CAGATAGGACA CAGATAGGACA CAGATAGGACA CAGATAGGACA CAGATAGCACA CACATACCAC CAC
GCCCGCCCC CANTICACIONES ANCIGAGEAC AGGGGACCCC CAGACAGAG AGGCCCCCC CATTIGGCCCC CATTICCCCC CAGACCCCCAGAGAG AGGCCCCCCA CCAGACCCCCAGAGAG AGGCCCCCCAGAGAGAG
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CCCCAGAGTIC CCCAGGCACT CCTIAGGTAG CTTCTGGANA TGGGGACAGA TCCCCTCGAA 582 GGACACAAAC COSCCTCCC CTTGTGTTG GCGTCCCTG TGTCCCCAGE 588 GCACACAAAC COSCCTCCC CTTGTGTTG GCGTCCCTG TGGCCCTACC TTGTTTCACT 1000 CAGCACGAAAC CCCCCCCCCCC CCTTGTGTTG GCGTCCCCCCCCCC
GEACACAMAC COGCOTTOCC CTTOGTOTTE GEOGRICCTO CASTIGNAC TRACTICACE (500 ACCTORAGE CAGGOTTGE ACCAGATING CREATED CASTIGNAC CASTIGN
ACCITICAGE COLOCITIGG TICALOGING CIRCALTICE CATTORISE TACCISCITE TOSTGAGCA ATTIOUTICA RESTRIAGGE CAGGAGGGG ASTIAGGGTC GCARGTICE TOSTGAGCA ATTIOUTICA TOTTGAGTIT CIRALOGOT ATTIOGRICA COCCAGINCE TITLOGITA GAGGGAGAAC TOTATION COCCAGOCA COTTATAMA ACCOCANAGA COTTCANAGA GAGGGAGAAC TOTATION COCCATOCA COTTATAMA ACCOCANAGA COTTCANAGA GAGGAGGAAC TOTATION COCCATOCA COTTATAMA ACCOCANAGA COTTCANAGA GAGGACTICOT GCACTACTOT CAGGGAGGTC TITCCACACA CAACTOTTTO GAGTCCATTC COCAGGTGGG AGCCAACTOT CAGGGAGGTC TITCCCACCA AACATOTTTC AGCTCATOGA AGGACTACT CAGGGAGGTC TITCCCACCA AACATCTTTC AGCTCACGGA AGGACTACT CAGGGAGGAT TAGTGGTGAT AGGGCCTGCT CANAGCCAG AGTCACAGGA AGGACTACT CAGGGAGGAT TAGTGGTGAT AGGGCCTGCT CANAGCCAGA AGTCACAGGA AGGACTACT CAGGGAGGAT TAGTGGTGAT AGGAGGGAG GTTAANATGA COCCAGTGCA CTATTAAAAA GATATCATT TAGAGTGAC CAGGAAAGTT GAATATGTTTC GGCTCAGTTC ATTTAAAAAA GATATCATT TAGAGTACA ATTACACAAG ACCATATC TAGGCATTTT CTTGTTGCA CAAAATTTCT TATGCTTAG AAAATTGAT CATAGGTTTA CACAGTACAGG ATCATACAA AAAATTTCT TATGCTTAG AAAATTGAT CATAGGTTTA CACAGTACAGG ATCATACAA AAAATTTCT TATGCTTAG AAAATTGAT CATAGGTTTA CACAGTACAGG ATCATACAA GAAATTTCT TATGCTTAGAAAA ACAAATTGAT TATGCTTAGAAATAC CAAAATTTCT TATGCTTAGAAAA GAAAATGATT CAGGAGAAAAC CTTTGCTTTTT TTCTTTGCC GAAATAGCTG GTCCTTTTC GAGGAGTACAA TTCCTTTTTTATTTATTTTTTTTATTATTTTTTTT
Tectaticit geagtictae aggragge cageagagg attaggete accaptice 612 Titeagete tectaate ections of the aggragage attaggete accaptance 612 Titeagete tectaate ections of the aggragage accaptance control of the aggragage accaptance control of the aggragage accaptance control of the aggragage accaptance accaptance control of the aggragage accaptance aggragage accaptance aggragage accaptance aggragage accaptance aggragage aggragate
TOGTGAGGCA ATTTOGCTGA TCTTGGGTGT CTGAGGGCT ATTGGGTCCA CCTATAGAG AGCCCAAGGG CTTTTTAGGTGT GCTGAGGGC CCTGATAGGA GGGCGAGGC CCTGATAGGA GGGCGAGGC CCTGAGGAGGAC CTTGAGGAGAC CTTGAGGAGG CACCAGAGGC CCTGAGAGA GGGCGAGAC CACCACACACA CAAACTCTTT CCCTGGGTC TGTGAGGAG AGCCACATGAGGAGGAGAC CCTCAAAGAC GGGCCGACC GGGTCCCCCA CCCCAACGC CACCACACACA CAAACTCTTT AGCCTCATAGA GGGCTGCCC GGGTCCCCCA CCCCCAACGA CACCACACACA CAAACTCTTTA AGCCTCTGC GGGTCCCCCC ACCCACACGACACA CAAACTCTTTC AGCCTCATAGA AGGACTCTCT CACGAGGAGGT TTTCCACCCA AACATCTTTC AGCCTCATAGACACA AGGACTTCT CACGAGGAGGAC TTTCCACACA AACATCTTTC AGCCTCATAGACACA AGGACTCTC TCTAGAGAGACACACACACACACACACACACACACACACA
TITICAGICIC TICTITANTIC CUTICITY COCTIGECCA CUTTATAGA AGGOCAAAGA COTCOTOTA AGGOGACAAA CTATATOTIC GUTTATATAT TIGCAGGAG CACCAGAGTC COTCOTOTA AGGOGACAAA CTATATAT COCCTATOCT GUCCAACCA CAAACTCTTT CUTTCAAAGA GOGCOTOCT GETCCTTCC CACCACTGC ACCCACACA CAAACTCTTC AGCTCCTTC CCCAGGTOGG AGCCAACTGT CAGGAGGTC TITCCCACCA AACATCTTC AGCTCCTGG AGGTACCAT AGGCCTCTCC TITTAAAGAT ATGCCTCTT CAAAGCCCA AGCTCCATGC TICTIGTCA CGGTTTGTT CAGGAGAGTT GAAAGCAGA GTTAAATAGA ACACTOTGAA AGGACTCTT CCAGGAGAT TAGTGGTAGT GAAAGCAGA GTTAAATAGA ACACTOTGAA ACCATTAGAG ATGTATTCAT TICAAAGCT CAGGAGTTT AAAGTTCTTCA GCTCAGTTC ATTTAAAAAA GATATCTATT TICAAAGCT ATTCACCAAG ACCATATCT GCTCAGTTC ATTTAAAAAA GATATCTATT TICAAAGCT ATTCACCAAG AGCAATATC ACAGGACTTT CTTGGTACAA AAAAGTTTCT TATTGCTTAA AAAATTGTTC ACAGGATTTT CTTGGTACAC CAAATTTCT TATTGCTTAA AAAATTGTT TTCTTTATCT TCTTGTTACC GAAATACTTC TCTGGTAGAATAC CTTGTCTTTT TTCTGTTGCC GAAATACGT GTCCTTTTTC GGGAGTTACA TGTATAGGT GTTTGTTATT TAACATTCAT TAAGGACTC ACCATAAACA AAGATATATT TTCTATTATT TATTATATG TGCACTTCAA GAAGTCACTC TCAGGAGAAA AAGATATATT TTCTATTTAT TATTATATG TGCACTTCAA GAAGTCACTC TCAGGAGAAA AAGATATATT TTCTATTTAT AAAGCTCTTA TCCTATGAT GAAGTCACTC TCAGGAGAAA AAGAATATT TTCTATTTAT AAAGCTCTTA TCCTATGAT GACCCCCCCGG ATTCACAAA TAACAATACA AAGATATATT TCCTATGATT AAAAGTCTTA TTCCTATGAT GCCCCCCTCGG ATTCACAAA TAACAATACA AAGATATACT TCCTAGAATAC TACACACTTAGA AACACTTAC TGCACACTTA AAAGCTCTTA TCCTCAGAATAC AGCTCATACAA AACACTAAAACA AAAACACTTAC TTCCAGACCTA AACACTACAAATAC TACACCTTAGA AACACTTACC TTCCAGAATACA AAATACTTCTTAG GACCCTCATCAAAAAACA AAATACTATTCA AACACCTTACA TTTCCTCAGAATACA AAATACTTTCTA AACACCTTACA ATTCCACACATTACA AACACCTTACA TTCCTCAGAATACA AAAATACTTTCTAGAAAAAAAAAA
GCTCCTOTAM GAGGAGAAC TCTATCTGTG GTTTATAMTC TTGCACGAGG ACCAGAGTC 624 TCCCTGGAGT CTTGTAGATAM CTACATTATAT COCCTTTCCT GCCCAACCA CAMACTCTTT 630 GGGTCATTC CCCAGGTGG AGCCACCTT GCTCCCC ACCGACTGC ACCCATGAGA CTCGGTCCAA AGCTCACGG AGGGGACCAT AGGCCTCTC TTTTAMACAT ATGCGTCGTC AAAGGCCAG AGTCACAGGA AGGACTCTTT CCAGGGAGGAT TAGTGGTGAT GAAGGCCAG AGTCACAGGA AGGACTCTTT CCAGGGAGGAT TAGTGGTGAT GGAGGAGGAG GTTAMATGG AGTCACAGGA AGGACTTCTT CCAGGGAGGAT TAGTGGTGAT GGAGGAGGAG GTTAMATGG ACACTGTGAA CCACTTAGGA TGTGATCACT TCAGGTGGC CAGGAATGTT GAAAGTCTAC ACACTGTGAA CCACTTAGGA TGTGATCACT TCAGGTGGC CAGGAATGTT GAAAGTTCC ACACTGAGGA ACCACTTAGAA TAGTGATCACT TCCAGAGTTGA CAAATGTTTC CACGTTCAGATTCACT AAAAGTTTCT TTAGAGTTCT CAGGGTTGA CAAATGTTTC ACACTACAGG ATCTGTACAT AAAAGTTTCT TATTGCTTAG AAAATGTTAC CTTGTATAT TTAGAGTTCT CTTGTTTCT TTTGGTTGCC GAAATACTGT TTTTTTTCTTTTTC TGTTAGCACT AACATTTCT TGTTAGGGAT ACCACTTAGT TTTTTTTTTT
TOCCTGGGTC TITGATGAA CTACATTIAT COCCTTTCCT GCCCAACCA CAACTCCTTT CCTTCAAAGA GGGCTGGCTC GGCTCCTCC ACCCAACTCA GCACATCGTT GAGGCTCCAC GAGTCCATTC CCCAGGTGGG AGCUAACTGT CAGGGAGGTC TITCCCACA AACACTTTC AGCTGCTGG AGCTGACCAT AGGGCTCTGC TITTAAAGAT ATGGCTCCTT CAAAGGCCAG AGCTCACTGTC CCAGGGAGAT TAGTGTGAT GAGGAGGAGA GTAAAATGA STCACAGGAA AGCACTTCTT CCAGGGAGAT TAGTGTGAT GAGAGGAGA GTAAAATGA CCTCATGTCC TICTIGTCCA CGGTTTTGTT GAAGTTCTA CTCTCTAAAG CAAGATGTT CATTCACCAG AGCATGTTGAAAATGA ACACTAGGAA CCACTTAGAA TAGAGTTCTT TTGAAAGTC TCTCCTAAAATG CAAGATGTTCT AACACTAGGA CCACTTAGAC CAAATTTTCT TATTCCTTAACC ATTCACCAAG AGCCAATATC ACAGTACGA ACCTTTCACAC CAAATTTTC TATTGCTTAG AAAATTGCT TCCTTGTATT ACACTACGA ACCTTTCCC CAAAATACCA TITCACACAG ACCCATTCT CCTGGAATG CTTTGTTTTT TCTGTTAGC CAAATTTTC TATTGCTTAG AAAATTGCT CTCTTGTATTT TAGGCATTTT CTTGGTAGC CAAAATTTCT TTTTCGTTAGA AAAAATTTC CTTGTTATTT TTCTTTATCT TAGGCAATTTT CTTGTTAGGT CAAAATTTCT TTTTTTTTTT
CCTTCANAGA GGGCTGCCT GGCTCCTC ACCCANCTGC ACCCATAGGA CTGGTCCAN GAGTCCATTC CCCAGGTGGG AGCCACTTCT CAGGGAGTC TTTCCCACCA ANCACCTTTC AGCTGCTCGG AGGGACACTA AGGGCTCTC TTTTAAACAT ATGCTGCTT CAAGGGCCG AGTCCACGG AGGACTCTT CCAGGGAGAT TAGTGGTAAT GGAGGAGGAG GTTAAAATGA AGTCACAGGA AGGACTTCTT CCAGGGAGAT TAGTGGTAAT GGAGGAGGAG GTTAAAATGA ACACTGTGAA CCACTTAGGA TGTGATCACT TCAGGTGCC CAGGAATGTT GAACTTTCA ACACTGGAA CCACTTAGGA TGTGATCACT TCAGGTGCC CAGGAATGTT GAACTTTCA ACACTGAGA CCACTTAGAA TATACTATT TAGAGTTCT CAGAGTTGTA CATATGTTTC ACACTACAGG ATCTGTTACAT AAAAGTTTCT TTCCATAGCC CAGGAATGTC CACTGTTAT TAGGCATTTT CTTGGTAGCA CAAATTTCT TATTGCTTAG ANAATTGTC TCCTTGTATAC TTGGTTGTA AGACTTAAA TGAGTTTGGT CTTTAGGAA AGCAGGCC CTCTGAAATG CTTGCTTTTT TTCTGTTGCC CAAATACTG TTTTAGGAA AGCAGGCC CTCTGAAATG CTTGCTTTTT TTCTGTTGCC CAAATACCG TCCTTTTC GGGAGTACA AGCATTATT TATATATTAT TGCACTTCAA GAAGTCACTC ACCATGAACA AAGAATATAT TTCTATTATA TTATATATG TGCACTTCAA GAAGTCACTC ACCATGAACA AAGAATATAT TTCTATTATAT TTATTATATG TGCACTTCAA GAAGTCACTC ACCATGAACA AAGAATATAT TCTTATATATG CCAGGCCTG TAGGCCTGC TC ACCAGGAAG GTCACCTGCT GGGAAAAGTG CTCAGACCTGT AGGCCTGATA GACTGATTAA ACCACGGAAG GTCACCTGCT GGGAAAAGTG ACCAGGAACATAC TGGGAAAAAC CTGCCTCTGC GTTAAGTG GGAGACAATG TCACAAGTTA AAAGCTCTTA TCCATGAT GACCGCTCGA ATTCAACAA TTTTCATCAC TTGGATGATG AAAGGAGATAC TCAAAACATA GATCCATCTT TTCAGGGAA ACCCCTTTCT TGGAGGAAA AAAGGGAATAC TCAAAACATA GATCCATCTT TTCAGGGAA ACCCCTTTCT TGGAGGAACA TTCAGGCGAG GAATGGAACT GATCCATCTT TTCAGGGAA ACCCCTTTCT TGGAGGAACAT TCCACAAGTTA AAAGGGAATAC TCAAAAGAAT GATCCATCTT TTCAGGGAA ACCCCTTTT TCCAGGAAAAACATA CTCTTAGGAAAAACATA CATCCATCTTA AAAAACACATAC TTCCGCCAAG ACCTTTCACCAGA GAATACAAGA AAAACTCCAT TCCACAAGTTA CTCCCCCTGG ACCAAAAAAAAAA
GAGTICCATTC CCCAGGTAGG AGCAACTOT CAGGGAGGTC TTTCCACCA MACATCTTTC AGCTGCTOG AGGTGACCAT AGGGCTCTGC TITTAMAGAT ATGGCTGCTT CAMAGGCCAG AGTCCACGAG AGCACTTCTT CCAGGGAGAT TAGTGGTGAT GAGGAGGAGA GTTAMATGA CCCCCATGTCC TICTIGTCCA CGGTTTTGTT GAGTTTTCAC TCTTCTAMAG CAAGGGTCTC ACACTGTGAA CCACTTAGA TTGGATCACT TTCAGGTGGC CAGGAATGTT GAAGGTCTT ACACGTGTGAA CACTTTAGAACA TGGATCACT TTCAGGTGGC CAGGAATGT GAAGTTCTTT GGCACTAGTC ATTAMAAAA GATATCTATT TGAAGTTCT CAGAGTTGTA CATATGTTTC ACAGTACAGA ACCATTAGAC TAGAGTTCTT TAGACACTTCACCAA GACCATACTC ACAGTACAGA ACCATTAGA CAAATTTCT TATTGCTTAG AMATTGCC TCCTGTAAT TTCTGTTTGT AAGACTTAAG TGAGTTAGAC TCTTAAACC ATTACACAA GACCACTTC CTCTGTAAT TTCTGTTTGT AAGACTTAAG TGAGTTAGAC TCTTTAAGGAA AGCACGCTC CTCTGAAATG GTTTGTATTT TTCTGTTGCC CAAATACGTG GTCCTTTTTC GGGAGTAGA TGATATGAGG GTTTGATGT AAACATTCC TGTAGGCATC ACCATGAACA AAGATATATT TTCTATTTAT TTATTATATG TGCACTTCAA GAAGTCACTG TCAGAGAAA AAGATATATT TTCTATTTAT TTATTATATG TGCACTTCAA GAAGTCACTG TCAGAGAAA AAAAATATAT TTCTATTTAT TTATATATG TGCACTTCAA GAAGTCACTG TCAGAGAAA AAAAAAAATAT TCATATATGC Seq ID NO: 13 DNA Sequence Nucleic Acid Accession 8: NM_012112 Coding sequence: 4292672 1 1 11 21 40 TCAGACCTGT AGGCCTGGATA GACCAGAAAG GTGACCTGCT GAGAAAAAGT GACACAGAAAAAC CTGCCTCTCT GCGTTAAGTG GGAGACAATG TCACAAGTTA AAAGCTCTTA TCCTATGAT GACCCTCTGG ATTTCACAA TTTTTCATCC TTGGATGATG AAAGGAGATAC TCAAAAAAC CTGCCTCTGG ATTTCACAA TTTTTCATCC TTGGATGATG AAAGGAGATAC TCAAAAAAC GGAGGACATT TTCAGGGAAA AACCCCTTTG AACACTTTGA AACACTTTGA CACACTTTGA CAACACTTAC CACACATTAC CATTCTTACAA CACATTACAA CACATTACAA CACACTTACA CACACATACACA TACCCTTTGA CACACATTACA CACACACACACACACACACACACACA
AGCTOCTOGG AGGTGACCAT AGGGCTCTGC TITTANAGAT ATGGCTGCTT CAAAGGCCAG 684 AGGTCACAGA AGGACTTCTT CCAGGGAAT TAGTGGTGAT GGAGAGGAG GTTAAAATGA 684 CCTCATGTCC TICTIGTCCA CGGTTTTGTT GAGTTTTCA CTCTTCTAATG CAAGGGTCTC 660 ACACTGTGAA CCACTTAGGA TGTGATCACT TTCAGGTGGC CAGGATGTT GAATGTCTTT 662 GCCTCAGTTC ATTTAAAAAA GATATCTATT TGAAAGTTCC CAGGTGTGTA CATATGTTTC 672 ACAGTACAGG ATCTGTACCAT AAAAGTTTCT TTCCTAAACC ATTCACCAGA AGCCATATC 678 ACAGTACAGG ATCTGTACCAT AAAAGTTTCT TTCTTATGTAGA AAAATTGTC TCTTGTTAT 672 ACAGTACAGG ATCTGTACCAT AAAAGTTTCT TATTGCTTAG AAAATTGTC TCTTGTTAT 673 TTCTGTTTTT TCTGTTGCC GAAATACGTG GTCCTTTTTC GGGAGTTAGA TGTATAGAGGT 678 GTTTGTTATT AAACATTTCT TGTAGGCATC ACCATGAACA AAGATATATT TCTTATTTATT GTATTATATG TGCACTTCAA GAAGTCACTG TCAGGAAAAA AAAGAATTGT CTTTATTTATT TTATTATATG TGCACTTCAA GAAGTCACTG TCAGGAAAAA AAAGAATTGT CTTAAATGTC 708 Seq 1D NO: 13 DNA Sequence Nucleic Acid Accession 8: NM_012112 Coding sequence: 4292672 1 11 21 31 41 51 1
ACTICACAGA AGGACTTCTT CCAGGGAGAT TAGTGGTGAT GAGAGAGAG GTTAAAATGA 656 CCTCATGTCC TTCTTGTCCA CGGTTTTGTT GAGTTTTCAC TCTCTAATG CAAGGGTCTC GCCTCAGTC ATTTAAAAAA GATACTATT TCAAGGTGC CAGGAATGTT GAATGTTTC ACAGTGCAGA ATCGTACACA AAAAGTTTCT TCCAAACC ATCACCAGA GATCGTACACA AAAGTTTCT TCAAACCATTCCACAGA GATCGTACACA AAAGTTTCT TCAAACCATTCCACAGA GATCGTACACA AAAGTTTCT TCAAACCATTCCACAGA GATCGTACACA AAAGTTTCT TATTGCTTAGA AAAATGTCC TCCTTGTATT 684 TTCGTTTTTT TCTGGTAGCA CAAATTTCT TATTGCTTAG AAAATGTCC TCCTTGTATT 684 CTTGTCTTTT TCTGTGCC GAAATAGCTG GTCCTTTTTC GGGAGTTAGA TGTATAGAGT GTCTTGTATTT TCTGTTGCC GAAATAGCTG GTCCTTTTTC GGGAGTTAGA TGTATAGAGT GTCTTGTATTT TCTGTTGTACC ACACAGAAAA AAAATATAT TCTATTTAT 702 TTATTATATATG TGCACCTCAA GAAGTCACT TCAGAGAAAA AAAAATATAT TCTATTTAT 702 TTATTATATATG TGCACCTCAA GAAGTCACT TCAGAGAAAA AAAAATATAT TCTATATATT TCAAAACAT GAAGGCACACAT AAAGAAATAT AAAGAAATAT TCTAAAACAT GACAGAAAA ACACACAAAAG GTGACCTGCT GAGAAAAAGT GAAGAAATAC TGGGAAAAAC CTGCTCTTCT GCGTTAAAGG GGGACAAAT TACAAAGTA AAAGCACTTA TCCCTATGAAA GAACAATAAA ACCACCTAGA GAAAAACAA CTGCCTCTCT GCGTTAAAGAT GAAGAAAAACAA CTGCCTCTCA GAAAAAAAAAA
CCCARAGROC TICTIGETCCA COGITTICIT GAGTITICAL EXTERNATE CAAGGGTECT 666 ACACTGRAN CCACTAGGA TUTGATCACT TICAGGTGGC CAGGANGT GAATGTCTT 666 ACACTGRAN CCACTAGAGA TUTGATCACT TICAGGTGGC CAGGANGT GAATGTCTT 666 ACACTGRACAG ATCTATACAT AAAAGTTTCT TICCTAAACC ATTCACCAGA AGCCATATAC 678 ACAGTTACAG ATCTATACAT AAAAGTTTCT TICCTAAACC ATTCACCAGA AGCCATATAC 678 AGGCATTTT CTTGGTAGCA CAAATTTCT TICTCATAACC ATTCACCAGA AGCCATATAC 678 AGGCATTTT CTTGGTAGCA CAAATTTCT TICTTAGGGAA AGCAACCACT CCCTGGAATG GTTTGTATTT AAGACTTAAG TGAGTTAGGT CTTTAAGGAA AGCAACTAGT TCTATATGT AACACTTCA GAAATTCT TGTAGGCATC ACCAGGAAAT AAAGAATTGT TTCTATTTAT TTATTATATG TGCACTTCAA GAAGTCACTG TCAGAGAAAT AAAGAATTGT TTCTATATGT 702 Seq ID NO: 13 DNA Sequence Nucleic Acid Accession 8: NM_012112 CODING Sequence: 4292672 1
GCCTCAGTTC AITTAAAAAA GATATCTATT TGAAAGTTCT CAGACTTGA CATATGTTC ACAGTACAGG ATCGTACAT AAAAGTTTCT TTCCTAAACC ATTCACCAAG AGCCAATATC TAGGCATTT CTTGTAGCA CAAATTTCT TATTGCTTAG AAAATTGTC TCCTTGTTAT TAGGCATTT CTTGGTAGCA CAAATTTCT TATTGCTTAG AAAATTGTC TCCTTGTTAT TTCTGTTTGT AAGACTTAAG TGAGTTAGGT CTTTAAGGAA AGCAACGCTC CTCTGAAATG GTTTGTTATT TAAACATTTCT TGTAGGCATC ACCATGAACA AAGATTATAT TTCTATTTAT TTATTATATG TGCACTTCAA GAAGTCACTG TCAGAGAAAT AAAGAATTGT CTTAAATGTC Seq ID NO: 13 DNA Sequence Nucleic Acid Accession #: NM_012112 Coding sequence: 4292672 1
ACAGTACAGG ATCTGTACAT AAAAGTTTCT TTCCTAAACC ATCACCAAG AGCCAATATC TAGGCATTIT CTTGTAGCA CAAATTTTCT TATTGCTIAG AAAATTGTCC TCCTTGTAATG TTCGTTTGT AAGACTTAAG TGGGTTAGGT CTTTAAGGAA AGCAACGCTC CTCTGAAATG GTTGTATGT AAGACTTACA GAAGTAGCTG GTCCTTTTC GGGAGTTAGA TGTATAGAGT GTTGTATGT AAAACTTCT TGTAGGCATC ACCATGAACA AAGAATATATI TTCTATTATAT TTATTATATG TGCACTTCAA GAAGTCACTG TCAGAGAAAT AAAGAATTGT CTTAAATGTC Seq ID NO: 13 DNA Sequence Nucleic Acid Accession #: NM_012112 Coding sequence: 4292672 1 11 21 31 41 51
TAGGCATTT CTIGITAGCA CARATTITICT TATTGCTIAG ANALTIGICA TCCTIGITAT TICTIGITIC ANGACTIANG TRAGITAGGT CITTANGGAN ACCANGGCA CICTIGANATI GITTIGITATI ANACATTICT TGTAGGCATC ACCATGAACA ANGATATAT TICTATTATAT TTATTATATAT GCACTICAN GANGTCACTG TCAGAGAAA ANGATATAT TICTATTATAT TATTATATATG TGCACTICAN GANGTCACTG TCAGAGAAA ANGATATAT TICTATTATAT TATTATATATG TGCACTICAN GANGTCACTG TCAGAGAAA ANGATATATT TICTATTATAT TATTATATATG TGCACTICAN GANGTCACTG TCAGAGAAAA ANAAGAATTGT CTTANATGTC Seq ID NO: 13 DNA Sequence Nucleic Acid Accession #: NM_012112 Coding sequence: 4292672 1
TICTGTTTGT AAGACTTAAG TGAGTTAGGT CTTTAAGGAA AGGAACGCTC CTCGAAATG GTTTGTATTT TTCTGTTGCC GAAATAGCTG GTCCTTTTC GGGAGTTAGA TGTATAGAGT GTTTGTATTT AAACATTTCT TGTAGGCATC ACCATGAACA AAGATATATT TTCTATTTAT TTATTATATG TGCACTTCAA GAAGTCACTG TCAGAGAAAT AAAGAATTGT CTTAAATGTC Seq ID NO: 13 DNA Sequence Nucleic Acid Accession #: NM_012112 Coding sequence: 4292672 1 11 21 31 41 51
CTITICTITI TICTOTICCC GARATAGCTG GICCITITTIC GGGAGTTAGA TIGTATAGAGT GTTGTATATA AACATITCT TGTAGGCATC ACCATGAACA AAGATATATI TICTATITAT TTATTATATG TGCACTICAA GAAGTCACTG TCAGAGAAAT AAAGATATATI TICTATITAT 708 35 Seq ID NO: 13 DNA Sequence Nucleic Acid Accession #: NM_012112 Coding sequence: 4292672 1 11 21 31 41 51
Seq ID NO: 13 DNA Sequence Nucleic Acid Accession #: NM_012112 Coding sequence: 4292672 1 11 21 31 41 51 TCAGACCTGT AGGCCTGATA GACTGATTAA ACCACAGAAG GTGACCTGCT GAGAAAGTG GTACAAATAC TGGGAAAAAC CTGCTCTTCT GGGTTAAGTG GGGAACAAGT TACACAGTTA AAGGCCTTA TTCCTATGAT GACCCCCCCGA TATTCATCAA ATTTCATCT TGGATGATG AAAGGCATTA TCCTATGAT GACCCTCGA ATTCATCAA ATTTCATCC TTGGATGATG AAAGGCATTA TCCTATGAT GACCCCTCGA ATTTCATCAA ATTTCATCC TTGGATGATG AAAGGCATTA TCCTATGAT GACCCCTCGA ATTTCATCAA ATTTTCATCC TTGGATGATG AAAGGCATTA TCCTATGAT GACCCCTCGA ATTTCATCAA ATTTTCATCC TTGGATGATG AAAGGCATA CTCAAACATA GATTCATGT TTGAGGGAA AGCCCATTG GAGAATAAGT TACTGGGGAA GAATGCAAT GATTCATCAT TTTCAGGGAAA AACCCCTTTG AGAAAGGCAA AACTCTTCATCCAA AGCATTGTG GAACAATCCA TTCCGTCAAA TCCTTTGT AGAAAGGGCTA TTGAGGCAGC CATATCAAGA AAAACTCCAG CCCAGCCTCA GAGAAGATA TCACAAGAGG CCAGAAAAGA AAAACTCCAG CCCAGCCTCA GAGAAGATA TCCACAGTAA GCCAAGGGAT CTGCTCCAGA GGAATTGGAA CAGAAAGAAA AGCACCATTA AAAAATGAAA GTTTCTAACA GTGCCACCC TGTAATCATC GATGAAATTC TACCCCTCAAA GAAAATGAAA GTTTCTAACA GTGCCACCC TGTAATCATC GATGAAATTC TACCCCTCTAA GAAAATGAAA GTTTCTAACA GTGCCACCC TGTAATCATC GATGAAATTC TACCCCTCTAA GAAAATGAAA GTTTCTAACA GTGCCACTCC TGTAATCATC GATGAAATTC TACCCCCTCAA GAAAATGAAA GTTTCTAACA GTGCCACCCAG GAAACCAAA GAAGGAAA GAACAACATA TCCTGCCTGT AAAACCAAACGAA AGCTTCCCCAAG GAAACCAAA GAAGAAAA ACCCCTCCACAGC TACCACAGAGAG TACCGCCTGAAACCAA GAACCAAGAGA TACCGCTGCACCACGCAGACAACAAACAAACAAT CCTGGAAACCAA CCAACCAGTCA CCAAACCAAA
Seq ID NO: 13 DNA Sequence Nucleic Acid Accession #: NM_012112 Coding sequence: 4292672 1 11 21 31 41 51 TCAGACCTCT AGGCCTGATA GACTGATTAA ACCACAGANG GTGACCAGTCT GAGAAAAGTG GTACAAATAC TEGGAAAAAC CTGCTCTCT GCGTTAAGTG GGAGACAAGT TCACAAAGTA AAAGCTCTTA TTCCTATGAT GCCCCCTCGG ATTTCATCAA AGCCCTCTCT GAGAAAAGTG AAAGCACAGAAG GTGACCATTT TCCTATGAT GCCCCCTCGG ATTTCATCAA TTTTTCATCC TTGGAGAAA GCCAATTTGA TACTGGGGAA GATTGATC TCAAAACACA GATTCATCAA TTTTTCATCC TTGGAGAAAA GCCAATTTGA TACTGGGGAA AACTCCTTTG AGAAAGAGA AAACTCCTTTG AGAAAGAGA AAACTCCTTTG AAACCAGTTA TCCTGCAAA AACCACTTAC TACAAAGAGG AACCAGAAAAAGA AAACTCTGG GAGAAAAAAA AAACTCCAG CCCAGCCCA GAGAAAAAGA AAACTCTGAAAAAAACAA CAGAAAAAAAAAA
Seq ID No: 13 DNA Sequence Nucleic Acid Accession #: NM_012112 Coding sequence: 4292672 1 11 21 31 41 51
Nucleic Acid Accession #: NM_012112 Coding sequence: 4292672 1 11 21 31 41 51 TCAGACCTGT AGCCCTGATA GACTGATTAA ACCACAGAAG GTGACCTGCT GAGAAAAGTG 60 GTACAAATAC TGGGAAAAAC CTGCTCTTCT GCGTTAAGTG GGAGACAAGT TCACAAGTTA 120 AAAGCTCTTA TTCCTATGAT GCCCCCTCGG ATTTCATCAA TTTTTCATCC TTGGAGTAAA 120 AAAGCTCTTA TTCCTATGAT GCCCCCTCGG ATTTCATCAA TTTTTCATCC TTGGAGTAAA 120 AAAGCAGATAC CTAAAACAATA GATTCATGGT TTGAGGAGAA AGCCCTTTG GAGAAAAGGCTA 300 ACAGAAAAAGA AAATCTTGTG GAACAATCCA TTCGGTCAAA ACCCCTTTG AGAAAGGGCAA TTGAGAGGAA GCCAATTTCA TCACAAGGAG 420 CAGAAAAAGA AAACTTTGTG GAACAATCCA TTCGGTCAAA TGCTTGTTCT TCCCTGGAAG 420 CTGCTCAGAA GGATTTGGAA CAGAAAAGAAA ACACATTAC TACAAAGAGG 420 CTGCTCAGAA GAGATCAGAA AAAACTCCAG CCCAGCCTCA GAGAAAGAATC CTTAAGGCTT 480 GTGCCACTCC TGTAATCATC GATGAAAAAAAAAAAAAA
Nucleic Acid Accession #: NM_012112 Coding sequence: 4292672 1 11 21 31 41 51 TCAGACCTGT AGCCCTGATA GACTGATTAA ACCACAGAAG GTGACCTGCT GAGAAAAGTG 60 GTACAAATAC TGGGAAAAAC CTGCTCTTCT GCGTTAAGTG GGAGACAAGT TCACAAGTTA 120 AAAGCTCTTA TTCCTATGAT GCCCCCTCGG ATTTCATCAA TTTTTCATCC TTGGAGTAAA 120 AAAGCTCTTA TTCCTATGAT GCCCCCTCGG ATTTCATCAA TTTTTCATCC TTGGAGTAAA 120 AAAGCAGATAC CTAAAACAATA GATTCATGGT TTGAGGAGAA AGCCCTTTG GAGAAAAGGCTA 300 ACAGAAAAAGA AAATCTTGTG GAACAATCCA TTCGGTCAAA ACCCCTTTG AGAAAGGGCAA TTGAGAGGAA GCCAATTTCA TCACAAGGAG 420 CAGAAAAAGA AAACTTTGTG GAACAATCCA TTCGGTCAAA TGCTTGTTCT TCCCTGGAAG 420 CTGCTCAGAA GGATTTGGAA CAGAAAAGAAA ACACATTAC TACAAAGAGG 420 CTGCTCAGAA GAGATCAGAA AAAACTCCAG CCCAGCCTCA GAGAAAGAATC CTTAAGGCTT 480 GTGCCACTCC TGTAATCATC GATGAAAAAAAAAAAAAA
40 1
40 TCAGAACTGT AGGCTGATA GACTGATTAA ACCACAGAAG GTGACCTGCT GAGAAAAGTG 60 GTACAAATAC TGGGAAAAAC CTGCTCTTCT GGGTTAAGTG GGAGACAATG TCACAAGTTA 126 AAAGCTCTTA TTCCTATGAT GCCCCCTCGG ATTTCATCAA TTTTTCATCC TTGGATGATG 126 AAAGGAGATAC TCAAAACATA GATTCATGGT TTGAGGAGAA GGCCAATTTG GAGAAAGACTA 246 ATCTTCAGGA AGCTATTGTC ACACCTTTGA AACCGTTGA ACACCTTTG AGAAAGAGAA ACCACCTGC ACACAGAAAAAGAA AAACTCCATGT AAAAACAAAA ACACCGTGCAACTCA TCCGCACAGA TTGAGGCAGC CATATCAAGA AAAACTCCAT TTCGAGGCAA AACTCCTTTG AGAAAGAGGA 426 CTGCCCACTCA GAGATACCAA TCCCTCTCAA GAAAAGAAAA
TCAGACCTGT AGGCCTGATA GACTGATTAN ACCACAGANG GTGACCTGCT GAGANAGGT 60 GTACANATAC TEGGANANAC CTGCTCTTCT GGGTTANGTG GAGACANTG TACAGAGTA ANAGCTCTTA TTCCTATGAT GCCCCCTCGG ATTTCATCAC TTTTCATCAC TTGGATGATG ANAGGAGATAC TCANAACATA GATTCATGGT TTGAGGAGAA GGCCAATTTG GAGAATAAGT TACTGGGGAA GAATGGAACT GGAGGGCTTT TTCAGGGCAA AACTCCTTTG AGAAAGAGG ACCACAGAAAAGAA AAAACTCCAG CCCAGCCTCA GAGAAGATCT TCAGAGAGAG TTGAGGCAG CATATCAAGA AAAACTCCAG CCCAGCCTCA GAGAAGATCT CTTAGGGCTT CTGCTCAGAA GCATATCAAGA AAAACTCCAG CCCAGCCTCA GAGAAGATCT CTTAGGCTTT GTGCCACTC TGTAATCATC GATGAAATACAA AGCATCATGT AAAAATGAAA GCCACAGGGTA GTGCCACTC TGTAATCATC GATGAAATTC TACCCTCTAA AAAATGAAA GCCACAGGAGA GTTCCCCCAGA GAAACAAA AGCACTCTG TACCCTCTAA AAAATGAAA GCCAAGAGAT AGTTTCTAACA AGAACCAAG GAAAGAAA ACCACCTCTA GAAAATGAAA GCCACAGAGA GTGCCACTC TGTAATCATC GATGAAAATTC TACCCTCTAA AAAATGAAA GCCACAGAGA GTGCCACTC TGTAATCATC GATGAAATTC TACCCTCTAA AAAATGAAA GCCACAGAGA AGTTTCTAAA AAGTACTGAG GACAGAGACT TCATCAAGA TACTGCTGAA AAGAATCAAT AGTTTCTAAA AAGTACTGAG GAGCAGAGAC TGGAGAAGAGA TACTGCTGAA AAGAATCAAT AGCCTTTCAAC GAAACAAAAA AATGAAAGAAT TCAAGAAAACT TGCTCTCGGC GAAAGCAGA AACCTGTGAA GAAATCAACT CCTGGAGAACC ACGAAGAGAG TATGAAATCAA GAAACAAACAA TCAAACAAACAA TCCAAGGAAT CAAACAACAA TCCAAGAAACAA TCAACAACAA TCCAAGAACAA TCAACAACAA TCCAAGAACAA TCAACAACAA TCCAAGAACAA TCAACAACAA TCCAACGAAT CAACAACAA TCAACAAACAA TACAAACCAATCCT TCCGCCAAGAACAA ACCACCGTC ACGAGAGAACAA ACCACCGAG GATGAATATT AACCTGTTAC CCTCCAAAAC AACAACCGTC ACGAGACAAA TCAACAAACAA TCCAACAAACAA TCCAACAAACA
GTACAAATAC TGGGAAAAAC CTGCTCTTCT GCGTTAAGTG GGAGACAATG TCACAAGTTA AAAGCTCTTA TTCCTATGAT GCCCCCTCGG ATTTCATCATACA AAAGCTCTTA TTCCTATGAT GCCCCCTCGG ATTTCATCATACA AAAGCTCTTA TTCCTATGAT GCCCCCTCGG ATTTCATCATCA AAAGCTCTTA TTCCTATGAT GCCCCCTCGG ATTTCATCATCA TACTGGGGAA GAATGGAACT GGAGGGCTTT TTGAGGGCAA ACCTCCTTTG GAGAATAAGT ACTTCAGGAA AAACTCTTTG GAACATTCA TTCAGAGAGG GCCAATTTG AGAAAGGGTA ATCTTCAGCAA GACTATTGTC ACACCTTTGA AACCAGTTGA CAACACTTAC TACAAAGAGG CAGAAAAAGA AAACTCTAGGA AAAACTCCAA TTCCGTCAAA TGCTTGTTCT TCCCTGGAAG TTGAGGCAGC CATATCAAGA AAAACTCCAG CCCAGGCTCA GAGAAGATCT CTTAGGGCTT CTGCTCAGAA GGATTTGGAA CAGAAAGAAA ACCACTCATG AAAAATGAAA GCCAAAGAGAT CTTCCCCCAG GAAAAGCAAA GAAGAAAA ACCACTCATGT AAAAATGAAA GCCAAAGAGAT CCTTCCCCCAG GAAAAGCAAA GAAGAAAT TACAAGAAGA TACTGCTGTAA AAAAATGAAA GCTTCTCAAA AAGTACTGAG GAGCAAGAGC TGGAGAAAGAAAT TGATGCCATG GCAAAGAGAG TGGTGGAGAT GAGGAAAAGAAAAACAAT CCTGAAGAAT TCAAGAAAAT TGACTCTCGG GGAATAGGGC AACCAGTGAA GAAACAACAAT CCTGAGAACC ACAAATCAAT TAGAGAAGT AACCATTGAACTAA CCTGCCCCAA GAGAAGAACA TACAGGAAGT TAGACTACAAT TACAGAAAACAA TACCAGTCAA CCAAACAAACAA CCCGAGGAAAAAACAAT CCTGAAAACAAACAT CCTGAAACCAA AGACATTCCA TAAACAAGAA TACCAGCAGAA GAAACAACAAT CCTGCAAACCAA AACACAGTGC TAAAGGAACT TACAGAAACAA TACCAGTCAA CCAAACCAAT TACAACAAACAA TACCAGTCAA CAAAACAAAA
ANAGCTCTTA TTCCTATGAT GCCCCCTCGG ATTTCATCA TTTTTCATCC TTGGATGATG 186 ANGGAGATAC TCANACATA GATTCATGGT TTGGAGGAA GGCCAATTTG GAGAATAGGT 24 45 ATCTTCAGCA GATTGATCA GATTCATGGT TTGAGGGCA ACTCCTTG GAGAAGGCTA 300 ATCTTCAGCA AGCTATTGC ACACCTTTGA AACCAGTTGA CAACACTTAC TACAAAGAGG 360 CAGAAAAAGA AAATCTCTGT GAACAATCCA TTCCGTCAAA TCCTTGTTCT TCCCTGGAAG TTGAGGCAGC CATATCAGA AAAACTCCAG CCCAGGCTCA GAGAAGATCT CTTAGGGTTT 486 CTGCCCAGCC GTATACACA CAACACTTCA TACACATGT AAAATGAAA GCCAAGAGAT 540 GTGCCACTCC TGTAATCATC GATGAAATTC TACCCCTCTAA GAAAATGAAA GCCAAGAGAT 540 ACAAAAAGAA GCCATGAGGAA GAAGGCAGTG CTCATCAGAG TACTGCTGAA AAGAATGCAA AGAATCCAA CCTCCCCAGC TCCCCAGA GAAAAGAAA AGAATGCAT 660 ACATTCCCCAGA GAAAGCCAAG GGTAGACATA CTGTCCCTTG TATGCCACCT GCAAAGCAGA 720 AGTTTCTAAA AAGTACTGGG GAGCAAGAGC TGAGAAGAGA TACTGCTGAA AAGAATGCAA TCGTCTGACA GAAAAAAAA AATCAGTG GAGCAAGAGC TGAGAAAGAA TCGCTCTGAC GCAAAGCAGA 720 AACCTGTGAA GAAAACAAAT CCTGAGAAGT TCAACAAAAT TCGCTCTGCC GGAATAGCGC 840 AACCTGTGAA GAAACACAT CCTGAGAAGC AGAGGAGAT TAAGGAAGT ACCACTGTTA CCTGACACAGA GAAACACAT CCTGAGAAGAC AGAACACAT TAAGGAAGT TAAGGAAGT ACCACTGTTA 100 AGCCCTTCA CACGAAGTT GAAACACAA CCCGAGAGGAA GAAACACAT CCTGAGAAAC AACACCGTGC AAACACAAT CCTGAAACCAA GAACACAT CCTTCCCCC AGCGAGGAT AAACACACT TCCTCCTCC CCCGAGTGGC TAAGGGAGT ACCACTGTTA 100 GGAGCACACA GACTACTTTA CTGCAAACCA AACACCGTGC ACGGGCTGT ACCTGCAAAA 120 GGAGCACACA GACTCCTTTA CTGCAAACCA AACACCGTGC ACGGGCTGT ACCTGCAAAA 120 GGAGCACACA GACTCCTTTA CTGCAAACCA AACACCGTGC ACGGGCTGT ACCTGCAAAA 120 GGAGCACCACA GACTCCTTTA CTGCAAACCA AACACCGTGC ACGAGGAGT ACCACTGTGA 130 AACCACCCCC CGAGCCTATT GGCTTTGATT TGGAAATTGA ACCACTCTGC AACACACT TCCCCAAAACAA CCACCTGTGA 130 AACCACCCCC CGAGCCTATT GGCTTTGATT TGGAAATTGA ACCACCCTCTCAACAC AACACCGTGC ACAAAACAAA
AAGAGATAC TOAMACATA GATTCATGGT TIGAGGAGAA GGCCAATTIG GAGAATAGGT 24 TACTGGGGAA GAATGGAACT GGAGGGCTTT TICAGGGCAA AACTCCTTIG AGAAAGGCTA 300 ATCTTCAGCA AGCTATIGTC GAACCATTIGA AACCAGTTGA CAACACTTAC TACAAAGAGG 36 CAGAAAAAGA AAAACTCTGIG GAACAATCCA TICCGTCAAA TGCTTGTTCT TCCCTGGAAG 42 TIGAGGCAGC CATATCAAGA AAAACTCCAG CCCAGCCTCA GAGAAGATCT CTTAGGCTTT CTGCTCAGAA GGATTGGAA CAGAAAGAAA AGCATCATGT AAAAATGAAA GCCACAGGGTT GTGCCACTC TGTAATCATC GATGAAATTC TACCCTCTAA GAAAATGAAA GCCACAGAGAT ACAAAAAGAA GCCAGAGGAA GAAGGCAGTG CTCATCAAGA TACTGCTGAA AAGAATCATA AGTTTCTAAA AAGTACTGAG GAGAGAATT CTACCCTTAA GAAAATGAAA GTTTCTAACA AGTTTCTAAA AAGTACTGAG GAAGGAATT CTACCACTGAA AAGAATGCAT TGGTGGAGAT GCGGAAAAAG AATGAAGAAT TCAAGAAACT TGCTCTGGCT GAAAGCAGA AACCTGTGAA GAAATCAGTG GACCAAGACC TGGAAGAGAG TATGAATACAC CAGAAGAAC AACCTGTGAA GAAATCAGTG AGCCAGGTCA CCAAATCAGT TGACTTCCAC TTCCGCACAG AACCTGTGAA GAAATCACAT CCTGGAGAACC ACGAGGAATA TAAGGAAGTG ACCATTGTTA 10 AGCCTTTCAA CCTGTCCCAA GGAAAGAAA GAACAATTGA TGAAACAGT TCACATTGTTA 10 GGAGCAAGAA GGATGATATT AACCTGTTAC CCTCCAAATC TTCTGTGCAGA AAGAATTTGCA GTACACCAC GACTCCTGTA CTGCAAACCA AACACCGTCC ACCAGGTTG ACCTGCAAAA GGAGACCCAC GACTCCTGTA CTGCAAACCA AACACCGTCC ACCAGGTTG ACCTGCAAAA GTGAACTTGA TCCCACAATA CTGCAAACCA AACACCGTC ACCAGGTTG ACCTGCAAAA AACCACCCCC CGAGCCTATT GGCATGAACT AACACCGTC CACCAAACAA TTCAAAGCAC 13 AACCACCCAC CGAGCCTATT GGCTTTGATT TGGAAATTGCA ACAATACAAA TTCAAAGCAC 13 AACCACCCAC CGAGCCTATT GGCTTTGATT TGGAAATTGCA ACAATACAAA TTCAAAGCAC 13 AACCACCCAC CGAGCCTATT GGCTTTGATT TGGAAATTGCA ACAATACAAA TTCAAAGCAC 13 AACCACCACC CGAGCCTATT GGCTTTGATT TGGAAATTGCA ACAATACAAA TTCAAAGCAC 13 AACCACCACC CGAGCCTATT GGCTTTGATT TGGAAATTGCA ACAATACAAA TTCAAAGCAC 13 AACCACCACC CGAGCCTATT GGCTTTGATT TTGAAATTGCA CCCCCTTCTA 13 AACCACCACC CGAGCCTATT GGCTTTGATT TGAAATTGCA CCCCCACTACA 14 AACTATTTGGA ACAATTTGTGT GGTGTTCTCTGAAAGCAA ACCACCGTCCCCA 15 AACTTCAAGAA GAAAACAAA TCTGAAAGCAA TCTCCAAAACA ACCACCTCTCAACA ACACCTTTCCA CCCCAACAAA CCCCCTCTCAACACA ACACTTTTCAATTTCA TTCCAAGACT TCCCCTTACAA CCCCTTCTAC 13 AACCACCACC
45 ATCITCAGGA AGATGGACT GGAGGGCTTT TEAGGGCAA AACTCCTTTG AGAAAGGCTA ATCITCAGCA AGCTATTGTC ACACCTTTGA AACCAGTTGA CAACACTTAC TACAAAGAGG CAGAAAAGA AAATCTTCTG GAACACTTACA TECCTGCAAG TTGAGGCAGC CATATCAAGA AAAACTCCAG CCCAGACTCA GAGAAGATCT CTTAGGCTTT CTGCTCAGAA CGATTTGGAA CAGAAAGAAA ACCACTCTA GAGAAGATCT CTTAGGCTTT ACAAAAAGAA GCCAGAGGAA GAAGAAAAAAAAAAAAA
ATCITCAGCA AGCTATTGTC ACACCTTTGA AACCAGTTGA CAACACTTAC TACAAAGAGG 36/ CAGAAAAAGAA AAAACTCTGTG GAACAATCCA TTCCGTCAAA TGCTTGTTCT TCCCTGGAAG TTGAGGCAGC CATATCAAGA AAAACTCCAG CCCAGGCTCA GAGAAGATCT CTTAGGCTTT CTGCTCAGAA GGATTTGGAA CAGAAAGAAA AGCATCATG AAAAATGAAA GCCAAGAGAT GTGCCACTCC TGTAATCATC GATGAAATCT TACCCTCTAA GAGAAAGAATA GCCAAGAGAT ACAAAAAGAA GCCAAGGGAA GAAGGCAATG CTCATCAAGA TACTCGTGAA AAGAATGCAA AGTTTCTAAA AAGTACTGAG GAGCAAGAC TGCAGCTAGA AAGAATGCAA GAAAAGAAGAA AGTTTCTAAA AAGTACTGAG GAGCAAGAGC TGGAGAAGAGA TATGAAAATG CAGCAAGAGG TGGTGGAGAT GCAGAAAAGA AATGAGAAT TCAAGAAACT TGCTCTGCCT GCAAAGCAGA AACCTGTGAA GAAACAACAT CCTGAGAAGC TCAAGAAAAT TAGAGAATGT CACCTTCCAC GCAAAGCACA AGCCTTTCAA CAACAACACAT CCTGAGAAAC AGAAGCAGT TAGAGAATGT ACCATTGTTA AGCCCTTTCA CCTGTCCCCAA GGAAAGAAAA GAACATTTGA TGAAACAGT TCTCACATTGC GGAGCAAGAA GGATGATATT AACCTGTTAC CCTCCAAATC TAGAGAAGT TCTACATTGC GGAGCAAGAA GGATGATATT AACCTGTTAC CCTCCAAATC TCTCTGTGCC AAGAATTTGCA GGAGCAAGAA GGATGATATT AACCTGTTAC CCTCCAAATC TCTCTGTGCC AAGAATTTGCA GGAGCAAGAA GGATGATATT AACCTGTTAC CCTCCAAATC TCTCTGTGCCAAAAA 12 GTACACCACA GACTCCTTGT CTGCAAACCA AACACCGTGC ACGGGCGTGT ACCTGCAAAAA 12 GTACACCACA GACTCCTGTA CTGCAAACCA AACACCGTGC ACGGGCGTGT ACCTGCAAAAA 12 GTACACCACC CGAGCCTATT GCCTTGAATT GAAAACAAT TCCAAAGACAC AACCACCCAC CGAGCCTATT GGCTTTGAATT GAAACAATT AACCACTTGC AACAAACAAT CCTGAAACCA TCCCTACAAG TACCACTGTGA AACCACCCAC CGAGCCTATT GGCTTTGATT TGGAAATTGA ACAATACAAA TCCAAAACCA AACCACCCAC CGAGCCTATT GGCTTTGAATT ACCCCTTGCAACAA CCACCTGTGA AACCACCCAC CGAGCCTATT GGCTTTGAATT ACCCCTACAACAA CCACCTGTGA AACCACCCAC CGAGCCTATT GGCTTTGATT TGGAAATTGA ACCACTCACAC TCCCCTACATA CCCCTTCTACACACA AACACCTTTGCA AACAACACAT CCCCTACAACCA AACACCCTTTGCAATACAA CCACCTTGTAA AACCACCCAC CAAACACACT TTCCAATTTCA TTCCAAGACCA CACACCCAC CAAACACACT TTCCAATTTCA TTCCAAACCAA AACACCTTTGAATTTCA TTCCAAGACAA CCACCTTGTAA AACCACCCAC CAAACACACT TTCCAATTTCA TTCCAAACCA TACCACTTTCA AACCACCACA CAAACACACT TTCCAATTTCA TCCCCAAAAAA CCACCTTCTATA AACCACTTTCAATTTCA TTCCAAACCA TACCACTTTCAATTTCAATTTCAATTTCAATTTCAATTCAATTCAATCACCAC
CAGAAAAGA AAATCTIGTG GAACAATCCA TTCGGTAAA TGCTTGTTCT TCCCTGGAAG TTGAGGCAGC CATATCAAGA AAAACTCCAG CCCAGCCTCA GAGAAGATCT TCTAGGCTTT CTGCTCAGAA GCATTTGGAA AAAACTCCAG CCCAGCCTCA GAGAAGATCT CTTAGGCTTT GTGCCACTC TGTAATCATC GATGAAAGAAA AGCATCATGT AAAAATGAAA GCCAAGAGAT TCCCCCAGA GAAAGCAAA GAAGGCAGTG CTCATCAAGA TACTGCTGAA AAAGAATCAA ACAAAAGAA GCCAGAGGAA GAAGGCAGTG CTCATCAAGA TACTGCTGAA AAGAATCAAT AGTTTCTAAA AAGTACTGAG GAGCAAGAGC TGGAGAAGAG TATGAAAATG CAGCAAGAGAG AGTTTCTAAA AAGTACTGAG GACCAAGAGC TGGAGAAGAG TATGAAAATG CAGCAAGAGAG AACCTGTGAA GAAATCAAGT GACCAAGACA CAGAAGAAACT TGCCCTTGGCT GGAATACGGC AACCTGTGAA GAAATCAACTA CCTGGGAAACC ACGAAGAAACT TGACTTCCAC TTCCGCACAG AGCCTTTCAA CAAGAAACTA CCTGGAGAACC AGGAGGAATA TAAAGGAAGT ACCATTGTTA AGCCTTTCAA CCTGTCCCAA GGAAAGAAA GAACAATTCA TGAAACAGT TCAACATATG TGCCCCTTGC ACAGCAAGTT GAAGACTTCC ATAAACGAAC CCCTAACAGA TATCATTTGA TGCCCCTTGC ACAGCAAGTT AACCTGTTAC CTCCCAAACCA TACCATTGTAA GGAGCCACA GACTCCTGTA CTGCAAACCA AACACCGTGC ACGGGCTGTG ACCTGCAAAA GAGACTCCAATA CTTGAAACCA AACACCGTGC ACGGGCTGTG ACCTGCAAAA TCAACACAC GACTCCTGTA CTGCAAAACCA AACACCGTGC ACGGGCTGTG ACCTGCAAAA AACCACCCAC CGAGCCTATT GCCTTGAAGTT GCCCAAGAAA TTCAAAGCAC AACCACCCAC CGAGCCTATT GGCTTTGATT TGGAAATTGCA ACAATACAAA TTCAAAGCAC AACCACCCAC CGAGCCTATT GGCTTTGATT TGGAAATTGCA ACAATACAAA TTCAAAGCAC AACACCCCAC CGAGCCTATT GGCTTTGATT TGGAAATTGA ACCACCTGTGA AACCACCCAC CGAGCCTATT GGCTTTGATT TGGAAATTGA ACCACCTGTGA AACCACCCAC CGAGCCTATT GGCTTTGATT TGCAAATACAA TTCCAATACCA TGCCCTACTAC AACCACCCAC CGAGCCTATT GGCTTTGATT TGCAAATTGA ACCACCTCTGCA AACCACCCAC CGAGCCTATT AGCTTTGAATTTCA TTCCAGACCT TGCCCTACAACA AACCACCCAC CGAGCCTATT AGCTTTGAATTTCA TTCCAGACCT TGCCCTACAACA AACCACCCAC CGAGCCTATT AGCTTTGAATTTCA TTCCAGACCT TGCCCTACAAC AACCACCCAC CGAGCCTATT AGCTTTGATT TGGAAATTGA CACCACTCTGCA AACCACCCAC CGAGCCTATT AGCTTTCATTTATTTTTATTTTCA TTCCAGACCT TGCCCTTACAACAAAC
TIGAGGAGG CATATCAAGA AAAACTCCAG CCCAGGCTCA GAGAAGATCT CTTAGGCTTT CTGCTCACAA GAGATCAGAA CAGAAAGAAAA ACACCACCA GAGAAGATCA CTTAAACAA CAGAAAGAAAAAAAAAA
50 AGAGACRCE COTANTCATC GATGANATTC TACCCTCTAA GAAAATGANA GTTTCTAACA 60 ACAAAAAGAA GACACCAGA GAAAGCAGA GAAAGCAGT CTCATCAAGA TACTGCTGAA AAAGAATGCAT 60 ACAAAAAGAA GAAAGCAGA GAAAGCAGA CTGCCCCTAGA GAAAGCAGA 72 AGATTCTAAA AAGAACCAGA GAAACAAAAA AAGAACCAGA AATCAAACAA CCACCCAGA GAAACAAAA AACAACCAG GAAACAAAC
ACAAAAAGAA GCCAGAGGAA GAAGGCAGTG CTCATCAAGA TACTGCTGAA AAGAATGCAT CTTCCCCAGA GAAAGCCAAG GGTAGACATA CTGTGCCTTG TATGCCACT GCAAAGCAGA GATTCTTAAA AAGTACTGAG GAGCAGAGAG TGGGGAAAAGA TACTGCACT GCAAAAGCAGA TGGTTGCAAAAAAAAAA
CTTCCCCAGA GAAAGCAAG GGTAGACATA CTGTGCCTTG TATGCCACCT GCAAAGCAGA 72/AGTTTCTAAA AAGTACTGAG GAGCAAGAGC TGGAGAAGAG TATGAAAATA CAGCACAGAGG TGGAGAGAGAG TGGAGAAGAGA TAGCAACAGA TGGTCGAGAT GCAAACAACAACA CATGAGAACT TGACTTCAC TTCCGCACAG 90/ATGAGCAACAACAACAACACAT CCTGAGAACA GAGAGACACAACAACAACAACAACAACAACAACAACAACA
AGTITICTANA ANGTACTGAG GAGCAAGAGC TGGAGAAGAGG TATGAAAATG CAGCAAGAGG TGGTGGAGT GCGGAAAAAG AATGAAGAAT TCAAGAAACT TGCTCTGGCT GGAATAGGGC AACCATGGAA GAATCAGTG AGCCAGGTCA CCAAATCAGT TGACTTCCAC TTCCGCACAG ATGAGCGAAT CAAACAACAT CCTGAGAACC AGGAGGAATA TAAGGAAGTG AACCATTGTTA AGCCTTTCAA CCTGTCCCAA GGAAAGAAA GAACATTGA TAAGGAAGT ACCATTGTTA TGCCCCTTGC ACAGCAAGTT GAAGACTTCC ATAAAGGAAC CCCTAACAGA TATCATTGTA TGCCCCTTGC ACAGCAAGTT GAAGACTTCC ATAAAGGAAC CCCTAACAGA TATCATTTGA GGAGCAAGAA GAATGATATT AACCTGTTAC CCTCCAAATC TTCTGTGACC AAGATTTGCA GTACAGCAGA GACTCCTGTA CTGCAAAACCA AACACCGTGC ACGGGCTGTG ACCTGCAAAA TCAACACCAC GAGCCAATT CTGCAAACCA AACACCGTGC ACGGGCTGTG ACCTGCAAAA AACCACCCAC CGAGCCTATT GGCTTTGAATT TGCAAATTGA CAAAAGAAAC CACCCTGCA AATCAAAGAA GAAAACAGAG GATGAACACT TTGAATTTCA TCCAGACCT TGCCCTACTAC AACACTCCAG CTTTGCATTG AGGTGTGGAAATTATTA TACCAGACCT TGCCCTACTAC AACCACCCAC CGAGCCTATT GGCTTTGATT TGGAAATTGA CAAAAGAAGA CCACCTGTGA LAACAACACA CAACAAGAA CCACTGTGAA AACCACCCAC CGAGCCTATTG GGCTTTGATT TGGAAATTGA CAAAAGAAGA CCACCTGTCA LAACAATTCAA TTCAAAGAA GAAAGAAGAA TCCACTGCAACAA AACACACGTG CACCAAGAA CCACCTGTGA LAACAACAAA CAAAACAAAA CAACACCGC CGAGCCTATT GGCTTTGATT TGGAAATTGA CAAAAGAAGA CACCCCCCAAAAA AACACCCGCC CGAGCCTATTA GGCTTTCAATTTCA TTCCAGACCT TGCCCTACTA LAACAATTCAA ACCATTCCCA AAAAAAAAAA
TGGTGGGAT GCGGAAAAG AATGAAGAAT TCAAGAAACT TGCTCTGGCT GGAATAGGCC 84 AACCTGTGAA GAATCAGTG AGCCAGGTCA CCAAATCAGT TGACTTCCAC TTCCGCACAG 96 ATGAGGGAT CAAACAACAT CCTGAGAACA AGCAGGAATA TAAGGAAGT ACCATTGTTA 10 AGCCTTTCAA CCTGTCCCAA GGAAAGAAAA GAACATTTAA TAAGGAACAGT TCATACTATAG 11 TGCCCCTTGC ACAGCAAGTT GAAGACTTCC ATAAACGAAC CCCTAACAGA TATCATTTGA 11 GGAGCAAGAA GGATGATATT AACCTGTTAC CCTCCAAATC TCTGTGACC AAGATTTGCA 12 GAGACCACAC GACTCCTGTA CTGCAAACCA AACACCGTGC ACGGCTGT ACCTGCAAAA GTACAGCAGA GCTGGAGGCT GAGGAGCTCG AAGAATTGCA ACAATACAAA CCCCTAACACAC GTGAACTTGA TCCCAGAATA CTTGAAGGTG GGCCCATCTT GCCCAAGAAA CCACCTGCA AACCACCCC CGAGCCTATT GCCTTTGATT TGGAATTCA GAAAAGAATC CAGGAGCGG 14 AATCAAAGAA GAAACCAGAG GATGACACT TTGAATTCA TCCCAGACT TGCCCTACTA AGCTTCGA GATGTTGTG GGTGTTCCTG AAAAGAAGT ACTTCCAATA CACGTCCCCA AGTTCACAGC CTTTGCATTG AAGAACAGAA TTCGAATGCC CACCAAGAA GATGAGGAAG 16
ACCTGTGNA GAAATCAGTG AGCCAGGTCA CCANATCAGT TGACTTCCAC TTCCGCACAG ATGAGCGNAT CANACAACAT CCTGAGAGACC AGGAGGANTA TARGGAAGTG NACTTTACAT CTGAACTACG AAAGCATCAT CCTGAGAGACC AGGAGGANTA TARGGAAGTG NACTTTACAT AGCCTTTCAA CCTGTCCCAA GGAAAGAAA GAACATTTGA TGAAACAGTT TCTACATATG TGCCCCTTGC ACAGCAAGTT GAAGACTTCC ATAMACGAAC CCCTAACAGA TATCAATTGA GGAGCACAGA GGATGATATT AACCTGTTAC CCTCCAAATC TCTGTGTAGCC AAGATTTGCA GTACAGCAGA GACTCCTGTA CTGCAAACCA AACACCGTGC ACGGGCTGTG ACCTGCAAAA GTACAGCAGA GGTCGAGGCT GAGGAGCTCG AGAAATTGCA ACAATACAAA TCCAAAGCAC GTGAACTTGA TCCCACAGATA CTTGAAGTG GGCCATCTT GCCCAAGAAA CCACCTGTGA AACCACCCAC CGAGCCTATT GGCTTTGATT TGGAAATTGA GAAAAGAATC CAGGGCGGG AATCAAAGAA GAAAACAGAG GATGACACCT TTCCATTTCA TCCCACACT TCCCTACTA AACCACCCAC CTTGCTTGTGT GGCTTCTGT TTGAATTTCA TCCCACACT TCCCTACTA AACCACCAC CTTGCATTG AGGAGAGAA TCCGAACCA AACACACAC AACACACCCAC CAGGAGCGAG AATCAAAGAA GAAAACAGAG GTTCCTGC AAAAGAAGT ACTCCCAATC ACCGTCCCCA AGGTCACCAGC CTTTGCATTG AAGAAAGAA TCCGAAACGAA GATGAGGAAG AGTCACCAGC CTTTGCATTG AAGAACAGAA TCCCAAACAA GATGAGAAGAGAGAGAA 12 13 14 15 16 17 18 18 19 19 10 11 11 11 11 11 11 11
55 ATGACGART CANACANCAY COTGAGAACC AGGAGGARTA TANGGARGTG AACTTACAT 6 CTGAACTACG AAAGCATCCT TCATCTCCTG CCCGAGTGAC TANGGGARGT ACCATTGATA AGCCTTTCAA CCTGTCCCAA GGAAAGAAA GAACATTGA TANGGARGT TCTACCATATG 10 TGCCCCTTGC ACAGCAAGTT GAAGACTTCC ATAAAGGAAC CCCTAACAGA TATCATTGA 11 GGAGACCAAC AGCTCCTGTA CTGCAAAACCA AACACCGTGC ACGGGCTGTG ACCTGCAAAA 12 GTACAGCAGA GACTCCTGTA CTGCAAAACCA AACACCGTGC ACGGGCTGTG ACCTGCAAAA 12 GTACAGCAGA GCTGGAGGCT GAGGAGCTCA AGAATTGCA ACAATACAAA TTCAAAGCAC 13 GTGAACTTGA TCCCAGAATA CTTGAAGGTG GCCCAACAAA AACACCCCCC CGAGCCTATT GGCTTTGATT TGGAAATTGA GAAAAGAAGT CAGGGAGCGAG 14 AACACCCCC CGAGCCTATT GGCTTTGATT TGGAAATTGA GAAAAGAAGT CAGGGAGCGAG 14 AACACCCAC CGAGCCTATT GGCTTTGATT TGGAAATTCA TCCCAGACCT TGCCCTACTA 13 AACACCCAC CGAGCCTATT GGCTTTCATT TGGATTTCA TCCAGACCT TGCCCTACTA 13 AACACCCAC CGAGCCTATT GGCTTTCATT TGGATTTCA TCCAGACCT TGCCCTACTA 13 AACACCCAC CGAGCCTATT GGCTTTCATT TGGAATTCA TCCCAGACC TGCCCTACTA 14 AACACCCAC CGAGCCTATT GGCTTTCATT TGAATTCA TCCAGACCT TCCCCTACTA 15 AACTTCAGA GAAAACAGAA TCGAACCAC TTCACATTCA ACGTCCCCCA 15 AGTTCACCAGC CTTTGCATTG AAGAACAGAA TTCGAATGCC CACCAAAGAA GATGAGGAGG 14
CTGAACTACG AAAGCATECT TEATCTCCTG CCCGAGTGAC TAAGGGATGT ACCATTGTTA AGCCTTTCAA CCTGTCCCAA GGAAGAGAAA GAACATTGA TATGAT TGCCCCTTGC ACAGCAAGT GAAGACTTCC ATAAACGAAC CCCTAACAGG TATCATTTGA GGAGCAAGAA GGATGATATT AACCTGTTAC CCTCCAAATC TTCTGTGACC AAGATTTGCA GGAGCCACAC GACTCCTGTA CTGCAAACCA AACACCGTGC ACGGCTGTG ACCTGCAAACAC GTACAGCAGA GCTGGAGGCT GAGGAGCTCG AAGATTGCA ACAATACAAA TTCAAAGCAC GTGAACTTGA TCCCAGAATA CTTGAAGGTG GGCCCATCTT GCCCAAGAAA CCACCTGGA AACCACCCCC CGAGCCTATT GGCTTTGAT TGGAATTCA GAAAAGAATC CAGGAGCGAG AATCAAAGAA GAAAACAGAG GATGAACACT TTGAATTTCA TTCCCAGACCT TGCCCTACTAA AGATTTGGA AGATGTTGTG GGTGTTCCTG AAAAGAAGC ACTCCCAATA CACGTCCCCA AGTCACCAGC CTTTGCATTG AAGAACAGAA TTCGAATGCC CACCAAGAA GATGAGGAAG AGTCACCAGC CTTTGCATTG AAGAACAGAA TTCGAATGCC CACCAAGAA GATGAGGAAG 16
AGCCTTTCA CCTOTCCCAA GGAAAGAAA GAACATTGA TGAAACAGTT TCTACATATG TGCCCCTTGC ACAGCAAGTT GAAGACTTCC ATAAACGAAC CCCTAAACAGA TATCATTTGA GGAGCAAGAA GGATGATATT AACCTGTTAC CCTCCAAATC TCTGTGTACC AAGATTTGCA GAGACCCACA GACTCCTGTA CTGCAAACCA AACACCGTGC ACGGGCTGT ACCTGCAAAA GTAACAGCAG GCTCGAGGCT GAGGAGCTCG AGAAATTGCA ACAATACAAA TTCAAAGCAC GTGAACTTGA TCCCACGAATA CTTGAAGGTG GCCCAACTTA GCCCAAGAAA CCACCTGTGA AACCACCCAC CGAGCCTATT GGCTTTGATT TGGAAATTGA GAAAAGAATC CAGGAGCGAG AATCAAAGAA GAAACAGGA GATGAACACT TTGAATTTCA TCCCAGACT TGCCCTACTA AACACTTGAA GAATATTGGT GGCTTCTGT TATCAATTCA CCCGTCCCCAC AGGTCACCAGC CTTTGCATTG AAGAAAGAA TCCGAACCCA AGTCACCAGC CTTTGCATTG AAGAAAGAA TCCCAAAGAA GATGAAGAAGA AGTCACCAGC CTTTGCATTG AAGAAAGAA TCCGAACCCA AGTCACCAGC CTTTGCATTG AAGAAACAGAA TCCGAACCCA AGTCACCAGC CTTTGCATTG AAGAACAGAA TCCGAACGCA GATGAAGAAGAG 16
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GTGAACTIGA TCCCAGAATA CTTGAAGGTG GGCCCATCTT GCCCAAGAAA CCACCTGTGA 13 AACCACCCAC CGAGCCTATT GGCTTTGATT TGGAATTGA GAAAGAATC CAGGAGCGAG 14 AATCAAAGAA GAAAACAAGA GATGAACACT TTGAATTTCA TTCCAGACCT TGCCCTACTA 15 AGATTTTGGA AGATGTTGTG GGTGTTCCTG AAAGAAGGA GATGACGAAC 15 AGTCACCAGC CTTTGCATTG AAGAACAGAA TTCGAATGCC CACCAAAGAA GATGAGGAAG 16
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65 AGATTITIGGA AGATGITGTG GGTGTTCCTG AAAAGAAGGT ACTTCCAATC ACCGTCCCCA 15 AGTCACCAGC CTITGCATTG AAGAACAGAA TTCGAATGCC CACCAAAGAA GATGAGGAAG 16
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40	ATTIGACTIC COCCUTICAT COGGECAACA GCATCCOTG GOTCCTCGAG CAGATCTTG CACTCCCTCC CCCCGTGCCT GGTGCCAACA GCATCCOTG GOTCCTCGAG CAGATCTTG GTCTGCAGCA GCAGCAGCTA CAGCAGATCC AGCTCACCGA GCAGATCCCG ATCCAGGTGA ACATGTGGGC CTCCCACGCC CTCCACTCAA GCGGGCAGG GGCCGACACT CTGAAGACCT TGGGCAGCCA CATGTCTCAG CAGGTTTCTG CAGCTGTGGC TTTGCTCAGC CAGAAAGCTG	720 780 840 900
45	GAAGCCAAGG TCTGTCTCTG GATGCCTTGA AACAAGCCAA GCTAACCTCAC GCCAACATCC CTTCTGCCAC CAGCTCCCTG TCCCCAGGGC TGGCACCCTT CACTCTGAAG CCGGATGGGA CCCGGGTGCT CCCGAACGTC ATGTCCCGCC TCCCGAGGGC TTTGCTTCCT CAGGCCCCGG	960 1020 1080 1140
50	GCTCGGTGCT CTTCCAGAGC CCTTTCTCCA CTGTGGCGCT AGACACATCC AAGAAAGGGA AGGGGAAGCC ACCGAACATC TCCGCGGTGG ATGTCAAACC CAAAGACGAG GCGGCCCTCT ACAAGCACAA GTGTAAGTAC TGTAGCAAGG TTTTTGGGAC TGATAGCTCC TTGCAGATCC ACCTCCGCTC CCACACTGGA GAGAGACCCT TCGTGTGCTC TGTCTGTGGT CATCGCTTCA	1200 1260 1320
5.5	CCACCARGG CAACCTCAAG GTGCACTTC ACCGACATCC CCAGGTGAAG GCAAACCCCC AGCTGTTTGC CGAGTTCCAG GACAAAGTGG CGGCCGGCAA TGGCATCCC TATGCACTCT CTGTACCTGA CCCCATAGAT GAACCGAGTC TTTCTTTAGA CAGCAAACCT GTCCTTGTAA CCACCTCTGT AGGGCTACCT CAGAATCTTT CTTCGGGGAC TAATCCCAAG GACCTCAGG	1380 1440 1500 1560
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60	CCCTCAGAT GCATTATCGC ACCCACACCG GGGAGAGACC GTTCCAGTGT AAGATCTGTG GCCGAGCCTT TTCTACCAAA GGTAACCTGA AGACACACCT TGGGGTTCAC CGAACCAAC CATCCATTAA GACGCAGCAT TCGTGCCCCA TCTGCCCAGAA GAAGTTACAT AATGCCGTGA TGCTGCAGCA ACATATTCGG ATGCACATGG GCGGTCAGAT TCCCAACACG CCCCTGCCAG	1860 1920 1980 2040
65	AGAATCCCTG TGACTITACG GGTTCTGAGC CAATGACCGT GGGTGAGAAC GGCAGCACCG GGGCTATCTG CCATGATGAT GTCATCGAAA GGATGATGT AGAGGAAGTC AGCTCCCCAG AGGCTCCCAG CAGCTCCTCC AAGGTCCCCA CGCCTCTTCC CAGCATCCAC TCGGCATCAC CCACGTAGG GTTTGCCATG ATGGTTTCCT TAGATGCCCC AGGGAAAGTG GGTCCTGCCC	2100 2160 2220 2280
70	CTTTTAACCT GCAGCGCCAG GGCAGCAGAG AAAACGGTTC CGTGGAGAGC GATGGCTTGA CCAACGACTC ATCCTGGCTG ATGGGAGACC AGGAGTATCA GAGCCGAAGC CCAGATATCC TGGAAACCAC ATCCTTCCAG GCACTCTCCC CGGCCAATAG TCAAGCCGAA AGCATCAAGT CAAGGTCTCC CGATGCTGGG AGCAAAGCAG AGAGCTCCGA GAACAGCCGC ACTGAGATGG	2340 2400 2460 2520
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		80
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25	INITIANGLE NOTIFICIALI INGIOUSINI INCIDENTI CITTORIA	00
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	AATTCTTAAA TTTCTTAACC TAGGCTTCAG GGAGCATATG AAACCAAAAT TATATGGAAC 32	40
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55	COCCOMODIO ISINICONILLI ITALIANI ITALIA	260 320
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43	CTCCACTCCA GTTCCTTCAA AGCAGTCAGC AAGGTGGCAA GTTGCAAAAG AGCTTTATCA	1320
	AACTGAAAGT AATTATGTTA ATATATTGGC AACAATTATT CAGTTATTTC AAGTACCATT	1380
	GGAAGAGAA GGACAACGTG GTGGACCTAT CCTTGCACCA GAGGAGATTA AGACTATTTT	1440
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15	GCACGAGTA GGGTGGCGG GTCAGTGCTG CTCGGGGGCT TCTCCATCCA GGTCCCTGGA GTTCCTGGTC CCTGGAGCTC CGCACTTGGC GCGCAACCTG CGTGAGGCAG CGGACTCTG GCGACTGGCC GGCCATGCCT TCCCGGGCTG AGGACTATGA AGTGTTGTAC ACCATTGGCA	60 120 180
	CAGGCTCCTA CGGCCGCTGC CAGAAGATCC GGAGGAAGAG TGATGGCAAG ATATTAGTTT GGAAAGAACT TGACTATGGC TCCATGACAG AAGCTGAGAA ACAGATGCTT GTTTCTGAAG TGAAATTTGCT TCGTGAACTG AAACATCCAA ACATCGTCG TTACTATGAT CGGATCATT ACCGGACCAA TACAACACTG TACATTGTAA TGGAATATTG TGAAGGAGGG GATCTGGCTA	240 300 360 420
20	GTGTAATTAC AAAGGGAACC AAGGAAAGGC AATACTTAGA TGAAGAGTTT GTTCTTCGAG TGATGACTCA GTGACTCTG GCCCTGAAGG AATACCACAG ACGAAGTGAT GGTGGTCATA CCGTATTGCA TCGGGATCTT AAACCAGCCA ATGTTTTCCT GGATGGCAAG CAAAACGTCA AGCTTGGAGA CTTTGGGCTA GCTAGAATAT TAAACCATGA CACGAGTTTT GCAAAAACAT	480 540 600 660
25	TIGITISCAC ACCITATIAC ATGICICCTG AACAATGAA TCGCATGTCC TACAATGAGA AATCAGATAI CIGGTCATTG GGCTGCTTGC TGTATGAGTI ATGICCATTA ATGCCTCCAT TTACAGCTTT TAGCCAGAAA GAACTCGCTG GGAAAATCAG AGAAGGCAAA TTCAGGCGAA TTCCATACCG TTACTCTGAT GAATTGAATG AAATTATAC GAGGATGTTA AACTTAAAGG	720 780 840 900
30	ATTACCATOR ACCTTCTGTT GAAGAAATTC TTGAGAACCC TTTAATAGCA GATTTOGTTG CAGACAGCA ACAAGAAAT CTTGAGAGA GAGGGGGACA ATTAGGAGAG CCAGAAAAAT CGCAGGATTC CAGCCTGTA TTGAGTGAGC TGAAACTGAA GGAAATTCAG TTACAGGAGC GAGAGGATC CTCCAAAGCA AGAGAAGAAA GATTGGAGCA GAAAGAACAG GAGCTTTGTG	960 1020 1080 1140
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33	GGCTTCACGC TGCCCAGCTG CGGGCTCAAG CCCTGTCAGA TATTGAGANA AATTACCAAC TGAAAAGCAG ACAGATCCTG GGCATGCGCT AGCCAGGTAG AGAGACACAG AGCTGTGTAC AGGATGTAT ATTACCAACC TTTAAAGACT GATATTCANA TGCTGTAGTG TTGAATACTT	1440 1500 1560 1620
40	GGCCCEATGA GCCATGCCTT TCTGTATAGT ACACATGATA TTTOGGAATT GGTTTTACTG TCTCTCAGCA ACTATTGTAC AAAATGTTCA CATTTAATT TTCTTTTCTT	1680 1740 1800
45	TATGCAGGAA GAGTAGCACT CACTGAATAG TITTAAATGA CTGAGTGGTA TGCTTACAAT TGTCATGTCT AGATTTAAAT TITTAAGTCTG AGATTTTAAA TGTTTTTTGAG CTTAGAAAAC CCAGTTAGAAT GCAATTTGGT CATTAAATACC ATGCACTCTT GCTTATAAAAT ATTCCATTGC TCTGTAGTTC AAATCTGTTA GCTTTGTGAA AATTCACCAC TGTGATGCTT GTATTCTTTT TTTTTTTTCTG TITAACAGAA TATGAGCTGT CTGTCATTTA CCTACTTCTT TCCCACTAAA	1980 2040
50	TAAAAGAATT CTTCAGTTA Seq ID NO: 28 DNA Sequence	2119
55	Nucleic Acid Accession #: Eos sequence 1 11 21 31 41 51 CGGAGCTACA ATGTTTTGTC ATTATCACT CTGATGGAA AAAGGCAGTG AATTTAATAG	60 120
33	ANANTARCTI CGTAGAGCAN ANTOCAGGI GIGITITITI AGTGCCGCAG TCTTGGATGA TGGGTTCCTA GAAGGTCTCA ACATCTCTTC TTAATTGGAG ANAGTGTTAA GCCCCANAGT AGCTGGAGCA GTACATCTTC ANTITITICAC AAGANAACAG GAACTTGAIT ACTTTGAGTG CTATTCATTA GTTTCTGCTT TCATTGAGAA TGCAACANAA GCCAACTAGG CTGCTGCTAA	180 240 300
60	CTCCTTGCNN NNNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNN	420 480 540
65	GAAATTACAG GAAAACTTIC CAAAGTTCCA TCTCACAGAA ATTATTITTA CAAAGAATTC CAAGATAAGI TTAGTTTTAT GGAAGACTTT TATGTGGTT TTACTCACTC TCCATCTCAG ACATCAACAG ATGATTACAT CACTTATTA GCTAGTAAAT TTATTAATAT AAAAACTCAG AGACATTCCA ATAATCCACAT TGCTTACACC ATTAGGGATA GATTCAGTGT CAGCTATGA	660 720- 780
70	ANTIGNANT ANGCTGTTTT GTGATTTANA GGTTTANTT TCTCTAACCA AACTGCTTGA TCCAGATGCA GGACTGCANA TGTTANTATT TGTCTGGAN GAACAATCAN ATAAGACTTA AGAGGANANG GANTGGCAC ANTCCACCTG ANATTTTTTT TTANANAGTG TGCAGCTTA TANATCGAN TGANANTAGA AGTACANGAT TATANACANA ATGCATCAN ACTTTTCTTA	4 960 4 960 2 1020
75	TAMICIAN INDUSTRIAL ANTIGORANT TICANGCARC TITIGTICANC ATTRANTIGE CANTCHARC TARCAGGICT TITIGAATITI TECANGGIAG TAAACATICT CICTATTAAC TOTATTACCT ANGCCTAAAC CTAAAATITI TAAGCAAAAT TAGAAAAATA GTCTTCACTC ATCAAAAAAT AAACTTTGIT ACATTTAGTA TITITCCCAAG AAAAAAAAA AAAAAAAAAAAAAAAAAAAAAA	1140 1200 1260
13	ATANAMAN ANGESTETS CANAMETER CTANAMATAN ATTAGCACTA GANATATTI CTANATACA ANAMANAN ANANTIGAGA TEGETTICCC ANGGANACA CTCCCANTCL ANCACANAN ACANAGANCA ANANGANTA GACANANAGA	T 1380
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15

	GCTCCAAAGG	ATGAAATTTC	ATTCTGATTT	TCTGGCTGAA	GACTATTCTC	TTTGTGTATG	120
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	GAGTGACTGC						720
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		AGCTAGTAAA					1080
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	0 ** **	21 000 0					
		31 DNA Seq					
50		id Accessio wence:91		quence			
50	1	11	21	31	41	51	
	i	i*	i*	i	7	i	
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	GTOGGCATGG TCTCCTAATG GAGGAGTGTY CATTGTATAA TAAGTTATTC ACCTGAGTAT	2400
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	Nucleic Acid Accession #: NM_032957.1	
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	CGGGAGCAGC TGTGCATCCA TCCTGAGGTG AAGAAACAAG AGAGTAACCA TCTACAGATC	480
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		720
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	TORGEROUR CONCERCET COUNCIECAS CONCARCOGT GOOTGOOGT GOOGGACOG	G 4260
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••	CONTRACTOR TEACHER TOCCGGAACC TGAAGCAGCA AGCCGACATC ATATTCA	rGC 1500
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	TOTAL COCCO CATCGATGCT GTTGAGCTGC CTGGAGACGA CAGCGGTGTC ACCAAGC	CAG 1860
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25	CTCTAATAAA	GCTGCTGGCA	GTGCCC				4946
		37 DNA Sequ		-43.0			
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20		uence: 246.				••	
30	1	11	21	31	41	51	
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٥U						G GGGAGCGGCT	
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	CCTTTGTGCA GCGCCGTGC CGCCGAGACA GCCCCACGAC GTGTGGCCCG TGTCCACCGC	660
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45 50	Nucleic Acid Accession #: NM_000593 Coding sequence: 1652591 1 11 21 31 41 51	120
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50	Nucleic Acid Accession #: NM_000593 Coding Bequence: 1652591 1 11 21 31 41 51	120 180 240 300 360 420 480
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50	Nucleic Acid Accession #: NM_000593 Coding Bequence: 1652591 1 11 21 31 41 51	120 180 240 300 360 420 480 540
50	Nucleic Acid Accession #: NM_000593 Coding Bequence: 165.2591 1 11 21 31 41 51 GGCACGAGGG TGGCGTGAT GGGAAAATT GGGCACAGG GCTGCTCCCC AGATTCTCAG ATCTGATTTC CAGGCTGGT ACCAAAATAG TCTGGGCAGG CCACTTTTGG AAGTAGGCGT TATCTAGTGA GCAGGGCAGC GCTTTCGATT TGGCTTTCCC CTAAATGGCT GAGCTTCTCG CCAGCGCAGG ATCAGCCTGT TCCTGGGACT TCCCGAGGC CCCGCCCTCG TTCCCTCCCC CAGCCGCAG ACCAGGCAGG CTCGCGGGTA CCCGGAGGT GCCAATGGCT AGCTCTAGGT ACAGTCCCAG ACCAGGCCGG GACCGGAAGG GCTCCAGAGGC CCCGCCCCCC TCCCCGCTCC CCCGGGGTCC CCCGGAGCTT CTCTGCATGG CTGGGGACAG TACTGCTACT TCTCGCCGGC TGGGTGCTC CCGGAGCGC GCTGCCCCCC ATATTCTCCC TCCTGGTGCC CACCGGGCTC CCACTGCTC CCGGAGCAG GCTGCCCCCC ATATTCTCCC TCCTGGTGCC CACCGGGCTC CCACTGCTTC TCAGGCAAG GCTGGGGCAA ACCAGGTCC CACGGGCTCG CTGCCTCC TCAGGGCAAC GCTTGCCTCC AAGAGCGAA ACCAGGTGC CAGGGCTCG CTGGCTCCTT TGAAGCCATT AGCTGCGGCA CTGGCTTGG	120 180 240 300 360 420 480 540 600 660
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50	Nucleic Acid Accession #: NM_000593 Coding Bequence: 1652591 1 11 21 31 41 51 GGCACGAGGGG TGTGCGTGAT GGAGAAAATT GGGCACCAGG GCTGCTCCCC AGATTCTCAG ATCTGATTTC CACGCTTGCT ACCAAAATAG TCTGGGCAGG CCACCTTTTGG AAGTAGGGT TATCTAGTGA GCAGGGGGGC GCTTTCGATT TCGCTTTCCC CTAAATGGCT GAGCTTCTCG CCAGGGCAGG ATCAGCCTGT TCCTGGGACT TTCCGAGAGG CCGGCCTGG TTCCTCCCC CAGGCCGCAG TAGGGGAGGA CTCGGCGGTA CCCGAGCTT CAGGCCCAG GCGGGAGGAG AGAGTCCCAG ACCCGGCCGG GACCGGAGGT CCGCAGCTT CAGGCCCAG TCCTGGTCC CCGCGGGTCC CGCTGCCTCC CCGGACCGC GTGCCCCCC AGCTCTCGGC TACTGGTTGC CACCGCGCTG CCACTGCTCC CGGGACCG GTGCCCCCC ATATTCTCCC CGCTGCTCC CACCGCGCTG CCACTGCTCC CCGGACCGC GTGCCCCCC AAGAGCAAA ACCCGGCCGG CTTGCTGCTC TCAGGCAAC GGTTGGCTC AAGAGCAAA ACCCGCGGG CTGCTTTTCCAAGGC CAATGGCT AAGAGCAAAA ACCGCGGCT CCAGGGCTCG CTGGCTCCTT TGAAGCCAAT AGCTGCGGCA CTGGCTTGGC ATAGCACAGG CCAGGCCTC TCCGGGACCG CTTGCTCCCC CCGGACCGC ATAGCACCAG CCAGCACCC CTGCTCCTT TGAAGCCAAT AGCTGCGGCA ACCCGCCCGGAACCGC CTTCGGGGAAAACCTT TACAAAGCA CAACCCCGGGACCC CGGTCCCCGGGAACGCCC CGGGCCCCGGGAACCCC CGGGCCCCC GGTCCCCGCGAACCCC CGCACCGCC CGCACCGCC CCGCACGCCC CGGTCCCCGGAACCCC CTTCGGGAAAACCTT TACAAAGACAAAAACCTACCAGAGGCCCCCCCGGGCCCCC GGTCCCCGCGAACCGCCCCCCCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
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50 55 60	Nucleic Acid Accession #: NM_000593 Coding Bequence: 1657591 1 11 21 31 41 51 GGCACGAGGG TGGCGTGAT GGAGAAAATT GGGCACGAGG GCTGCTCCCC AGATTCTCAG ATCTGATTTC CAGGCTGGT ACCAAAATAG TCTGGGCAGG CCACTTTTGG AAGTAGGCGT TATCTAGTGA GCAGGCAGGC GCTTTCGATT TCGCGAGGG CCACCTTTTGG AAGTAGGCGT TATCTAGTGA GCAGGCAGGC GCTTTCGATT TCGCGAGGC CCCGCCCTCG TTCCCTCCCC CAGCGCAGG ATCAGCCTGT TCCTGGGACT TCCCGAGGC CCCGCCCTCG TTCCCTCCCC CAGCGCAGG ACCAGGCAGG CCCGGCCTCC CCGGAGCTT CAGGCCCCAC GGGGCACGG AGAGTCCCAG ACCAGGCCGG GACCGGGACG GCTGCAGGT GCCAATGGCT AGCTCTAGGT TACTCCATCT TCTGCCCGG CAGCGGCTC CCCGGAGCTT TCTCCACTGC CTGGGACAG TACTGCTACT TCTGCCGGC CCACTGCCTC CCGGAGCTT TCTCCACTGC CTGGGGACAG TACTGCTACT TCTGCCGGGCTG CCACTGCTC CCGGAGCCCC GGTGGCCCG ATATTCTCCC TCCTGGTGCC CACCGCCCTC CCACTGCTC TCACGGCAGG GCTGCCCCC ATATTCTCCC CCGTGCTCTG GCTGGGGGCTG CGACTGCTC TCAAGGCAAA ACCAGGTGC CCAGGGCTG CTGGGGTCT TACAGGCAAT AGCTGCGGAA ACCAGGGTGC CCAGGGCTG CTGGGTGCTC TACAGGCAAT AGCTGCGGCA CTGGGCTGG CCCTGCCCGG ACTTGCCTTC TTCCGAGGC TGACTCACGC CTTCGTTGTC AGGGCCGGA ATAGCACCAG GCTACTTGCAC TGGGGAAGC AACCTACCGC CTTCGTTGTC AGTTAGCAGG AGGCGGCTC TGGAAACCCT GGGGTAGCA AACTCAGGGG CCTCTGGGTC CTGGGGTGC AGGGCGGCT TGGAAACCCT GGGGTGCC TTCTAGGCTG CCTGGGGTC CTGGGGTGC AGGCGGCTC TGGAAACCCT GGGGTGCC TTCTAGGCTG CCTGGGGTC CAGGAGCCCC GCCTCTCGCT TTCCTGGTC CTGGTGGTC TCTCCTCTTT TGGGAGAG CCCCCGCGGTC AGGCGGCTC TGGAAACCCT GGCGTGGCC TTCTAGGCTG CTTGGGGAGA CCCGCCCTCCT CTTTTTAGGG CCGCCTCACT GACTGGATT TCTCCTCTCTT TGGGAGAG CCCCTCCCG AGACTTAAC TCTCATGTCC ATCTCACAC TAGCCAATGGCA ATCTCACTC ACGGGATTAAC TCTCATGCCA ACTGGACTACGC CTTCCACGAGA ACCTTCACT GAAACTTAAC TCTCATGTCC ATCTCACAC TAGCCAATGCA CTTCCACGAGA ACCTTCACT GAGCTGTCCT GCGCCAGGAA ACCGAGTTTT TCCAAAGAACACCAC AGGCCAATTT TCCAAACACAC ATGCCCAACGAAC TTGCAACAGAACACACACACACACACACACACACACACAC	120 180 240 300 360 420 600 660 720 780 840 900 960 1020 1080 1140
50 55 60 65	Nucleic Acid Accession #: NM_000593 Coding Bequence: 1652591 1 11 21 31 41 51 GGCACGAGGG TGTGCGTGAT GGAGAAAATT GGGCACCAGG GCTGCTCCG AGATTCTCAG ATCTGATTC CACGCTTGCT ACCAAAATAG TCTGGGCAG CCACCTTTTGG AAGTAGGCGT TATCTAGTGA GCAGGGCGCC GCTTTCGATT TCGCTTTCCC CTAAATGGC GAGCTTCTCG CCAGGGCAGG ATCAGCCTGT TCCTGGGACT TCCGAGGC CCAGCCTGG TCCCTCCCC CAGCCGCAG ATCAGCCTGT TCCTGGGACT TCCGAAGGC CCAGCCTCG TCCCTCCCC CAGCCGCCAG ACCGGGGCC GCCTGCCTCC CCGGAGCTC CAGGCCCCAG GCCATGGCT AGCTCTAGGT TCCCGGCTC CCCGCGGGTC CCGCTGCCTC CCGGAACGC GCTGCCCCG ATATTCTCCC TCCTGGTGCC CACCGGGTC CCACTGCTCC CCGGAACGC GCTGCCCCG ATATTCTCCC CCGTGCTCC CCGCGGGTC CCACTGCTC CCGGAACGC GTTGCCCCG ATATTCTCCC TCCTGGTGCC CACCGCGTG CCACTGCTC TCAGGCAAAC GGTTGCCCCG ATATTCTCCC CCGTGCTCTG GCTGGGGGCC TCGGGGTCT TCAAGGCAAC GGTTGCCCCG ACTGCCTC ACGCCGGGA ACTTGCCTT TTCCGAAGGC TGATCTCAG GGGGCCCC GGTCCCGGG ATAGCACCAG GCTACTGCAC TGGGGAACAC AACTCGGGG CTTCTGGTTC AGGCACGCC CGGGCCCCG GCCCTCCCC GGCAGACGC CTGGGGACAA AACCCGGGGC CTGGGGCCCC GGTCCCGGG ACGCCCTC TCCTGTTCC TGGGGAACCC TTCTGTTGTC CCCGGGGTC CCCGGGGCCC GGCCCCC GGTCCCGGG GCCTCTCGCT GTTCCTGGTC CTGGTGGCC TTCTAGGGT CCTGGGCTC GGAGCGCCC GCCTCCCCT GTTCCTGTC TTCCAGGCACA AACCCGGGGCCC CGGGCCCCC GCCTCCCCC GGCCCCCC TCCGGGCCCC CGCCCCCC GGCCCCCC GCCCTCCCCC GCCCCCC TCCGGGCCCC TCCGGGGCCCC CGGCGCCCC GCCTCCCCC GGCCCCCC TCCGGGCCCC TCCGGGGCCCC GCCTCCCCC GCCCCCCCC TCCGGCGCCC TCCGGGGCCCC GCCTCCCCC GGCCCCCCC TCCGCGGCCC ACGCGCCC CGGACACCC TCCACCCCCC AACCCCCC CGGCGCCC ACGCCCCCCCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020 1080
50 55 60	Nucleic Acid Accession #: NM_000593 Coding Bequence: 1652591 1 11 21 31 41 51 GGCACGAGGG TETGCGTGGT GGAGAAAATT GGGCACCAGG GCTGCTCCCC AGATTCTCAG ATCTGATTC CACGCTTGCT ACCAAAATAG TCTGGGCAGG CCACTTTTGG AAGTAGGCT TATCTAGTGA GCAGGGCGCC GCTTTCGAT TCGGTTTCCC CTAAATGGCT GAGCTTCTCC CCAGCGCAGG ATCAGCCTGT TCCTGGGACT TCCGGAGGC CCGGCCCTG TTCCTCCCC CAGCCGCAG ACCAGGCCGG GACCGGGACG GCTGCCGCC CGGGGCCCG AGAGTCCCAG ACCAGGCCGG GACCGGGACG GCTGCAGGC CCGGCCCTG TTCCTCCCC TCCCGCTCC CCGCGGGTC CCCTGCCTC CCGGAGCTT CTCGCAAGC AGCTCTGGC TCCTGTTCC CACCGGGTC CCACTGCTC CCGGAGCTT TCTGCGAACG CTGGGCCAG GCTGCCCCC CCGTGCTCTG GCTGGGGGC CCGGGGTCT CACGGCACAG GCTGCGCCCC ATATTCTCC TCCTGTCCC CACCGGGTC CCACTGCTC TCAGGCAACG GTTGGCCTC AGAGCGAACA ACCAGGTGC CACGGGCTC CCACTGCTC TCAGGCAAC GGTTGGCCTC AGGCCAACA ACCAGGTGC CCAGGGCTC CCACTGCTC TCAGGCAAC GGTTGGCCTC AGGCCAACA ACCAGGTGC CCAGGGCTC CCACTGCTC TCAGGCAAC GGTTGGCCTC AGGCCAACA ACCAAGGTGC CCAGGGCTC CCACTGCTC TCAGGCAAC GGTTGGCTC AGGCCAACA ACCAGGCTCC CCAGGGCTC CCACTGCTC TCAGGCAAC GGTTGCTCC AGGCCAACA ACCAGGGTGC CCAGGGCTC CCACTGCTCT TCAGGCAAC CTTCGTTTC AGCCGACCAC CCCTCCCGGGCCC CTGGGGACAC AACTCCAGC CTTCGTTTC AGTTATGCAG CCGCACTGCC CGCAGCACC CTGGGGACAC AACTCCAGC CTTCGGTTTC AGTTATGCAG CCCTCTCGGT CTCCTGGTC TCCTGGTCTC TCTCCCTCT TCGGGAAGC CCCTCGGGTC TCTTTACGGG CCCTCCTGTC TCCTGGTCTC TCTCCCTCT TCGGGAAGC CCCTCCGGTTC TCTTTACGG CCCCTCACT GACTGGATTC TACAAGATG CTCAGCCAAT ACCTTCACC ACGGCACTCA TAACAACACA TAGGCCACA TCCAACACAA ACCAACACACA TAGCCCACTC AGGCCACTCAACACACACACACACACACACACACACACAC	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1140 1260 1260 1320
50 55 60 65	Nucleic Acid Accession #: NM_000593 Coding Bequence: 165Z591 1 11 21 31 41 51 GGCACGAGGG TGGCGTGAT GGAGAAAATT GGGCACAGG GCTGCTCCCC AGATTCTCAG ATCTGATTTC CAGGCTGGT ACCAAAATAG TCTGGGCAGG CCACTTTTGG AAGTAGGCGT TATCTAGTGA GCAGGCAGGC GCTTTCGATT TGCGTTTCCC CTAAATGGCT GAGCTTCTCC CCAGCGCAGG ATCAGCCTGT TCCTGGGACT TCCCGAGGC CCCGCCCTG TTCCCTCCC CAGCGCCAG TAGGGGAGGA CTCGGCGGTA CCCGGAGCTT CAGGCCCCAC GGGGCACG AGAGTCCCAG ACCAGGCCGG GACCGGAGAG GCCTCGAGGC CCCGCCCCCG TCCCCCC CGGCGCCAG TAGGGGAGGA CTCGGCGTC CCGGAGCTT CTCGCATGG CTGGGGACAG TACTGCTTCT TCTGCCGGC CACCGGACT CCCGGAGCTT CTCCCCCCC ATATTCTCC TCCTGGTGC CACCGGGCTC CACTGCTCC CCGGAGCTT TCTCCATGG CTGGGGACAG ACCAGGGTC CACGGGCTC CACTGCTC TCAGGCACG GCTGCCCCC ATATTCTCCC TCCTGGTGC CACGGGCTG CACTGGTCT TCAGGGCACG GCTGCCCCC ATATTCTCCC CCCTGCCCGG ACTGCCTT TTCCGAGGC TGAGCCATA GCTGCGGAAA ACCAAGGTCC CAGGGCTG CTGGCGTCC TCAGGGCACG GTGGCCCC AGAGCCTGGA AAGCACAG GCTACTGCAC TGGGGAAGC TGATCTCATG GGAGCCCCC GGGTCCCGGA AAGCACCAG CTATTGCAC TGGGGAAGC TGATCTCATG CGGACTGCC CGCAGCAGCC CTGTGGCACA AACTCAGGG CTTCCTTTC AGTTATCCAG CGGCACTGCC CGCAGCAGCC CTGTGGCACA AACTCAGGG CTTCCTGGTTC AGTTATCCAG CGGCACTGCC CGCAGCAGCC CTGTGGCACA AACTCAGGG CTTCCTGGTTC AGTTATCCAG CGGCACTGCC CGCAGCAGCC CTGTGGCACA AACTCAGGGG CTTCTGGTTC AGTTATCCAG CGCCTCTCCT TGCAAACCCT GGCGTCGCC TTCTTAGGCTG CTTGGGTGC CCCTCGCTTC TGCAACCCCT GACTGGATT TCCACAAAACACC TTCCACTCCAC	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080 1140 1250 1320 1380
50 55 60 65	Nucleic Acid Accession #: NM_000593 Coding Bequence: 1652591 1 11 21 31 41 51 GGCACGAGGG TUTGCGTGAT GGAGAAAATT GGGCACCAGG CCATTTTGG AAGTTCTCAG AATCTGATTTC CACGCTTGCT ACCAAAATAG TCTGGGCAGG CCACTTTTGG AAGTTCTCAG TATCTAGTGA GCAGGGCGCC GCTTTCGATT TCGCTTTCCC CTAAATGGCT GAGCTTCTCG CCAGGGCAG ATCAGCCTGT TCCTGGGACT TCCGCAGGGCCCAG GCAGCCTCCCC CAGGCCCAG TAGGGGAGGA CTCGGCGGTA CCCGGAGCTT CAGGCCCCAC GCAGCGCCCA TAGGGGAGGA CTCGGCGGTA CCCGGAGCTT CTCGCAGTGCT AGCCCTTGGG TCCCGGCTCC CCGGGGGTC CCGTGCCTCC CCGGAGCTC TCTCGCCATG CTGGGGACAG TACTCCTACT TCTCGCCGAC TGGGTGCTC CCGGAGCTC CTCGGCGCCCAC GGGGCCCCC CCGTGCCTCC CACGGGGTC CACTGCTCC CACGGCCCCC ATATTCTCCC TCCTGGTGCC CACGGGGTC CACTGCTC TCAGGCAAC GGTTGCCCCC AGCCCCCCC CCGTGCCTCC CACGGGGTC CACTGCTCT TCAGGCAAC GGTTGCCCCC AGCCCCCCGAACCCC CCGGACCCC CCCCCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 1020 1080 1140 1250 1320 1320
50 55 60 65	Nucleic Acid Accession #: NM_000593 Coding Bequence: 1652591 1 11 21 31 41 51 GGCAGGAGGG TGGGGTGAT GGAGAAAATT GGGCACCAGG GCTGGTCCCG AGATTCTCAG AACTGATTC CAGGCTGGT ACCAAAATAG TGTGGGCAGG CCACTTTTGG AAGTAGGGT TATCTAGTGA GCAGGGCGGC GCTTTCGATT TGGGTTTCCC CTAAATGGCT GAGCTTCTCC CCAGCGCAGG ATCAGCCTGT TCCTGGGACT TCCGGAGGC CCAGCCCCAG GAGCTTCCCG CCAGCGCCAG TAGGGGAGGA CTCGGCGGTA CCCGGAGCTT CAGGCCCCAC GGGGGCCGG AGAGTCCCAG ACCAGGCCGG GACCGGGACG GCGCCCAGGCCCCAC GGGGCCCG TCCCGCTCC CCGCGGGTC CCCTGCCTCC CCGGAGCTT CTCGCCAGG CTGGGCCCA TCTCCTGTCT TCTGCGCAC TGGGTGCTC CCCTGGCTCC CGGGGCCCG ATATTCTCC TCTGGTGCC CACCGGGTC CCACTGCTC CCGGAGCTT ACTCCAGG CGGGGCCGA AGCAGGTGC CACGGGCTG CCACTGCTC CCGGAGCTT AGCTCTAGGT CCCTGCCCGG ACTGGCTCC CTGGGGACG ACCGCGCCCC GGGCCCCG ATATTCTCCC CCCTGCCCGG CTGGGGCC CTGGGGCCCC CTGGGCCCC AGCGCCTGG CCCTCGCGGGCC CTGGGGCC CTGGGGACG AACTCCATT CCCTGGCCC CGGAGCCC CTGGGACAC AACTCCAGGC CTGGGCCCC AGGGCCGCC CGGAGCCC CTGGGGACG CTTCCAGGCACA CTGGGCTCC AGGCCGCCC CGGAGCCC CTGGGGACA AACTCCGGG CCTTCGGTTTC AGGCCACTC CCCTCCCGCCTCCC CGGGGGCCC CTGGGGCCCC CTGGGCTCC CTGGGCTCC GCCCTCTCGCT TCCTGGCCC CTCTGGGCCC CTTCGGTTTC AGGCCACTC TCTTTACGG CCCCCCACCT GACTGGATTC TACAAGATG CTCTGGGCTC AGGCCGCCC GCCCTCACT GACCGCACC CTGCGGTTC CTCCCCCTC TGGGGAAGC CCCTCGGCTC TCTTTACGG CCCCCCACCT GACTGGATTC TACAAGATG CTCAGGCCAG TCCATCCAT CCCGCACACC CTGCGCCTC CTCCCCCCC CTCGGCTCC AGGCCCCCC GCCCTCACT GACTGGATTC TACAAGATC ATGCCCACG CTTCCACCACA ACCTTCACT CCCGGCAACC TCCACCCACAC TCCACCACACACACACACACAC	120 180 240 300 350 420 480 540 600 660 720 960 1020 1020 1140 1260 1320 1380 1480
50 55 60 65 70	Nucleic Acid Accession #: NM 000593 Coding Bequence: 1652591 1 11 21 31 41 51 GGCACGAGGGG TGTGCGTGAT GGAGAAAATT GGGCACCAGG GCTGCTCCCG AGATTCTCAG ATCTGATTTC CACGCTTGCT ACCAAAATAG TCTGGGCAGG CCACTTTTGG AAGTAGGCGT TATCTAGTGA GCAGGGCGGC GCTTTCGATT TCGCTTTCCC CTAAATGGCT GAGCTTCTCG CCAGGCGAGG TTGAGCTGT TCCTGGGAGT TCCGCAGGG CCACGCTGG TTCCTCCCC CAGGCGCGAG ATCAGCCTGT TCCTGGGAGT TCCGCAGGC CCAGCCTCG TTCCTCCCC CAGCCGCAG ATCAGCCTGT TCCTGGGAGT TCCGCAGGC CCAGCCTGG TTCCTCCCC CAGCCGCAG TAGGGCAGGA CTCGGCGGTA CCCGAGCTT CAGGCCCAG GCGCTCCCCC CAGCCGCCC CCCGCGGTCC CCCTGCTCCC CCGGACCTC CACGCCCAC GCGGGCACG TACTGCTAGT TCTGGCGAG TGGGTGCTC CCGGACCGC GTGCCCCCC AAGGCCACA CCCGCGCCC CACCGCGCTC CCCTGCTCC CCGGACCGC GTTGCCCCCC AAGACCAAAAAAAAAA	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080 1140 1200 1250 1320 1380 1440 1560
50 55 60 65	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51	120 180 240 300 350 420 480 540 600 660 720 960 1020 1020 1140 1260 1320 1380 1480
50 55 60 65 70	Nucleic Acid Accession #: NM_000593 Coding Bequence: 1652591 1 11 21 31 41 51 GGCAGGAGGG TGTGCGTGAT GGAGAAAATT GGGCACCAGG GCTGCTCCCC AGATTCTCAG ATCTGATTTC CAGGCTGGT ACCAAAATAG TGTGGGCAGG CCACTTTTGG AAGTAGGCGT TATCTAGTGA GCAGGGCGGC GCTTTCGAT TGCGTTTCCC CTAAATGGC GAGCTTCTCC CAGCCGCAG ATCAGCCTGT TCCTGGGACT TCCGGAGGC CCAGCCCCAG GAGCTTCCCC CAGCCGCAG ACCAGCCCGG GACCGGGAC GCTCCGAGGC CCGCCCCCC GGGGCCCG AGAGTCCCAG ACCAGGCCGG GACCGGGACG GCGCCCGAGCCTC TCCCCCCCC TCCCGCTCC CCGCGGGTC CCCTGCCTCC CCGGAGCTT CTCGCAACG CTGGGCCCA AGAGTCCCAG CCCGGACCT CCACTGCTC CCGGAGCTT CTCGCAACG CTGGGCCCA TACTCCTCTC CCCCGGGGTC CCACTGCTC CCGGAGCTT CTCCGCAGC GTGGCCCCA AGAGTCCCAG CCCAGGCCTG CCACTGCTC CCGGAGCTT ACGCCCCCC CCCTGCCCCC CACGGCCTG CCACTGCTC TGAGGCCAA GGTTGCCTC AGAGCCAAC ACCAGGTCC CACGGCCTG CCACTGCTC TGAGGCACG GCTGCCCCC ATATTCTCC CCCTGCCCGG CTTGCCTTC TTCCGAAACCCT TCAGGCAAA GGTTGCTTCA GAGGCGAAA ACCAGGTCC CGGAGCCC CTGGGAACCC TTCAGGCAAC GCTTGGGTCC CAGGGCCAACG ATAGCACCAG CCTATCGCA TGGGGAAGC AACTCCAGC CCCTCTCGCT TCCGGAACCCT TCCGGGAACC CTTCGTTTTC AGTTATCCAG CCCCTCACCT GCGAGCCC CTGTGGCACA AACTCCGGGA CCCTCGGCTC GAGACCCCC GCCCTCACCT GACCAGCC TTCCAGCCACA CCCTACCCC CTTCGGTTG CCCGGCGCTC TCTTTACGG CCCCCCACCT GACTGGATTC TACAAGAAC ACCTACCAC ACGGCACTCC CGCCCTCACT GACTGGATTC TACAAGATG CCTCAGGCCAG TCCATCCAT TCTTTACGG CCCCCCACCT GACTGGATTC TACAAGATG CCTCTCCCCCC GCCCTCACCT GCCCCCACC GACCCCCC CTCCCCCCCC CTCGGCTCC GCCCTCACCT GCCCCCACC GACCGCTTTCTCTCTCCCCC AGGCCCCCC GCCCTCACCT GCCCCCCCC TCCCCCCCCC CTCCCCCCCCCC	120 180 240 300 360 420 480 540 600 660 720 960 1020 1020 1140 1260 1320 1440 1500 1560 1680
50 55 60 65 70	Nucleic Acid Accession #: NM_000593 Coding sequence: 1652591 1 11 21 31 41 51 GGCACGAGGG TGTGCGTGAT GGAGAAAATT GGGCACCAGG GCTGCTCCCG AGATTCTCAG AACTGATTTC CACGCTTGCT ACCAAAATAG TCTGGGCAG CCACTTTTGG AAGTAGGCGT TACTGAGTAT CACGAAATAG TCTGGGCAGG CCACTTTTGG AAGTAGGCGT TACTGAGAGA ACCTCAGCTT TCCTGGGAACT TCCGAAGGC CCAGCGCAGG ACAGCCTGCT CCCGCGGCAGG ACCAGCGCGAG ACCAGCGCGAG ACCGGGCGCG GCCGGCCTC TCCGCCGCGAGCCTC CACGCCAGG ACCCGGCCGG GCCGGGCCCG GCCGCCCCC CCGGGGGTC CACGCGCCCC CACGCGCTC CCCGCGGTC CCCGCGGGTC CACGCGCCC CACGCGCTC CACGCCCCC CACCGCCTC CCCCCCC CACCGCCTC CCCCCCCC CACCGCCTC CCCCGGGGTC CACCGCCCC CACCGCCTC CCCCGGGGCTC CACCGCCCC CACCGCCTC CCCCCCCC CACCGCCTC CCCCCCCC CACCGCCTC CCCCCCCC CACCGCCTC CCCCGGGGCCC CACCGCCTC CACCGCCCC CACCGCCTC CACCGCGTC CACCGCCTC CACCCCTCC CACCCCTCC CACCCCTCC CACCCCTC CACCCTC CACCCTC CACCCCTC CACCCCTC CACCCCTC CACCCCTC CACCCTC CACCCTC CACCCTC CACCTCCCTC	120 180 240 300 360 420 480 540 600 660 720 780 840 1020 1080 1140 1200 1260 1320 1380 1440 1560 1620 1620
50 55 60 65 70	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51 GGCACGAGGG TGTGCGTGAT GGAGAAAATT GGGCACCAGG GCTGCTCCCG AGATTCTCAG ATCTGATTC CACGCTTGCT ACCAAAATAG TCTGGGCAGG CCACTTTTGG AAGTAGGCT TATCTAGTGA GCAGGCAGC GCTTTCCATT TCGGTTTCCC CTAAATGGCT GAGCTTCTCG CCAGCGCAGG ATCAGCCTGT TCCTGGGACT TCCGGAGGCCCCC CCAGCGCCAG ATCAGCCTGT TCCTGGGACT TCCGAGGCCCCAG GAGGTCCCAG ACCAGGCCGG GACCGGCACC CCGGAGCTT CAGGCCCCAC CAGCCGCCAG TAGGGGAGGA CTCGGCGGTA CCCGAGCTT CTCGCAGCT TACTGCTACT TCTCGCCGG GACCGGCCCC CCGGAGCTT CTCGCCAGG AGCTCTCGC CCGTGCCTC CCGCGGGTCC CACCTGCTCC CCGGAGCTT CTCCCCAGG GCTGCCCCC CAGCCGCCC CACCGGGTC CACTGCTCC CCGGAGCTT CTCCCCAGG CTGGGCCCG CCGTGCTCC CCGGGGGTC CACTGCTCC CCGGGGCCG GCTGCCCCC ATATTCTCC CCCTGCCTCC CACCGGGTC CACTGCTCT CACGGCACCG GTGGCCCCG ATATTCTCC CCCTGCCCGG ACTGCCTTC TTCCGAGAGC TCAGGCACAG GTTGGCTCC AAGGCGAAA ACCAAGGTC CAAGGGCCC CTGGGTCTC TCAGGCAAC GGTTGGCTC AAGGCGAAA ACCAAGGTC CAAGGGCCC CTGGGTCTC TCAGGCAAC GGTTGGCTC AAGGCGAAA ACCAAGGTC CAAGGGCCC CTGGGTCTC TTCAGGCAAC CTTCGTTGTC AGTTATCCAG CAGCACCAG CTTACTTCAC TGGGGAACT CACCTTACGC CTTCGTTGTC AGTTATCCAG CAGCACTCC GCACAGCC CTGGGGTCC CTGGGTCC CTGGGCTC CAGGGCCCC GCCTCTCGCT TGAAAACCT TGCGTTGCC TTCTCAGGCTA CCCTTACGC CTTCGGTTG CCCGGGGTC TCTTTACGG CCGCCTCACT GACTGGTTC TCCAGCAGAA CCCTTCCGT TCCAGGCCAC GCCTCTCGCT TGAAACCCT TGCGTTCC TTCTAGGCT CCTCGGGTTC CTGGGTCC GCAACTTACA TAACAACACA AACGCGAACGT TAACAACAGA AACTCCATCAT TCTCATGTC ATTCTCACCA TAGCCAATGC CTTCGGGTA TCTCTGCGTT CCTGGGTAC AGAGGAACACT TCTCATGTC ATTCTCACCA TAGCCAATGC ATTCCAGGAA ACCTTCACTC GGAACTTACA TAACAACACA AACGGCAACT TAACAACAGA ACCTTCACTC GGAACTTACA TAACAACACA AACGGCAACGT AACACTCAT TCCAGGGAAC CTTCCAGCAAC AGAGGCACC TCCACCTGA GAGAGGCACC TCCACCTAC CACTCACTCA CACCACACAA AACCCCACACAC AACACCACACAC AACCCCACACACAC AACCCCACCA	120 180 240 300 360 420 480 600 660 720 720 780 840 1020 1140 1250 1320 1320 1350 1440 1500 1680 1760 1680
50 55 60 65 70	Nucleic Acid Accession #: NM_000593 Coding Bequence: 1652591 1 11 21 31 41 51 GGCAGGAGGG TGTGCGTGAT GGAGAAAATT GGGCACAGG GCTGCTCCCG AGATTCTCAG ATCTGATTTC CAGGCTGGT ACCAAAATAG TCTGGGCAGG CCACTTTTGG AAGTAGGCGT TATCTAGTGA GCAGGGCGC GCTTTCGATT TCGCTTTCCC CTAAATGGCT GAGCTTCTCC CCAGCGCAGG ATCAGCCTGT TCCTGGGACT TCCCGAGGC CCAGCCCCAG GAGCTTCCCG GGCGCCAG TAGGGGAGGA CTCGGCGGTA CCCGGAGCTT CAGGCCCCAC GGGGGCCGG AGAGTCCCAG ACCAGGCCGG GACCGGGACG GCTGCCGGC CCGGGCCTG TCCCTCCCC CGGCGCCCC CCGCGGGTC CCCTGCCTCC CCGGAGCTT CTCGCATGG CTGGGGACA ACCAGGCTCC CCGCGGGTC CCACTGCTCC CCGGAGCTT CTCGCATGG CTGGGACAG TACTGCTACT TCTGCGCGAC TGGGTGCTC CCCGGAGCTT CTCGCATGG CTGGGACAG ACCAGGCTCC CCCGGGGTC CCACTGCTC CCCGGAGCTT ACTGCATGG CTGGGGACAG ACCAGGCTCC CACGGCCTG CCACTGCTC CCCGGAGCTT AGCTCCCGC CGGGGCCCG CCCTGCTCTG GCTGGGGGCC TGGGGTCC TCAGGGCAAC GGTTGCCCCC ATATTCTCCC CCCTGCCGGG ACTTGCCTTT TTCGGAGAGC TGAGCCCAAT AGCTCCGGCAC AAGCAGGTCC CACGGGCTG CGACTGCTC CCCGGAGCTC CTGGGTCC CTGGGCCCAC AAGCACGGC CTGGGGGCC TGGGGTCC TCAGGGCAAC GGTTGCCTC AAGGCCAAA ACCAAGGTCC CGGAGCCCC TGGGGTACC TGAGGCCAAT AGCTCCGGCAC AGGCCGCTC CCGGGGCCC CTGGGGACC TTGCAGCCAA ACCCTACCAC CCCTCCCGCG CTTCCCCT TTCGGAAACCCT GTGGGTACC CTTGGGTTG CCTTGGGTTG CCCTGCCTC CGCAGCAGCC CTGGGGAAC CACCTACCAC CTTCGGTTG CCCGGCGCTC TCTTTACGGG CCCCTCACT GACTGGATTC TACAAGATCA CTTCAGGCCAC CTGGGGCAC GCCCTCTCGGT TCCTGGTCC CTGGGGTAC CTCTCCACTC TGGGGAAC GCATTCCAT TCTTTACGG CCCCCCACT GACTGGATTC TACAAGATCA CATCATCACACACA AACCACACA TACACACACA	120 180 240 300 360 420 480 540 600 660 720 1020 1020 1140 1200 1140 1260 1320 1500 1560 1680 1740 1860
50 55 60 65 70	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51 GGCACGAGGGG TGTGCGTGAT GGAGAAAATT GGGCACCAGG GCTGCTCCG AGATTCTCAG ATCTGATTTC CACGCTTGCT ACCAAAATAG TCTGGGCAG CCACCTTTTGG AAGTAGGCGT TATCTAGTGA GCAGGGCGCC GCTTTCGATT TCGCTTTCCC CTAAATGGC GAGCTTCTCG CCAGGGCAG ATCAGCCTGT TCCTGGGACT TCCGCAGGG CCACCTGG TCCCTCCCC CCAGGCGAG ATCAGCCTGT TCCTGGGACT TCCGAGAGC CCGCCCCGG TCCCTCCCC CAGCCGCAG ACCAGGGGGC GCTTCGGTT TCCGAGAGC CCAGCCCCAC GCGGGCCAG GAGATCCCAG ACCAGGGGC GCCTGCTCCC CCGGAGCTT CAGCCCCAC GCGGGCACG TCCTGGTCC CCCGGGGTC CCGCTGCTCC CCGGACCGC GTGCCCCCC TCCTGGTGCC CCACGGGTC CCACTGCTCC CCGGACCGC GTGCCCCCC TCTGTGTCCC CACCGGGTC CCACTGCTCC CCGGACCGC GTGCCCCCC TCCTGGTGCC CACCGCGCTG CCACTGCTC TCCAGGCCAAC GGTTGCCCCC TCCTGGTGCC CACGGGGTC CCACTGCTCC TCACGCCAAC GGTTGCCCCC ACGCCGCAC TCCGGGGTC TCAGGGCAAC GGTTGCCTC AAGACCAAAA ACCAGGTGC CCAGGGCTC TCCGGGGTC TCAGGCAAC GGTTGCCCCC ATACCACAG CCTACTCCAC TCCGGGTCC TCACGCCAAC GCTTGCTCCA AGGCCGGCC CGAGACCCC TGGGGGACA AACCCCGGCTC ACCCCCCAACCCC CGTCCCCCC GCCCTCCCCG ACTTGCTCT TTCCGAGAGC TCACTCCCCC CTTCGTTGTC AGTTATGCAG CCGCACTGCC CGCAGCAGCC CTGGGGACAA AACCCCGGCGCC CGGCCCCCC GCCTCCCCC GCCCTCCCCT GTTCCTGGTC CTGGTGGCCC CTTCGGTGC CCCGGGGTC GCCTCTCGCT GTTCCTGGTC CTGGTGGCCC CTTCGGTGC CCCGGGGTC GCCTCTCGCT GTTCCTGGTC CTGGTGTCC TCCCCCCTC AGGCGCCCC GCCTCCCCC GCCCTCACCT GCCCAGGAACCCC TGGCGTGCC TCCAGCGAT ACCTTCACTC TCTTTACCGG CCCCCCACACCCC ACCCCCCAACCCC AGGCGCCC CCCGGGACACCC TGCCCCCAACACCC TTCCACCCTA ACCTCACTC TCCTGCTCC CCCCCAGGAA ACCCCTACCCTA GCCCAGCACCC ATGCCCCTAA ACCCCAAGACACCT TCCACCCCTAA GCACACCC ATGCCCCAACCCC TCCCCCCACCAACCCC ACCCCCCAACCCCC ACCCCCCAACCCC CCCCACCAACCCC AGCACACCC ATCCCCCTAACCTA TCCCCCTAACCTA TCCCCCCCAACCC	120 180 240 300 360 420 480 540 600 660 720 780 840 1020 1080 1140 1260 1320 1380 1440 1560 1620 1680 1740 1800 1800
50 55 60 65 70	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51	120 180 240 300 360 420 480 600 660 720 780 840 900 960 1020 1140 1260 1320 1380 1440 1500 1680 1740 1680 1740 1860 1860 1980
50 55 60 65 70	Nucleic Acid Accession #: NM_000593 Coding Bequence: 1652591 1 11 21 31 41 51 GGCAGAGGG TGTGCGTGAT GGAGAAAATT GGGCACCAGG GCTGCTCCCG AGATTCTCAG ATCTGATTTC CAGGCTGGT ACCAAAATAG TCTGGGCAGG CCACTTTTGG AAGTAGGCGT TATCTAGTGA GCAGGGCGCC GCTTTCGATT TCGGTGTCCC CAAATGGCT GAGCTTCTCC CCAGCGCAGG ATCAGCCTGT TCCTGGGACT TCCGGAGGC CCACCTTTTGG AAGTAGGCG CCAGCGCCAG TAGGGGAGGA CTCGGCGGTT CCCGGAGGCT CCGGCCCTG TCCCTCCCC CGGCGCCAG TAGGGGAGGA CTCGGCGGTA CCCGGAGCT CAGGCCCCAC GGGGGCCGG AGAGTCCCAG ACCGGGCCG GACCGGGACG GCGTCCGGG GCCAATGGCT AGCTCTAGGT TCTCGCTCC CCGCGGGTC CCACTGCCTC CCGGAGCTT CTCGCAAGC GTGGGCCCA AGAGTCCCAG CCCGGGGTC CCACTGCCTC CCGGAGCTT CTCGCAAGG CTGGGACAG TACTGCTAT TCTGCGCGAC TGGGTGCTC CCACTGCTC TCCGCACCAG GCTGCCCCC CCTGCTCTG GCTGGGGGC TGCGGGGTC TCAGGGCAAG GGTTGCCTC AGGCCCAG GCTGCCCCC CCCTGCCCGG ACTGCCTC CCACGGGCTC TCAGGCAAA GGCTGCGCCCA ATATTCTCCC TCCTGGTGCC CACGGGCTC CCACTGCTC TCAGGCAAA GGCTGCGCCC AGCGCCTGG CCCTGCCGGG CCTCGGGGCC TCCGGGGTCC TCAGGGCAAG GGTTGCCTC AGGCCAAAG AGCAGGTGC CACGGGCTC CCACTGCCTC TCAGGCAAG GGTTGCCTC AGGCCAAAG AGCACGGTC CCAGGGCCC TGCGGGTCC TCAGGGCAAG GGTTCCAT TCGGAACCCC CGGGGCCCCC GGGTCCCCC CCCTGCCGGG ACTTGCCTT TTCGGAAGC TTAGAGCCAAT AGCTGCGGA AAGCACAG GCTATCTCACA TGGGGAAGT AACCTCAATT GGGAAGCCCC CGGGGCCCCC GGGGCCCCC GCCCTCACC TGGGGAACCC TGCGTGCCC CTTGGGTGC CCTGGGCTC AGGACCCCC GCCCTCACCT GGCGAGCC CTGGGGACAAACTCAAACACCA AACTCAGAC AGGGCGGCTC TGGGGAAGC CTCTGCGCTC CTCCCCTCT TCGGGAAACCCT TCCAGCCAGA ACCTTCAAT TCCTTGGGTA CCGGCAAGA ACGAGTTTT TCCAACACACA AACCACCA AACCACCA AACCACCA AACCACC	120 180 240 300 360 420 480 540 600 660 720 1020 1020 1140 1200 1140 1500 1560 1680 1740 1860 1920 1980
50 55 60 65 70	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51	120 180 240 300 360 420 480 540 660 660 720 780 840 1020 1080 1140 1250 1320 1320 1440 1560 1620 1680 1740 1860 1920 1980 2040

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55	CATACCAGTT TAAAACTCCT GAATCTTCTC CACCGGGGAC ACCAATTGGC AGAATCAAAG CCAGCGACGC TGATGTGGGA GAAAATGCTG AAATTGAGTA CAGCATCACA GACGGTGAGG	1260
	GGCTGGATAT GTTTGATGTC ATCACCGACC AGGAAACCCA GGAAGGGATT ATAACTGTCA	1320
	AAAAGCTCTT GGACTTTGAA AAGAAGAAAG TGTATACCCT TAAAGTGGAA GCCTCCAATC	1380
	CTTATGTTGA GCCACGATTT CTCTACTTGG GGCCTTTCAA AGATTCAGCC ACGGTTAGAA TTGTGGTGGA GGATGTAGAT GAGCCACCTG TCTTCAGCAA ACTGGCCTAC ATCTTACAAA	1440 1500
60	TAGAGAAGA TGCTCAGATA AACACCACAA TAGGCTCCGT CACAGCCCAA GATCCAGATG	1560
•	CTGCCAGGAA TCCTGTCAAG TACTCTGTAG ATCGACACAC AGATATGGAC AGAATATTCA	1620
	ACATTGATTC TGGAAATGGT TCGATTTTTA CATCGAAACT TCTTGACCGA GAAACACTGC	1680
	TATGGCACAA CATTACAGTG ATAGCAACAG AGATCAATAA TCCAAAGCAA AGTAGTCGAG TACCTCTATA TATTAAAGTT CTAGATGTCA ATGACAACGC CCCAGAATTT GCTGAGTTCT	1740 1800
65	ATGARACTIT TOTCTGTGAR ARAGCARAGG CAGATCAGTT GATTCAGACC CTGCATGCTG	1860
	TTGACAAGGA TGACCCTTAT AGTGGACACC AATTTTCGTT TTCCTTGGCC CCTGAAGCAG	1920
	CCAGTGGCTC AAACTTTACC ATTCAAGACA ACAAAGACAA CACGGCGGGA ATCTTAACTC	1980
	GGAAAAATGG CTATAATAGA CACGAGATGA GCACCTATCT CTTGCCTGTG GTCATTTCAG	2040 2100
70	ACAACGACTA CCCAGTTCAA AGCAGCACTG GGACAGTGAC TGTCCGGGTC TGTGCATGTG ACCACCACGG GAACATGCAA TCCTGCCATG CGGAGGGGCT CATCCACCCC ACGGGACTGA	2160
,,	GCACGGGGC TCTGGTTGCC ATCCTTCTGT GCATCGTGAT CCTACTAGTG ACAGTGGTGC	2220
	TGTTTGCAGC TCTGAGGCGG CAGCGAAAAA AAGAGCCTTT GATCATTTCC AAAGAGGACA	2280
	TCAGAGATAA CATTGTCAGT TACAACGACG AAGGTGGTGG AGAGGAGGAC ACCCAGGCTT	2340
75	TTGATATCGG CACCCTGAGG AATCCTGAAG CCATAGAGGA CAACAAATTA CGAAGGGACA TTGTGCCCGA AGCCCTTTTC CTACCCCGAC GGACTCCAAC AGCTCGCGAC AACACCGATG	2400 2460
13	TCAGAGATTT CATTAACCAA AGGTTAAAGG AAAATGACAC GGACCCCACT GCCCCGCCAT	2520
	ACGACTECTT GGCCACTTAC GCCTATGAAG GCACTGGCTC CGTGGCGGAT TCCCTGAGCT	2580
	CGCTGGAGTC AGTGACCACG GATGCAGATC AAGACTATGA TTACCTTAGT GACTGGGGAC	2640
80	CTCGATTCAA AAAGCTTGCA GATATGTATG GAGGAGTGGA CAGTGACAAA GACTCCTAAT CTGTTGCCTT TTTCATTTTC CAATACGACA CTGAAATATG TGAAGTGGCT ATTTCTTTAT	2700 2760
60	ATTITATECAE TACTECGIGA AGGETTETET GITETACCG TICCAAAAGE CAATGETIGE	2820
	AGTECGTGTG GATCCAATGT TAGAGACTTT TTTCTAGTAC ACTTTTATGA GCTTCCAAGG	2880
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	GTCCTGGTGT TTTACTA					3060
	CAGGCTAATG GGATAAA					3120
	TGAGGGCATA TCGGCTC					3180
_	GAATTTAAAA TAACACT	TGC CCATGCTATT	TGTTCTTCAA (GAACTITCTC :	IGCCATCAAC	3240
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	CACTAACTCA TAGTTTG					3420
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• •	TAAAGTTTTG GCCACCA					3540
10	CTAATGTCAA AATTGTT	TAA AAATTCTTGA	AAGAATTTTC (CTGAGACAAA	TTTTAACTTC	3600
	TTGTCTATAG TTGTCAG					3660
	CAATAATTCA TATTCTT					3720
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	ATATACTTAA GAATATO					
~ -	TTAATTTTCT ACAAATI	VATT TTAGTGTCAT	TTCCATTTGG	GGATATTGTC	ATATCAGCAC	4440
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	AGAAGTAAAG ATGGAA	ACGT T				4521
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	TITITITITI TITITA					60
	ACAAAAATTG ATTTGC					120
26	ATTCTTTTCA AATTTA					180
35	AGTGCGTATT TGCCAT					240
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60	TAGACTGCTT GGATTT					1680 1740
OU	TTGATAAACA TAAAA	TTAA GATTACACT	A TAAIGAICCI	IGITAGAGGA	TACATTICAA	1800
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	ATGCCGTGAA CCCGG					2280
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	GAGCTGCGCC CAGGG					120
80	GGGCGGCGCT AGCGC					180
50	CGGCCTGTCT GTCGG					240
	GTGCTTGGCA CAGCC					300
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	CGGCAGCCAC CGCGC					420
	coordinate event					

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	GAAGGGCGCC '	TTGCAGGATC	CICCCCCCC :	CCAACOGGA 1	POCTGGGTCT	AGAGCTCCCC	540
	AGAGCGAGGC (GCTCGCCAGG	ACTCCTGCCC (DGCCAACCCT (GACCGCCGGG	GGGTGCCCCC	600
_	GGGACGTAGC (GCCGCGGAGA	GGAAGCGGCA	AAGGGGACCA '	TGCGGGGGCCT	GACTCGTCGG	660
5	CTGGTTCTGC	CAGTCTTCGG	GGTGCTCTGG	ATCACGGTGC	TGCTGTTCTT	CTGGGTAACC	720 780
	AAGAGGAAGT	TGGAGGTGCC	GACGGGACCT (GAAGTGCAGA	TOCTOTATO	ACCACTOT	840
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10	CTGCTGGTGT	ATTGCACGGA	CCTTCCACCC .	ACTAGCATCA	TCATCACCTT	CCACAACGAG	1020
• •	GCCCGCTCCA	CGCTGCTCAG	GACCATCCCC	AGTGTATTAA	ACCGCACCCC	TACGCATCTG	1080
	ATCCGGGAAA	TCATATTAGT	GGATGACTTC	AGCAATGACC	CTGATGACTG	TAAACAGCTC	1140
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15	CGGATTCGGG	GCGCTGACAT	CGCCCAGGGC	ACCACTCTGA	CTTTCCTCGA	CAGCCACTGT	1260 1320
13	GAGGTGAACA	GGGACTGGCT	CCAGCCTCTG TATCATTAAC	TIGCACAGGG	TCACCTACAT	CIACACGCGG	1380
	TOTAL	CACCCCCCTT	TGACTGGAGC	CTCCACTTCC	AGTGGGAGCA	GCTCTCCCCA	1440
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25			GGACCTGAGG				1860 1920
23			TGAACTCAGC GTGCCTGGAA				1980
	AATATCCGAC	TORCOCCOTO	TGCCAAGGTC	AAACCCCAAG	ATCCAAAGTC	CCAGGTATGG	2040
			GATCCTCCAG				2100
	TTCCCTGGCG	CCCCAGTGGT	TCTTGTCCTT	TGCAAGAATG	GAGATGACCG	ACAGCAATGG	2160
30	ACCAAAACTG	GTTCCCACAT	CGAGCACATA	GCATCCCACC	TCTGCCTCGA	TACAGATATG	2320
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	ATGAGCCAGC	ACTOGGACAT	GGTGAGCTCT	TGAGGACCCC	TGCCAGAAGC	AGCAAGGGCC	2340
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33			AACATCACAA CCAGTCCTGG				2520 2580
			TTATTGTTCC				2640
	CCAGAAAGAA	AAGCCTTCTT	TTTCACTAGG	CCAGGACTAC	ATTGAGAGAT	GAAGAATGGA	
			AAGAGAAACT				2746
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	Coding seq	uence: 641.	.2299				
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45	Coding seq	uence: 641. 11 	2299 21 	31 	1	1	60
45	Coding seq	uence: 641. 11 GTGCACCGCT	2299 21 CCCGCCCCGC	31 CCCGCCTTGC	CCCAACCCAC	 GATGGTCTGG	60 120
45	Coding seq 1 GCCATCCCGA GAGCTGCGCC	puence: 641. 11 GTGCACCGCT CAGGGCTTGC	2299 21 r cccsccccsc r cscrsscssc	31 CCCGCCTTGC CCCGCAACAG	CCCAACCCAC CACCGAGCGT	GATGGTCTGG TTCGGTCGGC	
	Coding seq 1	uence: 641. 11 GTGCACCGCTGC CAGGGCTTGC AGGGCCCCCT	2299 21	31 CCCGCCTTGC CCCGCAACAG CGCTCACTCC TCACTCCCTC	CCCAACCCAC CACCGAGGGG CACCTGGGCGCGGGGGGGGGG	 GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCCGG	120 180 240
45 50	Coding seq 1 GGCATCCCGA GAGCTGCCGGT CGCCTGTCT GGTGCTTGGC	uence: 641. 11 GTGCACCGCT CAGGGCTTGC AGGGCCCCCT GTCGGGCCCCCT	2299 21	31 CCCGCCTTGC CCCGCAACAG CGCTCACTCC TCACTCCCTC	CCCAACCCAC CACCGAGCGT CACCTGGGCT CGCCCTCGTC	 C GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCGG CCCTATCGGC	120 180 240 300
	Coding seq 1 GGCATCCCGA GAGCTGCGC GGCGCGGT CGGCCTGTCT GGTGCTTGGC GGCAGCGGG	puence: 641. 11	2299 21	31 CCCGCCTTGC CCCGCAACAG CGCTCACTCC TCACTCCCTC CTCGCTGCTCC	 CCCAACCCAC CACCGAGCGT CACCTGGGCT CGCCCTCGTC GAGTCAGTTT GTGGCGGCGT	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCCGG CCCTATCGGC	120 180 240 300 360
	Coding seq 1 GGCATCCCGA GAGCTGCGCC GGCCGCGGT CGGCAGCGGC TCGCCAGCGGC TCGCCAGCCA	puence: 641. 11	2299 21 CCCGCCCGC G CGCTGGCGGC C CTCAGAGCCC G CCCTCCCGG G ATTCCTCCCG T CCCGCGGGGGGGGC C CCCGCTGGAG	31	CCCAACCCAC CACCGAGCGT CACCTGGGCT CGCCCTCGTC GAGTCAGTTT GTGGCGGCGT	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCTCCCCGG CCCTATCGGC GGGGAACATC CCTCGGTCCT	120 180 240 300 360 420
	Coding seq 1 	puence: 641 11	2299 21	31	CCCAACCCAC CACCGAGCGT CACCGAGCGT CACCTGGGCT CGCCTCGTT GGGTCAGTTT GGGGGGCGT AGCTGGCTGCT GCTCGCTTCC	GATGGTCTGG TTCGGTCGGC CGCTCCCGG CCCTATCGGC GGGGAACATC CCTCGGTCCT CTTCGAAGCG	120 180 240 300 360 420 480
50	Coding seq 1 1 GGCATCCCGA GACCTGCCC GGCCGCTGTCT GGTCCTTGGC GCAGCCGG TCGCCAGCCA TCCCTGCCAC	puence: 641. 11	2299 21	31 CCCGCCTTGC CCCGCAACAG CGCTCACTCC CTCGCTGCTC CGCGCGTCCCC CGCGCGTCCCACCCCACCCACCCACCCACCCACCCACCCA	CCCAACCCAC CACCGAGCGT CACCGAGCGT CACCTGGGCT CGAGTCAGTTT GGGGGGGGG GGTTGGCTGC GCTTGGCTGCT GCTTGGCTGCTGCTTC GTTGGCTGCTGCTGCTTC GTTGGCTGCTGCTGCTGCTTC GCTTGGCTGCTGCTGCTTC GTTGGCTGCTTC GTTGGCTGCTGCTTC GTTGGCTGCTTC GTTGGCTGCTTC	GATGGTCTGG GATGGTCTGGC CGCTCCGAGT GCTCTCCCGG CCCTATCGGC GGGGAACATC CTTCGAAGCG TTCGAAGCG	120 180 240 300 360 420 480 540
	Coding seq 1 1 GGCATCCCGA GAGCTGCGCC GGGCGGCGGT CGGCCTGTCT GGTGCTTCGC GCAGCGGCC TCCCTGCCAG GGAAGGGCGC CAAAGGGAGGCCC	nuence: 641. 11 GTGCACCGCT CAGGGCTTGC AGGGCCCCCT AAGGCCCCCT AAGGCCCCCT CACAGCTCGC ACAGCTCGC CACGGCTTC CCTTTCGGGTC CTTTCAGGT CCTTGCAGGA GCCCGCCAGG	2299 21	31	COCAACCCAG CACCGAGCGT CACCTGGGCT CGCCTCGTY GGGTCAGTTT GGGGGGGGT GCTTGGCTGG AGCTTGGCTGG ATCCTGGGTG TGACCGCCG	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCCGG CCCTATCGGC GGGGAACATC CCTCGGTCCT CTTCGAAGCG TAGAGCTCCC	120 180 240 300 360 420 480 540
50	Coding seq 1 1 GGCATCCGSA GAGCTGCCC GGCGGCGGT GGCGGCGGC TCGCCAGCCA TCCTGCCA GGAAGGGGG CGGAAGGGGG CGGAAGGGGGG CGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	Number: 641 11 GTGCACCGCT CAGGGCTTGC AGGGCCCCCT AGGGCTCGC AGGGCGCGC AGGGCGCGC CAGGCGCGC CAGGCGCGC CAGGCGCGC CAGGCGCGGA CCGGCGCTCC CGTTGCAGGA CGGCCGGGA GGCCCGGGA	2299 21	31 CCCGCATGC CCGCAACAG GCGCTACTCC TCACTCCCTC CTCGCTGCTC CCCCACCAGC CCCCACCACCAGC CCCCCACCCAGC AAAGGGGACC AAAGGGGACC AAAGGGGACC AAAGGGGACC AAAGGGGACC AAAGGGGACC AAAGGGGACC AAAGGGGACC AAAGGGACC	CCCAACCCAC CACCAGGGGGGGGGGGGGGGGGGGGGGG	GATGGTCTGG TTCGGTCGGC CGCTCCGGGT CCCTATCGGC CCTGGTCCT CCTGGGTCCT CTTCGAAGCG TAGAGCTCCC GGGGGGCCCC TGACTCGTCCC	120 180 240 300 360 420 480 540
50	Coding seq 1	nuence: 641	2299 21	31 CCCGCCTTGC CCCGCACAGC GGGCGTCCACTCC GGCAGCCGC GGGGGTCCA CCCCACCAGC CCCCCAAACCC AAAGGGACC AAAGGGACC TGAAGTGCAC TGAAGTGAAG	CCCAACCCAC CACCTGGGC CACCTGGGC CGCCTCGTC GGGTCGGTC GGTTGGCTGC GGTTGGCTGC TGACCGCGC TGACCGGGGGGGGGG	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CCCTTCCCGG CCCTTCGGC CGCGGACATC CTTCGAAGCTCC CTTCGAAGCC TAGAGCTCCC TGACTGCCC TGACTGCCC TTCGGATAC	120 180 240 300 360 420 480 540 600
50	Coding seq 1 GGCATCCCGA GGCTGCCCC GGCGGCGGT GGCTGCTTGGC GGCAGCGGG TCCTGCCA GGAAGGGGG CGGAAGGAGGA GCTGGTTCTC CAAGAGGAAG GCTGGTTCTC CAAGAGGAAG GTGGTTCTC CAAGAGGAAG	Number: 641.	.2299 21	31 CCCGCCTTGC CCCGCAACAG GGCTCACTCC GGCAACAG CCCGCGCGCGCGCGCGCGCGCGCGCGCG	CCCAACCCAG CACCGAGCGG CACCGGGCGGGGGGGGGG	I GATGGTCTGG TTCGGTCGCCCCGGGGACATC CCCTCCCGGGTCCTGTCGGCCCCCGGGGGACATCCCCCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840
50	Coding seq 1 GGCATCCOGA GGCAGCGGGCGGGGGGGGGGGGGGGGGGGGGGGG	Nuence: 641.	2299 21	31 COGCCTTGG CCCGCCTTGG CCCGCACAGG GGCACCGG CGGCACCGG CCCCCCCAG CCGCCACCGG CCGCCACCGG CCGCCACCGG CCGCCACCGG CCGCCACCGG CCGCCACCGG CCGCCACCGG CCGCCACCGG CCGCCACCC CCGCCACCG CCGCCACCG CCGCCACCG CCGCCACCG CCGCCACCG CCGCCACCG CCCACCG CCGCCACCG CCGCCACCG CCGCCACCG CCGCCACCG CCGCCACCG CCGCCACCC CCGCCACCG CCGCCACCG CCGCCACCG CCGCCACCG CCGCCACCG CCGCCACCG CCCACCG CCCCACCG CCGCCACCG CCCACCG CCGCCACCG CCCCACCG CCGCCACCG CCGCCACCG CCGCCACCG CCGCCACCG CCGCCACCG CCGCCACCC CCCCCCCC	CCCAACCCAG CACCAGGGGGGGGGGGGGGGGGGGGGGG	I GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CCCTTCCGGG GGGGAACATC CCTCGAGGC TGTCGAAGGG TAGAGCTCCC GGGGTGCCCC TGACTGGTCG TCTTCGAAGG TCTTCGGAGG TCTTCGGAGG CTCTCGGAGG CTCTCGGAGG CTCAAAAAGT AGTGAGGGAA	120 180 240 300 360 420 480 540 600 720 780 840 900
50	Coding seq 1	Nuence: 641	.2299 21	31 CCCGCCTTGC CCCGCACAGE GGGTCCACTCC TCACTCCTC TCACTCCTC CCCGCCACCAG CCCCCACCAG CCCCCACCAG CCCCCACCACCAG AAAGGGACC TAGAGTGCAC TGAATGCAG CCCTCCACCAG A TAGAGGACC CCACCTGAGGGACC CCACCTGAGGGACC CCACCTGAGGGACC CCACCTGAGGGACC	CCCAACCCAG CACCGAGCG CACCGAGCG CACCGAGCG CACCGGGC CACCGGGC CACCGGGC CACCGGGC CACCGGGC CACCGGGC CACCGGGC CACCGGGC CACCGGGC CACCGGGC CACCGGGC CACCGGGC CACCGGGC CACCGGGC CACCGGGC CACCGGGGC CACCGGGGC CACCGGGGC CACCGGGGC CACCGGGGAC CACCGGGAC CACCGGGAC CACCGGGAC CACCGGGAC CACCGGGAC CACCGGGAC CACCGGGAC CACCGGGAC CACCGGACACGGGAC CACCGGGAC CACCGGGAC CACCGGACACGGGAC CACCGGGAC CACCGGGAC CACCGGGAC CACCGGACACGGGAC CACCGGACACGGGAC CACCGGACACGGACACGGACACGGACACGACACGGACACGACACGGACACGACACGGACACGACACGGACACGACACGGACACACGACACACGACACACGACACACGACACACGACACACACGACACACACGACACACGACACACACGACACACGACACACACGACACACACACGAC	GATGGTCTGG TTCGGTCGCC CGCTCCGAGT CCCTATCGGC GGGGAACATC CTTCGAAGCGC TTCGAAGCGCCC TGACTCCCCC TGACTCCCCC TGACTCCCCCC TGACTCCCCCCCCCC	120 180 240 300 360 420 480 540 660 720 780 840 900 960
50	Coding seq 1 GGCATCCGGA GGCTGCCGC GGCGGCGGT GGCTGCTTGGC GGCAGCGGGC TCCTGCCAC GGAAGGGGGC CGGAAGGAGGA CGCGAGTAG GCTGGTTCTC CAAGAGGAAG GCCGTTGGT CTCCAGGAAG CTCCAGGAAC CCCAGGAAC CCCAGGAAC CCCAGGAAC CCCAGGAAC CCCAGGAAC CCCAGGAAC CCCAGGAAC CCCAGGAAC CCCAGGAAC CCCAGGAAC CACAGGAAC CACAGGAAC CACAGGAAC	Nuence: 641 11	.2299 21	31 CCCGCCTTGC CCCGCACAG GCCTCACTCC TCACTCCCTC GCCACCCG GCGCGTCCCG CCCCACCCG CCCCACCCG CTCCAACGG CTCCAACGG CTCCAACGG AAAGGGAC GATCACGT TAAGTGCAA TGACTTCAA	CCCAACCCAG CACCAGGGGGGGGGGGGGGGGGGGGGGG	i GATGGTCTGG TTCGGTCGCCCCCCCCCCGG CCTCTCCCCCCGG CCTCTCTCCCCCCGG CCTCGGTCCT CCTCGAAGCG TAGAGCTCCCCCCCGGGTGCCCCCCCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 900 1020
50	Coding seq 1 GGCATCCOGA GGCAGCGGT GGGCGGGGGGGGGGGGGGGGGGGGGGG	Nuence: 641.	2299 21	31	CCCAACCCAG CACCAGGGGGGGGGGGGGGGGGGGGGGG	COGGAAATCAT	120 180 240 300 360 420 480 540 600 660 720 840 900 960 1020 1080
50	Coding seq 1	Number: 641. 11 GIGACCGCT COMMENT	2299 21	31	CCCAACCCAG CACCGAGCG CACCGAGCG CACCGGGCG CACCTGGCG CAGCTAGTT GGGGGGGG GGTCGCTTC ATCCTGGCTG ATCCTGGCTG TACCGGGG TATCCGGGG TATCCGGGG TATCCGGGG TATCCGGGG TATCTGATT CACGGGGGG TATCTGATT CACGGGGGG TATCTGATT CACGGGGGGG TATCTGATG CACGGGGGGG CATGTGTT CACGGGGGGGG CATGTGTT CACGGGGGGGG CACGGGGGGGG CACGGGGGGGGG CACGGGGGGGG	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CCCTATCGGC CCCTGGTCCT CTTCGAAGCG TAGAGCTCCC TTTCGAAGCG TAGAGCTCCC TGACTCGTCCC TGACTCGTCCC TGACTCGTCCC TGACTCGTACC CTTCGAAGC CTTCGAAGC CTTCGAAGC CTTCGAAGC CTTCGAAGC CTTCGAACC TGACTCATC TGGTAATG CGGAAATATT CGGGAAATCAT AATTGCCCAA	120 180 240 300 360 420 480 540 600 660 720 780 840 900 1020
50 55 60	Coding seq 1 GGCATCCOGA GGCAGCGGCGGGCGGGGGGGGGGGGGGGGGGGGG	Nuence: 641.	2299 21	31 CCCCGACAGE CCCGCACAGE CGCACAGE CGCACAGE CGCACCAGE CCCCACCAGE CCCCCACCAGE CCCCCACCAGE CCCCCACCAGE CCCCCACCAGE CCCCCACCAGE CCCCCACCAGE CCCCCACCAGE CCCCCACCAGE CCCCCACCAGE CCACCCCTACCAGE CCCCCACAGE E CCCCCACACAGE CCCCCACACAGE CCCCCACACAGE CCCCCACACACACACACACACACACACACACACACACA	CCCAACCCAG CACCGAGCG CACCGAGCG CACCGAGCG CACCGGGC CAGGCGCGG CACCGGGCG CACCGGGCG CACCGGGGGG CACCGGGGGGG CACCGGGGGGGG	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CCCTTACCGC CGCGAGACATC CGTCGTCCT CTTCGAAGCCCC CAGCGTCCCCC CAGCGTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	120 180 240 300 360 420 660 720 780 840 900 960 1020 1080 1140
50 55 60	Coding seq 1	Number: 641. 11	219 21 7 CCGGCCCGC 6 CCTCCCGG 7 CTCAGAGCCC 6 CCTCCCCGC 7 CCGCTGGAC 7 CCGCTGGAC 7 CCGCTGGAC 8 CGCCTGCAC 8 CGCCTGCAC 9 CGCCTGCAC 9 AGGAACGGC 9 AGGAACGGC 9 ACCAGTTTG 1 ATTAAACGGT 1 ATTAAACGGT 1 ATGAACGGC 1 ATGAACGGC 1 ATGAACGGC 1 CCTGCCCT 1 ATGAACGGC 1 CACAGGTCA 1 ATGAACGGC 1 ATGAACGGC 1 ATGAACGGC 1 ATGAACGGC 1 ATGAACGCC 1 ATGAACGGC 1 ATGAACGGC 1 ATGAACGGC 1 ATGAACGGC 1 ATGAACGGC 1 ATGAACGGC 1 ATGAACGGC 1 ATGAACC 1 ATGAACGC 1 ATGAACGC 1 ATGAACGC 1 ATGAACGC 1 ATGAACGC 1 ATGAACGC 1 ATGAACGC 1 ATGAACGC 1 ATGAACGC 1 ATGAACGC 1 ATGAACGC 1 ATGAACGC 1 ATGAACC 1 ATGAACC 1 ATGAACC 1 ATGAACC 1 ATGAACC 1 ATGAACC	31	CCCAACCCAG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CAGCCAGC	CONTRACTOR CONTRACTOR	120 180 240 300 360 420 480 540 600 660 720 840 900 1020 1020 1140 1200 1320
50 55 60	Coding seq 1	Nuence: 641 11	.2299 21	31 CCCGCCTTGC CCCGCCTTGC CCCGCACAG CCCGCACAG CCCGCACCG CCGCGCGC CCGCCACCC CCCCACCCA	CCCAACCCAG CACCGAGCGG CACCGAGCGG CACCTGGGCG CACCTGGGCG CACCTGGTG CGGCGCGGG ATCCGGGGG TGACCCCGG TATCCGGGGG TATCTGATT CACGGGGGGG TATCTGATT CACGGGGGGGGGG	I GATCGTCTGG TTCGGTCCGG CCTCCTCCCGG CCTCGGTCCT CCTCGGTCCT CCTGGTCCT CTTCGAAGCG TAGAGCTCCC TAGAGCTCCC TAGAGCTCCC CTTCGGAAGCG CTTCGGAAGCG CTTCGGAAGCG CTTCGGACGC CCTTCGGACGC CCTTCGGACGC CCTTCGGACGC CCTAGGTAAT ATTCGCACGCT CGGGAAAATAT AATTGCCCAA ATTCGCGGCGC GTGAACAGGGA ATTCGCGCCTGT GAACAGGGA ATTCGCCCTGT GAACAGGGA ATTCGCCCTGT GAACAGGGA ATTCGCCCTGT GAACAGGGA TTGCCCCTGT GACCTCTGGACGCG GTGAACAGGGA TTGCCCCTGT GACCTCAGAGG	120 180 240 300 360 420 480 540 660 720 840 900 1020 1020 1200 1200 1220 1380
50 55 60 65	Coding seq 1 GGCATCCOGA GGCTGGCCG GGCGGGGGGGGGGGGGGGGGGGGGGGG	Number: 641.	2299 21	31	CCCAACCCAG CACCGAGCGG CACCGAGCGGGGGGGGGG	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CCCTTATCGGC CGCGAGACATC CGGGAACATC CTTCGAAGCGC TAGAGCTCCC TAGAGCTCCC TAGAGCTCCC TAGAGCTCCCC TAGAGCTGCCC TAGAGCTGCCCC TAGAGCGGAT CTTCGGAAGGGAT CTTCGGAAGGGAT CTGGTTATTG CGCAAAAATATT CGGGAAATCAT AATTGCCCAA ATTCGGGGGGC TGAACAGGGA TGTGCCCTGT TAGAGGGAGGCCCGC TGAACAGGGAGGAT TGGTGCCCTGT TAGACAGGGAGGAT TGGCCCCTGT TAGACAGGGAGGATCATAGAGGAGGACCCCGCCCCCCCCC	120 180 240 300 360 420 480 600 660 720 720 780 840 900 960 1140 1200 1320 1320
50 55 60	Coding seq 1 GGCATCCGAA GAGCTGCGA GGCGGGGGGGGGGGGGGG	NUMBER : 641. 11 GIGACCGCT CAGGGCTTCK AGGGCCCCCT GIGGGCCCCCT GIGGGCCCCCT GIGGGCCCCCT GIGGGCCCCCT GIGGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	219 21 7 CCGGCCCGCC 6 CCTCCCGGC 7 CTCAGAGCCC 6 CCTCCCCGC 6 CCTCCCCGC 7 CCGCTGGAC 7 CCGCTGGAC 7 CCGCTGGAC 8 GGCTCCTGCC 8 GGCTCTCGCC 8 GGCTCTCGCC 9 AGGAAGCGC 6 GGGTGCTCT 1 CTGACTT 1 ATAACTGTT 2 CGGACACTC A GCATCATCA A TGACCCT A ATGACCT A ATGACCT A ATGACCT C CACAGGTCA C CACAGGTCA C CACAGGTCA C CACAGGTCA C CACAGGTCA C CACAGGTCA C CACAGGTCA C CACAGGTCA C CCATCAGGTCA C C CCATCAGGTCA C C CCATCAGGTCA C C CCATCAGGTCA C C CCATCAGGTCA C C CCATCAGGTCA C C CCATCAGGTCA C C CCATCAGGTCA C C CCATCAGGTCA C C CCATCAGGTCA C C C C C C C C C C C C C C C C C C C	31 CCCGCCTTGC CCCGCCTGC CCCGCACAG GGTCACTCC GGCAGCGC GGGGGTCCA CCCGCCACCC CCCGCCACCC AAAGGGGAC CTGAACGG CTGAACGG CTGAACGG CTGCAACGG CTGCAACGG CTGCAACGG ATAGGGT AAAGGGAC ATGACTTCAA ACGCTTCCAC AAGGGACC AAGGCACCCTACC CCCCCTACCC CCCCCTACCC CCCCCTACCC CCCCCACCC CCCCCTACC CCCCCTACC CCCCTACC CCCCTACC CCCCTACC CCCCCCC CCCCCCC CCCCCCC CCCCCCC CCCCC	CCCAACCCAG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CAGCCAGC	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CCCTATCGGC CGCGAGACATC CTTCGAAGGG TAGAGCTCCC TGAGCTCCG TGACTCGTCG TGAGCGGAGG TGTGCCCTGT TGGGGGGGC TGACAGGGGAGGAAGCTCG TGACAGGGGCCC TGACAGGGGAGGAAGCTCG TGAAGGCTCG TGAAGGCTCG TGAAGGCTCG TCTTCGTGAT	120 180 240 300 360 420 480 600 660 720 840 900 1020 1140 1200 1320 1340 1440 1500
50 55 60 65	Coding seq 1	Nuence: 641 11	.2299 21	31 CCCGCCTTGC CCCGCACAG GCCTCACTCC TCACTCCCTC GGCAGCGGG GCGGGGTGCT CCCCACCGG CCCGCACCG CCCCACCC AAAGGGGAC GGTCTTCAAC GCATTCAG CCTCTATCAT AAATATGATAT	CCCAACCCAC CACCAGGGGGGGGGGGGGGGGGGGGGGG	I GATGGTCTGG TTCGGTCGGC CGCTCCGGGGG CTCTCTCCCGG CCTCGGTCCT CTCTGAAGGG TTCGGAGGG TTCGGAGGGG TTCGGAGGGGGGG TTCGGAGGGGGGGGGG	120 180 240 300 360 420 480 600 660 720 780 840 960 1020 1120 1260 1320 1440 1560
50 55 60 65	Coding seq 1 GGCATCCOGA GGCAGCGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Nuence: 641 11	2299 21 1	31	CCCAACCCAG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGG CACCGAGG CACCCAGG CACCGAGG CACCCAGC CACCCAGG CACCCAGG CACCCAGG CACCCAGC CACCCAGC CACCCAGC CACCCAGC CACCCAGC CACCCAGC CACCCAGC CACCCAGC CACCCAGC CACCCAGC CACCCAGC CACCCAGC CACCCAGC CACCCAGC CACCCAGC CACCCAGC CACCCAGC CACCC	GATGGTCTGG TTCGGTCGCC CGCTCCGAGT CCCTTATCGGC CGCGGAGCATCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	120 180 240 300 360 420 480 600 660 720 720 780 840 1020 1140 1220 1320 1440 1500 1500
50 55 60 65 70	Coding seq 1 GGCATCCGAA GAGCTGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGGAGGA	Number: 641. 11	219 21 1 CCGGCCCCGC GCCCGCCCGC GCCCCGCC GCCCCCGC GCCCCCGC GCCCCGCC GCCCCGCC GCCCCGCC GCCCCGCCC GCCCCGCCC GCCCCGCCC GCCCCGCCC GCCCCCC	31 CCCGCCTTGC CCCGCACAG GGCTCACTCC TCACTCCCTC GGCAGCGC GGCGCTCCA CCCCCACCCC AAAGGGACC TGACTCCACCG TGACTCCACCG CTCCAACCG CTCCAACCG CTCCAACCG CTCCAACCG CTCCAACCG CTCCAACCG CATCACTCAC AAAGGGACC ATGACTTCAAC CTCCACCGG CACCCTTCCA AAGGGACC TCCACCGT CCCTTCCACCG CACCCTTCCAC CGCACCCTACC CTCCACCGG CCCCTTCCACCG CCCCTTCCACCG CCCCTTCCACCG CCCCTTCCACCG CCCCTTCCACCG CCCCTTCCACCG CCCCTTCCACCG CCCCTTCCACCG CCCCTTCCACCG CCCCTTCCACCG CCCTTCCACCG CCCCTTCCACCG CTTCCC CCCCTTCCCC CCCCTTCCCC CCC	CCCAACCCAG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CAGCCAGC	I GATGGTCTGG TTCGGTCGGC CGCTCCGGGGG CTCTCTCCCGG CCTCGGTCCT CTCTGAAGGG TTCGGAGGG TTCGGAGGGG TTCGGAGGGGGGG TTCGGAGGGGGGGGGG	120 180 240 300 360 420 480 540 600 660 720 960 1020 1020 1140 1200 1320 1320 140 1500 1560 1620
50 55 60 65	Coding seq 1 GGCATCCGA GGCATCCGA GGCATCCGA GGCATCGGCA GGCAGCAGCCA GGCAGCAGCA GGCAGCAGCA GGAAGGGGG CGGAAGGGGG CGGAAGGGAG CGGAAGGAG GCGCTTGA GCAGCAGCA GCAGCAGAG GCGCTTGGA GCGCAGTAG GCGCATTGG GCTCAGGAC ATTAGTGGA GGTGAATTG GGTTAATGG GGTGAATTG GGGTTGA GCGCTTGGA CCGGACATACGC CTGGCTCCAC GACAAAGG CGACAAAGC CGACAAAGC CGACAAAGC CGACAAAGC CGACAAAGC CGACAAAGC CGACAAAGC GGACAAAGC GGACAAAGC GGACAAAGC GGACAAAGC GGACAAAGC GGACAAAC CTGCAACC GCAATACTA	Number: 641. 11 GIGACCGCT GAGGCCCCCT GAGGCCCCCC GAGGCCCCCC GAGGCCCCCC GAGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	219 21 1 CCGGCCCGCC CCGCCCGCC CCCCCCCCC CCGCCGGGGGG	31 CCOGCCTTGC CCOGCAACAG CGCTCACTCC CTCACTCCCT CAGCGCACACAG CGCACCCAC CCCCCACCCAC AAAGGGGAC TGACTTCACTCC AAAGGGAC ATGACTTCAAC ATGACTTCAAC ATGACTTCAAC AAGGGACCAC AAAGGGACCAC AAAGGACTAC AAAGGGACCACCACCCTACC CCCCTACCACAGG CCTCTACCACAGG CCTCTACTACACAGG AAAAGGACTACAAAAAAAAAA	CCCAACCCAG CACCGAGCGG CACCGAGCGGGGGGGGGG	CATCGGTCTGG CATCGGTCTGGC CGCTCCGGGC CGCTCCGGGCCCCCCCCGGCGGGGGGCGCGCGTCTGGAGGCGGAGGGGGGGG	120 180 240 300 360 420 480 600 660 720 780 840 960 1020 1140 1220 1320 1320 1440 1500 1620 1680 1780
50 55 60 65 70	Coding seq 1 GGCATCCGA GGCATCCGA GGCATCCGGA GGCTGTCT GGTGCTTGGC GGCAGCCA TCCCTGCCA GGCAGCCA TCCCTGCCA GGAAGGGAGC CGGAAGGGAGC CGGAAGGGAGC CGGAAGGGAGC CGGAAGGAGC GCCCTTGGT CTCCAGCAC ATTAGTGGA GGTGAATGG GGTGAATGG GGGTTTGA GGGTTTGA GGGCTGGA GGCCTGGA GGCCTGGA CGACAAAGC GGACAAAGC GCACAAAGC GCACAACAC GCAATACT CGCAGCCG TGCCAACAC GCAATACT CAGCACCT CGCAACACA CGCAATACT CAGCACCT CGCAACACA CGCAATACT CAGCAGCCG CGCAATACT CAGCAGCCG CGCAATACT CAGCAGCCG CGCAATACT CAGCAGCCG CGCAATACT CAGCAGCCG CGCAATACT CAGCAGCCG CGCAATACT CAGCAGCCG CGCAATACT CAGCAGCCG CGCAATACT CAGCAGCCG CGCAATACT CAGCAGCCG CAGAATTCCA	Nuence: 641 11	219 21 1 CCGGCCCCGC GCGCCCCGC GCCTGGAGGCC GCCTCCCCGG GCCTCCCCGG GCCTCCCCGG GCCTCCCGC GCCTCGAC GCGCTGGAC GCGCTGGAC GCGCTGGAC GCGCTGGAC GAGAAGGGGAC GACAGTTGG AACAGTAC AACACAAC GACCTCACCC GACCCCGCC AACACCCCGAC AACACCCCGAC AACACCCCGAC AACACCCCGAC CCACCCCCCCC	31 CCCGCCTTGC CCCGCACAG GGCTCACTCC GGCACAG GGCACCCG GGCACCCG CCCCCACCCG CCCCCACCCG CTCCAACCGG CTCCAACCGG CTCCAACCGG CTCCAACCGG CTCCAACCGG CTCCAACCGG CTCCAACCGG CTCCAACCGG CACCCTACC AAAGGGACCG ATGACTGCAG ATGACTGCAG CCCCTACCG CACCCTTACC CCCCTACCG CACCCTACC CTCCACCGG GGAGCACCT AATGGTAA AAGGTCTGTAA AAGGTCTGTAA AAGGTCTGGACGG CTACATCGACGG GAAGCACT AATATGATATA AATATGATATA AATATGATATA AATATGATATA GAAGGCCCG GAAAGCACCG GAAAGCACCG GCACAGCG GCACAGCTGACGG GCACAGCTGACGG GCACAGCTGACGG GCACAGCTGACGG GCACAGCTGACGG GCACAGCTGACGG GCACAGCTGACGG GCACAGCTGACGG GCACAGCTGACGG GCACAGCTGACGG GCACAGCTGACGG GCACAGCTGACGG GCACAGCTGACGG GCACAGCTGACGG GCACAGCTCACGACGG GCACAGCTGACGG GCACAGCTGACGG GCACAGCTGACGG GCACAGCTGACGG GCACAGCTGACGC GCACAGCTCACACGG GCACAGCTCACACGG GCACAGCTCACACG GCACAGCTCACACG GCACAGCTCACACCG GCACAGCTCACACCG GCACAGCTCACACCC GCACAGCTCACCCC GCACAGCCC GCACAGCTCACCC GCACAGCTCACCC GCACAGCTCACC GCACAGCTCACC GCACAGCTCACC GCACAGCTCACCC GCACAGCTCACCC GCACAGCTCACCC GCACAGCTCACCC GCACAGCTCACCC GCACAGCTCACCC GCACAGCTCACCC GCACAGCTCACCC GCACAGCTCACCC GCACAGCTCACCC GCACAGCTCACCC GCACACCC GCACAGCTCACCC GCACAGCC GCACAGCC GCACAC	CCCAACCCAC CACCGAGGGG CACCGAGGGG CACCGAGGGGG GAGTCAGTT GAGGGGGG ATGCGGGG TATCCTGGTT CACCGGGGG TATCCTGGTT CACCGGGGGG TATCCTGGTT CACCGGGGGG TATCCTGGTT CACCGGGGGG TATCCTGGTT CACCGGGGGG TATCCTGAT CACGGGGGG CACGGGGGG CACGGGGGG CACGGGGGG CACGGGGGG CACGGGGGG CACGGGGGG CACGGGGGG CACGGGGGG CACGGGGGG CACGGGGGG CACGGGGGG CACGGGGGG CACGGGGGG CACGCTT CACGGGGGG CACGCTT CACGGGGGG CACGCT CACGGGGGG CACGCT CACGGGGGG CACGCT CACGGGGGG CACGCT CACGGGGGG CACGCT CACGGGGGG CACCCT CACGGGGGG CACCCT CACGGGGGG CACCCT CACGGGGGG CACCCT CACGGGGGG CACGCT CACGGGGGG CACCCT CACGGGGGG CACCCT CACGGGGGG CACCT CACGGGGGG CACCCT CACGGGGGG CACCCT CACGGGGGG CACCT CACGGGGGG CACGCT CACGGGGGGG CACGCT CACGGGGGGGGG CACGGGGGGGG CACGGGGGGGGGG	CATCGTCTGG TTCGGTCGGC CGCTCCGGGTCCTGGCCCCCCCGGGGGGGGCCCCCCCCC	120 180 240 300 360 420 480 540 600 660 720 960 1020 1140 1200 1140 1120 1150 1150 1150 1150 1168 1174 1180 1180
50 55 60 65 70	Coding seq 1 GGCATCCGAA GAGCTGCGCCCGGCCGGCTGTCT GGTCCTTGGCCACCCC GGAGGGGCCCCCGGCCGTTCCCGCACCCCAC CCGCACGTTCCCCACCCCCCCCCC	Nuence: 641 11	2299 21 1 COGGCCCCGC GCCCCCGCGCGCGCGCGCGCGCGCGCGCG	31 CCCCGCCTTGG CCCGCCTTGG CCCGCCACAGG CCCGCACAGG CCGCGCGCCCCAGG CCGCGCACCCCAGG CCGCCACCCCAGG CCGCCACCCCAGG CCGCCACCCCAGG CCGCCACCCAGG CCGCCACCCAGG CCGCCACCCAGG CCGCCACCCAGG CCGCCACCCAGG CCGCCACCCAGG CCACCCCAGG CCACCCCAGG CCACCCCAGG ACAGGCCCACCCA	CCCAACCCAG CACCGAGCGG CACCGAGCGGGGGGGGGG	CATGGTCTGG CATGGTCGGC CATGGTCGGCC CATGGTCGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	120 180 240 300 360 420 480 600 660 720 780 840 900 960 1140 1200 1320 1320 1440 1500 1620 1680 1740 1800 1800
50 55 60 65 70	Coding seq 1 GGCATCCGA GGCATCCGA GGCATCGGC GGCGGGGGGGGGG	Number: 641. 11	221 21 7 CCGGCCCGCC 6 CCTCCCGGC 7 CTCAGAGCCC 6 CCCTCCCCGC 8 CCCTCCCCGC 7 CCGGCCGGAC 7 CCGGCGGAC 8 GACTCCTCGCC 8 GACCACTCCA 8 GACCACTCA 9 ACCACTCA A CCACCACA A TGACCCTG A ATGACCCTG A ATGACCCTG A CTCTGACT C CACCAGGAC T CCGGACACTC C CACCAGGAC T CCCACCAGGAC C CCACCAGGAC C CCCACCAGGAC C C CCCACCAGGAC C C CCCACCAGGAC C C CCCACCAGGAC C C CCCACCAGGAC C C CCCACCAGGAC C C CCCACCAGGAC C C CCCACCAGGAC C C CCCACCAGGAC C C CCCACCAGGAC C C CCCACCAGGAC C C CCCACCAGGAC C C CCCACCAGGAC C C CCCACCAGGAC C C CCCACCAGGAC C C CCCACCAGGAC C C C CCCACCAGCAC C C C C C C C C C C C C C C C C C C	31 CCCGCCTTGC CCCGCACAGG GGCTCACTCC TCACTCCCTC GGCAGCGC GGGGGTCCA GGCACCCAC CCCCACCCAC CCCCCACCCAC CCCCCC	CCCAACCCAG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CAGGCAGC CACCGAGC CAGGCAGC CAGGCAGC CAGGCAGC CAGGCAGC CAGGCAGC CAGGCAGC CAGGCAGC CAGGCAGC CACCGAGAGC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCAAAC CACCCAAAC CACCCAAAC CACCAAACAAC	CONTROLLED	120 180 240 300 360 420 480 600 660 720 780 840 900 960 1020 1140 1200 1320 1320 1440 1500 1620 1680 1740 1860 1860 1980
50 55 60 65 70	Coding seq 1 GGCATCCGAA GAGCTGCCT GGGCGGCGGT GGGCGGCGGCT GGGCTGTCT GGGCAGCCAC TCCCTGCCAC GGAAGGGAGC CGGAAGGGAGC CGGAAGGGAGC CGGAAGGGAGC CGGAAGGGAGC CGGAAGGAGC GGCAGTACT GCTCCAGGACT GCTCAGGACT GCTCAGGACT GCTCAGGACT GGGAATT GGGAATT GGGAATT CGGAAAAGC GGAAAAGC GGAAAAGC GGAAAAGC GGAAAAGC GCAAAAGC GCAAAAGC GCAAAAGC CGACAAAAC CCAAACAC CAAAACAC CCAATTGGA CTACCCTGGC CCCTGGCC CCCCTGGCC CCCCCTGGCC CCCCCTGCC CCCCCCC CCCCCCC CCCCCCCC	Nuence: 641. 11	219 21 1 CCGGCCCCCC GCCCGCCCCCC GCCCCCCCCC GCCCCCC	31 CCCGCCTTGC CCCGCACAG GCCTCACTCC TCACTCCCTC GCCACCCG GCGCGTCCC GCCCACCC CCCCACCCG CTCCACCGG CTCCACCGG CTCCACCGG CTCCACCGG CTCCACCGG CTCCACCGG CTCCACCGG CTCCACCGG CTCCACCGG CTCCACCGG CTCCACCGG CTCCACCGG CACCCTACC CTCCACCGG CCCCTACC CTCCACCGG CCCCTACC CTCCACCGG CCCCTACC CTCCACCGG GGAGCACT CTCCACCGG GGACACCT ATATGATAT ATATGATAT ATATGATAT ATATGATAT ATATGATAT GGATCTGCAC GGACACCT CTCTCTCCACCGG GGACACCT CTCCACCGG GCACAGCT CTCCACCGG CCCACCGC CCCCTCCCACCG CCCCCTCCC CCCCCCCCC CCCCCCCCC CCCCCCCC	CCCAACCCAC CACCGAGGGG CACCGAGGGG CACCGAGGGGGG CACCGAGGGGGG CACCGAGGGGGGG CACCGAGGGGGGGG	CATCOLOGICAL CONTROL	120 180 240 300 360 420 480 660 720 840 960 1020 1140 1200 1150 1560 1680 1740 1860 1920 1980
50 55 60 65 70	Coding seq 1 GGCATCCGA GAGCTGCGC GGCGGGGGGGGGGGGGGG	Number: 641 11	2299 21 1 1 1 1 1 1 1 1 1 1	31 CCCGCCTTGC CCCGCCTTGC CCCGCACAG CCCGCACAG CCCGCACAG CCCGCCACCC CCGCCACCCAG CCCGCCACCC CCGCCACCC CCCCCCCC	CCCAACCCAG CACCGAGCGG CACCGAGCGGGGGGGGGG	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CGCTCCGAGT CGCTCTCCCCG CGCGGACATC CGCGACACATC CTTCGAAGCCCC TACAGGCTCCC TACAGGCTCCC TACAGGCTCCCC TACAGGCTCCCC TACAGGCTCCCC TACAGGCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	120 180 240 300 360 420 480 600 660 720 780 840 1020 1140 1200 1320 1380 1440 1500 1620 1680 1740 1800 1800 1800 1920 1980 2040
50 55 60 65 70	Coding seq 1 GGCATCCGA GGCATCCGA GGCATCCGA GGCATCGCA GGCAGCAGCA GGCAGCAGCA GGCAGCAGCA GGCAGCAGCA GGCAGCAGCA GGCAGCAGCA GGAAGGGAGCA GGAAGGGAGCA GCAGCAGCA GCAGCAGCA GCAGCAGCA GCAGCAGCA GCAGCAGCA ATAGTGA GCGCATGAG GCGCATGAG GCGCATAGA GCGCACA GATCAGAACT GCAACAG GCAATACT GCCAACAG GCAATACT GCCACACA GCAATACT CCCAGCAC CAGAATCC CAGCAGAT ACTGCT CCAGCAGAT ACTGGTT CCAGCAGAT ACTGGTT CCAGCAGAT ACTGGTT CCAGCAGAT ACTGGTT CCAGCAGAT ACTGGTT CCTGTC CAGCAGAT CCCTGTC CAGCAGAT ACTGGTT CCTCTC CAGCAGAT CCCTGTC CAGCAGAT CCCTGTC CAGCAGAT CCCTGTC CAGCAGAT CCCTGTC CAGCAGAT CCCTGTC CAGCAGAT CCCTGTC CAGCAGAT CCCTGTC CCCTGTC CCTGTC TGTC CCT CCT	Number: 641. 11	221 21 7 CCGGCCCGCC 6 CCTCCCGGC 7 CTCAGAGCCC 6 CCTCCCCGC 6 CCTCCCCGC 7 CCGCCGGCG 7 CCGGCGGGC 8 CGCCTGGAC 8 CGCCTGGAC 8 CGCCTGGAC 9 CGGCCGGAC 9 CGGCGGGCG 9 AGGAAGCGG 9 ACCAGTTGA 10 TATAAACGGT 10 TATAAACGAAG 10 TATAAAC	31 CCCGCCTTGC CCCGCCTTGC CCCGCCACAG GGCTCACTCC GGCACCGC GGCGCCCC AAAGGGACC CCCCCACCCA	CCCAACCCAC CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGC CACCCAAC CACC	CONTROLLED	120 180 240 300 360 420 480 600 660 720 780 840 900 960 1020 1140 1200 1320 1320 1440 1500 1680 1740 1880 1860 1980 1980 1980 1980 1980 1980 1980 198
50 55 60 65 70	Coding seq 1 GGCATCCGAA GAGCTGCCGC GGCGGCGGTGTCT GGTCCTGGCAGCCAC TCCCTGCCAG GGAGGGGGG CGGAGGGGGG CGGAGGGGGG CGGAGGGGGG CGGAGGGAG	Number: 641 11	.2299 21 1 1 1 1 1 2 2 2 2 1 2 2 2 2 2 3 3 5 5 5 5 6 6 6 7 7 7 7 7 7 7 7 7 7	31 CCCGCCTTGC CCCGCATACAG CCCCGCACAG CCCCGCACAG CCCGCACCCG CGGCGCTCCG CGCGCACCCG CCCCACCCG CCCCACCCG CCCCACCCG CTCCAACGGC CTCCAACGGC CTCCAACGGC CTCCAACGGC CTCCAACGGC CTCCAACGGC CTCCAACGGC CTCCAACGGC CACCTCCAC CACCTCCAC CACCTCCAC CACCTCCAC CACCTCCAC CACCCTACC CACCTCCAC CACCTCGACGG CACCTCGACG CACCTCGACGG CACCTCGACG CACCTCGACGG CCCCTCGACGG CCCCTCGACGG CCCCTCGACGG CCCCTCGACGG CCCCTCCACCG CCCCTCCACCG CCCCTCCACCG CCCCTCCACCG CCCCTCCACCG CCCCTCCACCG CCCCTCCACCG CCCCTCCACCG CCCCTCCACCG CCCCCTCCACCG CCCCCCCC CCCCTCCACCG CCCCCCCCC CCCCTCCACCG CCCCCCCCC CCCCTCCCACCG CCCCCCCC CCCCTCCCACCG CCCCCCCC CCCCCCCCC CCCCCCCCC CCCCCCC	CCCAACCCAC CACCGAGGGG CACCGAGGGGG CACCGGGGGGG CACCGGGGGGGG	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CGCTCCGAGT CGCTCTCCCCG CGCGGACATC CGCGACACATC CTTCGAAGCCCC TACAGGCTCCC TACAGGCTCCC TACAGGCTCCCC TACAGGCTCCCC TACAGGCTCCCC TACAGGCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	120 180 240 300 360 420 480 600 660 720 780 840 1020 1020 1140 1150 1620 1680 1740 1880 1890 1990 1990 1990 1990 1990 199
50 55 60 65 70	Coding seq 1 GGCATCCGA GGCATCCGA GGCATCCGA GGCATCGGCA GGCGGGGGG GGCAGCGGC GGCAGCGCA GGCAGCGGG GGCAGCGGG GGCAGCGGG GGCAGCGGG GGAAGGGGG CGGAAGGGGG CGGAAGGGAG GCGGTTGG CAAGAGGAG GCGCTTGGG GTCAGGAA CACGGACTTGG GTCAGGAA CTAGGAATGG GGGTTAGA GGGTTTGA GGGTTTGA GGGTTTGA GCGCTCGG CGACAAG GCACATCGC CCAGAGCG CCAGAGCG CCAGAGCG CCAGAGCG CCAGAGCG CCAGAGCG CCAGAGCG CCACATCGA CCACATCGC CCACATCGC CCACATCGC CCACATCGC CCACATCGC CCACATCGC CCACATCGC CCACATCC CCACATCC CCAC	Number: 641. 11 11 13 14 15 16 17 16 17 17 17 17 17 17 17	219 21 7 CCCGGCCCCCC 6 CCTCCCCCC 7 CCTCCCCCC 8 CCCTCCCCCC 8 CCCTCCCCCC 9 CCCCCCCCC 9 CCCCCCCCC 9 CCCCCCCC	31 CCCGCCTTGC CCCGCACACA GCCTCACTCC GGCAACAG GCCTCACTCC GGCAACCC GCCCCACCCA CCCCACCCAC ATGAGGGGCC TGAACCGC ATGAGGGGCC ATGAGGGAC ATGAGGGAC ATGAGGGAC ATGAGGAC ATGACGACA ATGACACA ATGACGACA ATGACGACA ATGACGACA ATGACGACA ATGACGACA ATGACGACA ATGACGACA ATGACGACA ATGACGACA ATGACGACA ATGACGACA ATGACGACA ATGACGACA ATGACACA	CCCAACCCAG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGCG CACCGAGG CACCGAGG CACCGAGG CACCGAGG CACCGAGG CACCGAGG CACCGAGG CACCGAGG CACCGAGG CACCGAGG CACCGAGG CACCGAGG CACCGAGG CACCGAGG CACCGAGG CACCGAGG CACCGAGG CACCGAGG CACCGAGG CACCGAGG CACCCCAGAG CACCCAAAC CACCCAAC CACCCA	i GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CCCTTCCCGG CCCTCGGTCCT CCCTCGGTCCT CCTTGGAAGGC TAGAGCTCCC CTTGGAAGGC CTTCGGACGC CTTCGGACGC CTTCGGACGC CTTCGGACGC CTTCGGACGC CTTCGGACGC CTTCGGACGC CTTCGGACGC CTTCGACGCT CGGGAAATCAT AATTGCCAA ATTCGGGGCCC CTGACTGGACCC CTGACTGGACCC CTGACTGGACCC CTGACTGACCC CTGACCCT CTGACTGACCC CTGACCCT CTGTGGACACGC CAAAAGTGA ATTCGGGGCCC CTGATGGAAA CTTCGGGTGG CAAAAGTGAC CTGACACAGG CTGACACAGG CTGACACAGG CTGACACAGG CTGACACAGG CTGACACAGG CTGACACAGG CTAAAGTTGACC CTGACACACG CTGACACAGG CTAAAGTTGACC CTGGCCCCC CAAACTGGTCC CAAACTGGTTC	120 180 240 300 360 420 480 540 600 660 720 780 840 1020 1140 1220 1380 1440 1500 1680 17560 1880 1880 1880 1980 2040 2160 2220

CCCTGCCACG TTTCGGGTCG CCCTGCACCC CCCACCCAGG CTCGCTTCTC TTCGAAGGGG 480

	CCCTGGACCA GAACAGACTG GAAACTGGGC AGCAAGCAGC CTGGAACCAC CTCAGACATC CTGGACTGGG AGGTGGAGGC AGAGCCCCCC AGGACAGGAG CAACTGTCTC AGGAAGAACA	2400 2460
	GAGGAAAACA TCACAAGCCA ATGGGGCTCA AAGACAAATC CCACATGTTC TCAAGGCCGT	2520
	TARGETTICAG TICTGGCCAG TEATTECETG ATTGGTATET GGAGACAGAA ACCTAATGGG	2580
5	AAGTGTTTAT TGTTCCTTTT CCTACAAAGG AAGCAGTCTC TGGAGGCCAG AAAGAAAAGC	2640
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25	Nucleic Acid			218			
	Coding seque		080 21	31	41	51	
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		151	

		1020
	CHOMINGH MIGGIGINGS CHICAGOSTIC MINORAGOSTIC INCIDENTIAL	1080
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		3480
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33	GTACACA	667
	(Inche)	
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	Nucleic Acid Accession #: Eos sequence	
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5		63 DNA Sequid Accession		7			
	1			31	41	51	
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	AAATTGAAAJ	AAAAAAA					1398
	Sea ID NO	: 64 DNA Sec	nuence				
35		cid Accessio					
	1	11	21	31	41	51	
	CCCACCACC	L CAGAAACTC	TATCTCARAGE	CAAAACAAC	CAAAACAAA	AAAGAAGAGA	60
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	CTCAGTCACA TTGACTGACG GGGACCAGGG CTTGTGTGGG TCGAGAGCGC CCTCATGGTG CTGGTGCTGT TGTGTGTAGG TCCCCTGGGG ACACAAGCAG GCGCCAATGG TATCTGGGCG	1860
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	TGGTGTGCAT CCAGCGCTTC GCACAGGCTC AGCAGCAGCT GCCGCTCGAG TCACTTGGGT	300
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	GGCAGGGGG CCCAGCACTG GGCCGCTCCT TCCTGCATGG ACCAGAGCTG GACAAGGGGC	420
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5		540
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	TGATCAATAC CAGTATCCTG TTGATTTTTA TCTTTATTGT ACTTCTCATC CACTTTGAGG	
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	TTARGITITE CAIMANGIG HAMAHING TTTATICAM HINGMANIG ATTAINTED	
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15	GCTGGTGTGA TCATTCCACC CAACTTGCCC CCTCTCCGT GTGTTGACCC ACCCAGCAC CTGCCTCCTG CITCTCAGAA TGTGTTTTAC ATTTATTTAA TAAACGATGT TATTTGAGCA TTTA	540 600 604
20	Seq ID NO: 78 DNA Sequence Nucleic Acid Accession #: Eos sequence	
20	1 11 21 31 41 51	
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	ATATTIAGIG CCICCTIGGI CITICIGIC CITITGATCI CIGIACACAC GAATACGITG TACTATCTAC AGATGACTAA TITAGITATC IGIGIGIAAC ACTICITITG AGITTATIGI	300 360
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40	CTTCAGATAG ATTATATCTG GAGTGAAGAA TCCTGCCACC TATGTATCTG GCATAGTATT	60
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-	TOCCONTOR TITABACTAC ATTAGATOTT TIBACCCAT CAATTATAGA AAGCCAAATC	1620 1680
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	THE CONTROL OF A CANADITY OF A CONTROL OF A	2040
75	TATTOCTOCC AAAGACAGAA GCCTCACTGC AAGCACTGCA TGGGCAAGCT TGGCTGTAGA	2100 2160
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	TECTICAL CONCERN CALLED A ACCORDANCE TOTAL CONCERN CONTRACT TOTAL CONCERN CONTRACT TOTAL CONCERN CONTRACT TOTAL CONCERN CONTRACT TOTAL CONCERN CONTRACT TOTAL CONCERN CONTRACT TOTAL CONCERN CONTRACT TOTAL CONCERN CONTRACT TOTAL CONCERN CONTRACT TOTAL CONCERN CONTRACT TOTAL CONCERN CONTRACT TOTAL CONCERN CONTRACT TOTAL CONTRACT CONTRACT CONTRACT TOTAL CONTRACT CONTRACT TOTAL CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT	360
	AGGTTGAGCA TCCTAATCCT GAAATCTGAA ATGCTCCAGA ATCTGAACCT TCTTGAGCAC	420
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	PENETRAL COMMUNICATION CONTROL TATACCCARGA CARCOCCACA ACCACCACAC	
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	ATCCTGATCC TGATCAAGCA CAGGCCTTCA CAGTGACATT TCACTGTGAC CCTGGCCCAG	1860
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	Adjustment districts districts of the same state	

		1980
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03		
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	The second secon	
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60	AAGAGGCAGA ACTGCTAACA GTGACAGGCC CTGCAGTCAG CAGCTGTGA TITTATTATGCAGAGAGAGT GATCTGGAAA ATGGGAAGAG CTGACTGCAC ATAACACCTT GGGGGAGGT TTGTTCAGTG CATCTCCTA CTCCTTGTAT ACCTCTGATG ACATGCAGAA GCTTAGGAAA TAAAACACAC TTGTAACATC ACAGGGTGCA AGTAAGTACA TGTGGATGCC AGTGTAGAAA TCTCCCAGTCC ATGGTTTCCT GGTGTTCCTA GAGTCCTATT AAAAAAAAA AAAAAAAA Seq ID NO: 85 DNA Sequence Nucleic Acid Accession #: NM_004861.1 Coding sequence: 204.1475 1 11 21 31 41 51	180 240 300 360 420 480 539 60 120 180 240 300 360 420
60 65 70	AAGAGGCAGA ACTGCTAACA GTGACAGGCC CTGCAGTCAG CAGCTGTGAG ATTATATTGC AGGGCAGACT GATCTGGAAA ATGGGAAGAG CTGACTGCCA ATAACACCTT GGGGGAGGT TTGTTCAGTG CATCTCCTA CTCCTTGTAT ACCTCTGATG ACATGCAGAA GCTTAGGAAA TAAAACACAC TTGTAACATC ACAGGGTGCA AGTAAGTACA TGTGGATGCC AGTGTAGAGA GAAGCGAAAG CTAGTTTCAT TTGCAAGAAT CCAAACAGAG TAACAGGCT TTGTCACTG TCTCCCAGTCC ATGGTTCCCT GGTGTTCCTA GAGTCCTATT AAAAAAAAA AAAAAAAA Seq ID NO: 85 DNA Sequence Nucleic Acid Accession #: NM_004861.1 Coding sequence: 2041475 1 11 21 31 41 51 GGCAGCCTGG GAGTTGGACG TGGCTCAGGC AGTGGGTAGA AAGGGGCAGC CAGGCACAGC CCGAGGGTCT CACTGGTGCA TCCGAGAGCT GAGTGGGTAGA AAGGGGCAGC CAGCCAGGG CCGAGGGTCT CACTGGTGCA TCCGAGGCT GGCTCTCAAG TAACTAGGAC TACAGGCATG TGCCACCAGG CCTGGTGTCT GAGATGCTGC CACCGCAGAA GAAGCCCTGG GAGTCCATGG CCTAAGGGCT GGGCTGGGG GGCTCTTCA CTAGTTCCT GCTGCTGGTT TACAGGCATG CCTAAGGGCT GGGCTGGGG GGCTCTTCA CTAGTTCCT GCTGCTGGTT TACTCCTATG CCGTGCCCC GCTGCATGC GGCCTCTCA CTAGTTCCT GCTGCTGGTT TACTCCTATG CCGTGCCCC ACCAGCACAC CAGGCAGGAG TCCGGCGGGG GAACATCAT TCTGCAGCACGC GCGCCGCGG GGGGGTGCC CTCCACCTGC ACCAGCCA GAGGCAGTGA TCCGGCCCA GCCTCCGGG GGGGGGGCC ACCGGGGGG CAACATCCTT TTCTTGAAGA CGCACAAGAC GGCCCGCAGC ACCCTGCTA	180 240 300 360 420 480 539 60 120 180 360 420 480
60	AAGAGGCAGA ACTGCTAACA GTGACAGGCC CTGCAGTCAG CAGCTGTGA TTTTTTTTTT	180 240 300 360 420 480 539 60 120 180 240 480 540
60 65 70	AAGAGGCAGA ACTGCTAACA GTGACAGGCC CTGCAGTCAG CAGCTGTGA TITTATTATGCAGAGAGAGT GATCTGGAAA ATGGGAAGAG CTGACTGCACA ATAACACCTT GGGGGAGGT TTGTTCAGTG CATCTCCTA CTCCTTGTAT ACCTCTGATG ACATGCAGAA GCTTAGGAAA TAAAACACAC TTGTAACATC ACAGGGTGCA AGTAAGTACA TGTGGATGCC AGTGTAGAAA GAAGCGAAAG CTAGTTTTCA TTGCAAGAAT CCAAACAGAG TAACAGGGT TTGTCACTAT TCTCCAGTCC ATGGTTCCCT GGTGTTCCTA GAGTCCTATT AAAAAAAAA AAAAAAAA Seq ID NO: 85 DNA Sequence Nucleic Acid Accession #: NM_004861.1 Coding sequence: 2041475 1 11 21 31 41 51	180 240 360 420 480 539 60 120 240 300 360 420 480 540
60 65 70	AAGAGGCAGA ACTGCTAACA GTGACAGGCC CTGCAGTCAG CAGCTGTGA TITATTATGAC AGGGCAGACT GATCTGGAAA ATGGGAAGAG CTGACTGCCA ATAACACCTT GGGGGAGGT TTGTTCAGTG CATCTCCTA CTCCTTGTAT ACCTCTGATG ACATGCAGAA GCTTAGGAAA GAAGCGAAAG CTGATTTCA TTGCAAGAAT CCAAACAGAG TAACAGGCT TTGTCACTG GAGCGAAAG CTAGTTTTCA TTGCAAGAAT CCAAACAGAG TAACAGGGT TTGTCACTG TCTCCAGTCC ATGGTTCCCT GGTGTTCCTA GAGTCCTATT AAAAAAAAA AAAAAAAA SEQ ID NO: 85 DNA SEQUENCE Nucleic Acid Accession #: NM_004861.1 Coding sequence: 2041475 1 11 21 31 41 51	180 240 300 360 420 480 539 60 120 180 240 360 420 540 660
60 65 70	AGGGCAGA ACTGCTAACA GTGACAGGCC CTGCAGTCAG CAGCTGTGA TTTTATTGTGAGAAAAAAAAAA	60 120 120 120 120 120 120 140 300 420 420 480 539
60 65 70 75	AAGAGGCAGA ACTGCTAACA GTGACAGGCC CTGCAGTCAG CAGCTGTGA TTTTTTTTTT	180 240 300 360 420 539 60 120 180 360 420 480 540 660 720 780
60 65 70	AAGAGGCAGA ACTGCTAACA GTGACAGGCC CTGCAGTCAG CAGCTGTGA TTATATGCA AGGGCAGACT GATCTGGAAA ATGGGAAGAG CTGACTGCCA ATAAACACCT GGGGGAGGT TTGTTCAGTG CATCTCCTA CTCCTTGTAT ACCTCTGATG ACATGCAGAA GCTTAGGAAA GAAGCGAAAG CTGATTTCA TTGCAAGAAT CCAAACAGAG TAACAGGCT TTGTCACTG TTCTCCAGTCC ATGGTTTCCT GGTGTTCCTA GAGTCCTATT AAAAAAAAA AAAAAAAA Seq ID NO: 85 DNA Sequence Nucleic Acid Accession 8: NM_004861.1 Coding sequence: 2041475 1 11 21 31 41 51	180 240 300 360 420 480 539 60 120 180 240 360 420 540 600 720 780 840
60 65 70 75	AGGGCAGA ACTGCTAACA GTGACAGGCC CTGCAGTCAG CAGCTGTGA TTATTATGC AGGGCAGACT GATCTGGAAA ATGGGAAGAG GTGACTGCCA ATAACACCTT GGGGGAGGT TTGTTCAGTG CATCTCCTA CTCCTTGTAT ACCTCTGATG ACATGCAGAA GCTTAGGAAA GAAGCGAAAG CTAGTTTTCA TTGCAGGAAT CCAAACAGG TAACAGGCT TTGTCACTA TCTCCAGTCC ATGGTTCCCT GGTGTTCCTA GAGTCCTATT AAAAAAAAA AAAAAAAA Seq ID NO: 85 DNA Sequence Nucleic Acid Accession #: NM_004861.1 Coding sequence: 2041475 1 11 21 31 41 51	180 240 300 360 420 480 539 60 120 180 360 420 480 540 660 720 780 890
60 65 70 75	AGGGCAGA ACTGCTAACA GTGACAGGCC CTGCAGTCAG CAGCTGTGA TTATTATGC AGGGCAGACT GATCTGGAAA ATGGGAAGAG GTGACTGCCA ATAACACCTT GGGGGAGGT TTGTTCAGTG CATCTCCTA CTCCTTGTAT ACCTCTGATG ACATGCAGAA GCTTAGGAAA GAAGCGAAAG CTAGTTTTCA TTGCAGGAAT CCAAACAGG TAACAGGCT TTGTCACTA TCTCCAGTCC ATGGTTCCCT GGTGTTCCTA GAGTCCTATT AAAAAAAAA AAAAAAAA Seq ID NO: 85 DNA Sequence Nucleic Acid Accession #: NM_004861.1 Coding sequence: 2041475 1 11 21 31 41 51	180 240 300 360 420 480 539 60 120 180 360 420 480 540 660 720 780 890
60 65 70 75	AAGAGGCAGA ACTGCTAACA GTGACAGGCC CTGCAGTCAG CAGCTGTGA TTTTTTTTTT	60 120 180 240 480 539 60 120 180 240 300 360 420 420 420 420 480 540 600 720 780 900 900 9102
60 65 70 75	AGGGCAGA ACTGCTAACA GTGACAGGCC CTGCAGTCAG CAGCTGTGA TTATTATGC AGGGCAGACT GATCTGGAAA ATGGGAAGAG GTGACTGCCA ATAACACCTT GGGGGAGGT TTGTTCAGTG CATCTCCTA CTCCTTGTAT ACCTCTGATG ACATGCAGAA GCTTAGGAAA GAAGCGAAAG CTAGTTTTCA TTGCAGGAAT CCAAACAGG TAACAGGCT TTGTCACTA TCTCCAGTCC ATGGTTCCCT GGTGTTCCTA GAGTCCTATT AAAAAAAAA AAAAAAAA Seq ID NO: 85 DNA Sequence Nucleic Acid Accession #: NM_004861.1 Coding sequence: 2041475 1 11 21 31 41 51	60 120 180 240 480 539 60 120 180 240 360 420 420 420 420 420 420 420 420 420 42

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	CONCERNITY REGENERATE GARGETTEG GGCGGGAGCG CATGGCCCGC GAGGTGGCCG	1200
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)	TCCTGGGCTA CAACCTCAAG AAGAGCATCG GGCAGCGGCA CGCGCAGCTC TGCCGGCGCA TGCTCACGCC CGAGATCCAG TACCTGATGG ACCTCGGCGC CAACCTGTGG GTCACCAAGC	1440
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25	CCTGCAGCCA GTGCAGATGC AGACGTGCCG ACCTCAGGAG TGGCACCAGA CGGGATCCCA	2820
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	CTGTGGGGTG GGGAGCACAG GGACCCGAGA TGGGGGGGCGC ATTGATGGCA TTCCTCTTCT	2940 3000
	CCACATCTGC TOSTTCTTGC CGAGGGTGCA GTGGTGGGGT GGAAGCCCTG TCACCCCACC CCAGGCCACC CTCTCCCAGA GGACGCCATC TCCCTTACTG TTGCTGGGAG CCTCGCCCTT	3060
30	TGTCCCAACT GGGTAGAGCC CCCAGGTGCT GTTTGCTCAG GAGGCTGCTG TGGGGGTGCT	3120
	TTCCTCAGCC TCTGGCCCTC TTGGCTCAGA TTCAATCAAA TGTTGCTTCC CTCTCCTGTC	3180
	TTTCCCACTG GAGCCGCCCA AGCTTGTAGG TGGGTGGTGT GCATAGGCCA CGTGTGCCCC	3240
	ACATATGCAG GOGGTGCCCC ACACAGCTAG AGCGGCCAGG AGAGCGCCTC CTAACCACCA GCCGTTCCTG ATCTCAGGAG CCTTGAAGGG CTGGGCTCTT GCCTTCCTGG AGTAAATATT	3300 3360
35	GCCACAGATT TCATTIGAGA GAACTCAGCC CCCTGGTCTA AGCTGGACTT ACCTCTGTGG	3420
75	ATTCTGAAAT TAAAGAAGTG AGTTGCCAAA AAAAAAAAAA	3464
	Seq ID NO: 92 DNA Sequence	
40	Nucleic Acid Accession #: BC029071.1 Coding sequence:771	
	. 1 11 21 31 41 51	
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	60
	COGACGCOTO GOCGGACGCO TOGGCOGCTO AGGACTOGGG TGATGATGCC ACTGGCAGAA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACGG AGTGGGCCTG CATTCTGCGG	120
45	ACCARGACY CYRCGURA GURGUCUACO TTACTGATGG TCAGAGCATC CAGAAGAAGT	180
1.5	GGCAAGACTT CAGCTGTCCT CAAAGCAGGA AGACAGAGTG TTTCTGGCAG AAAGAACAGC	
	GGCAGACTI CAGCIGICCI CAAAGCAGGA MGACAGAGTO TITELGGGGG	240
	ACAAGCAAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAG AGGACACCCC	300
	ACAAGCAAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGAGAG AGGACACCCC CTCCACCCA GACATAGGAA AGGAGTCGAC CTGCGCACCA GGGGCAGGAC ACGTGGCTGG	300 360
50	ACAAGCAAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAG AGGACACCCC CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGGGCACCA GGGGCAGGAC ACGTGGCTGG CTCCAGACGC TGGCCCGAT GTCGCGAGG ACTCGCGGGC CGGTAGAGGC GGGCGGGGG	300
50	ACAGGAAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAG AGGACACCCC CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGGCGACCA GGGGAGGAC AGGTGGGTGG GTGCAGAGCG TGGCCCGGAT GTCGCCGAGG ACTCGCGCGC CGGTAGAGC CGCGCGGGGG GCGGGGGGG CGGCCGGGG AGGAGAGCA GGTCAGGCC CCTTCCCACC ACCTCCCGCC GCTCGAGCGGC CGGCCGCGCG AGGAGAGCAC GGTCAGGCA CTCCTAGAGG ACTGCGTCTG GCTCGATCGGCC CGCCGCCGCC GGAGAGGCCC GGACAGGTGA CTCCTAGAGG ACTGCGTCTG	300 360 420 480 540
50	ACAGCAAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAG AGGACACCCC CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGGGCACCA GGGGCAGGAC ACGTGGTGG GTGCAGAGGC TGGCCGGAT GTCGCGGAGG ACTCGCGGGC CGGTAGAGGG CGCGCGGGG GCGGCGGGG CGGCGCGGC AGGAGACGCA GGTCACGCCC CCTTCCCACC ACTCCCGGC GCCGACGGGG CGGCGCGCGC CAGGAGCCCG GGACAGGTGA CTCCTAGAGG ACTGGCTCT CCCTTCCCC GGCGGGAGTC CTTCTTCGC GGCCTCTGCC GCCCCCTGGG TCCCCTCCTG	300 360 420 480 540 600
50	ACAGCAMA ATCTGGTANC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAG AGGACACCCC CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGGGCACCA GGGGCAGGAC ACTGGCTGG GTGCAGAGCC TGCCCGGAT GTCCCGGAGG ACTCGCGCC CGTACAGAGC CGCGCGGGC GCGCGGGGG CGGCGGGGC AGGAGACGCA GGTCACGCCC CCTTCCCACC ACCTCCCGCC GCCACGGGG CGCGCGGGCC GAGGAGCCC GGACAGGTGA CTCCTAGAGG ACTGCGTCTG GCCTTCCCCC GGCGGGAGTC CCTTCTTCGC GGCCTCTGCC GCCCCCTGCC TCCCCTTGC GGCTTCCCAG AGTCTGACTC AGCCAAGCCG GCATCGCTTC GCCTCCTACA ACACACCCCC	300 360 420 480 540 600 660
	ACAGGAAAA ANCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAA AGGACACCCC CTCACCCCA GACATAGGAA AGCAGTCCAC CTGGCGACCA GGGGAGGAC AGGTGGCTGG GTGCAGAGCG TGGCCCGGAT GTCGCCGAGG ACTGCGCGC CGGTAGAGCG CGCGGCGGG GCGGCGGGG CGGCGCGGG AGGAGAGCA GGTCACGCCC CCTTCCCACC ACCTCCCGCC GCCACGGGC CGGCGCGCG CAGGAGCCCG GGACAGGTGA CTCCTAGAGG ACTGGTCTG GCCTCCCCC GGCGGGAGTC CCTTCTTCGC GGCCTCTGCC GCCCCTGCG TCCCCTCCTG GCCTCCCAGA GATCTGACTC AGCCAAGCCG GCACCGCTTA TGCCCTTCAA TACCCACCC	300 360 420 480 540 600
50 55	ACAGCAAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAG AGGACACCCC CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGGGCACCA GGGGCAGGAC ACGTGGTGG GTGCAGAGACG CGGCGCGGCG	300 360 420 480 540 600 660 720 780 840
	ACAGGAAAA ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAA AGGACACCCC CTCACCCCA GACATAGGAA AGCAGTCCAC CCGCCCACCA GGGGAGGAGA AGGACACCCC GTCCAGACGC TGCCCCGAT GTCCCCGAGG ACTCGCCGCC CGGTAGAGGC CGCGCGGGG GCGGCGGGG CGGCGCGGC GAGGAGAGCA GGTCACGCCC CCTTCCCACC ACCTCCCGCC GCCTCCCCC GGGGGGAGTC CCTTCTTCGC GGCCTCTGCC GCCCCTGCG TCCCCTCCTG GCCTTCCCAG AGTCTGACTC AGCCAACCCC GCATCGCTTC GCCTCCTACA ACACACCCCC CCGCTGTCAT CCCCGGCGCT CGGCGGGTT GGGCCAACGC GCCCTTAATTA AGACCCCCC CCCCGTTCAT CCCCGGCCCT CTTCGCCACC CCCACCCCAC	300 360 420 480 540 600 660 720 780 840 900
	ACAGGCAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAG AGGACACCCC CTCCACCCCA GACATAGGAA AGGAGTCCAC CTGGCGACA GGGGAGGAGA AGGAGCACCCC CTCCACCCCA GACATAGGAA AGCAGCCCCC CTGGCGACCA GGGGAGGAGA AGGGGGGGGGG	300 360 420 480 540 600 660 720 780 840 900
55	ACAGCAAAG ATCTGGTAAC CTTAGGTGC TCCAGTTTGA GGGAGGAGAG AGGACACCCC CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGGGCACCA GGGGCAGGAC ACGTGGTGG GTGCAGAGGC TGGCCGCGGA GTCCGCGAGGA ACTGGCTGG GCGGGGGGG CGGCGCGGC AGGAGAGGCA GGTCAGGGC CCTTCCCACC ACTCCCGCC GCCGCGGGGG CGGCGCGCGC CAGGAGCCCG GGACAGGTGA CTCCTAGAGG ACTGGCTCT CGCTTCCCAG GCGCCGCGCC CAGGAGCCCG GGACAGGTGA CTCCTAGAGG ACTGGCTCT GGCTTCCGAG AGTCTGACTC AGCCAAGCCG GCACCGCTTC GCCCCCTGCG TCCCCTCTG AGGGGAGAA GAAATTACAG GATTGCAGG GCACCGCTTA TGCCTCTAA TTACCCACCG CCCCTGTCAT CCCCGGCCT CCGCGGCGCT GGGCCAAGGC GCCGTAATTA AGACCCGCT CCCCGGTCCC GGAACCCTCC CTTCGCCACC CTCCACCCAC CACCTCCCG GTCCCCAGGA CCACTGGCTG CAAACTCCTG CCGCCCTCTG GGACTGCCCC TCAGTCCCAG GAGAGCTAAC AGGCCTCACT GGGGCAAGA CTTCGGGAGA CCGAAGCCCG CCCTTCCACT CCCCTAAACC TACAGTCCTG GAAGGTCTCT GCTGGAAGAA ACTGGGAGAG TCGGGAGAGG CCCAAGGACCT TACAGTCCTG GAAGGTCTCT GCTGGAAGAA ACTGGGAGAG TCGGGAGAGC CCCCTAAACC TACAGTCCTG GAAGGTCTCT GCTGGAAGAA ACTGGGAGAG TCGGGAGAGC CCCCAGGACCT	300 360 420 480 540 600 660 720 780 840 900
	ACAGGCAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAG AGGACACCCC CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGGCGACCA GGGGAGGAG AGGAGCGCGG GTGCAGGAGG TGCGCGGAG AGGAGGAGGA AGGAGCACGCG GCGGGGGGG GGGGGGGG	300 360 420 480 540 600 660 720 780 840 900 960 1020 1140
55	ACAGGCAMA ATCTGGTANC CTTAGGTGCC TCCAGTTTGA GGGAGGAGA AGGACACCCC CTCACCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGAGGAC AGGTGGTGG GTGCAGAGCG TGGCCCGGAT GTGCCGGAGG ACTGCGCGCAC GGGGAGGAC AGGTGGCGGG GCGCGGGGG CGGCGCGGG AGGAGAGCAC GGTCACGCCC CCTTCCCACC ACCTCCCGCC GCCCACGGGG CGGCGCGCG AGGAGACGCC GGTCAGGCAC CCTCCTACC ACCTCCCGCC GCCTCCCCC GGCGGAGTC CCTTCTTCGC GGCCTCTGCC GCCCCTCGGC TCCCCTCCC GGCTTCCAGA AGTCTGACTC AGCCAACCCC GCATGGCTTC GCCTCTACA ACACACCCCG CCGCTGTCAT CGCGGGGCT CGGCGCGCT GGGCCACGC GCCCTAATTA AGACGCGCT CCCCGGTCCC GGAACCCTCC CTTCGCCACC CTCCACCAC CCACCTCCGC GTCCCAGGA CCACTGGCTG CCAACTCCTG CTCGCCACC TCCACCCCC CCACCTCCGC GGAGACGTA AGAGGCACCAC GAAGCCTC GCTGGAAGAC ACTGGCAGA CTCCAGACCGC ATTCCTTG CAGAAACACT GCTGGAAGAC ACTGGCAGA GGGGGGGCCCCC ATTCCTCA CCAGAAACACT GAGGTCTAT GGAAAGTTAG CCTTCAGTCG AAGCCCCCA GCGGAACCTC CTCGAACCCC TCAGTCCCC TCAGTCCCC ATTCCCTCA GCAGAACCAT GAGGCCGTTAT GGAAAGTTAG CCTTCAGTCG AAGCCCCCA GCGGAACCT CCCAGACCCC TCCACCAC CCCCTCCACCAC CCCCTCCACCAC ACTCCCCCACAACCCCC CCCCACACCCCC TCAGTCCCCC AGGACCTAACCCC ACTCCCCCACACACCCCC CCCCCACCAC CCCCTCCACCAC CCCCTCAAACCCC ACTCCCCCCACACCCCC CCCCACACCCCCCCCCC	300 360 420 480 540 600 660 720 780 840 900 960 1020 1080 1140 1200
55	ACAGGCAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAG AGGACACCCC CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGGCGACCA GGGGAGGAGA AGGGACACCCC CTCCACCCCA GGGCAGGAG AGGGAGGAGGA GGTGGCTGG GGGGAGGAGGA GGGGCGGGGGGGGAGGAGGAGAGA GGGCAGGGAGAGAGA	300 360 420 480 540 600 660 720 780 840 900 960 1020 1140 1200 1260
55	ACAGGCAAG ATCTGGTAAC CCTAGGTGC TCCAGTTTGA GGGAGGAGAG AGGACACCCC TCCACCCCA GACATAGGAA AGCAGTCCAC CTGGCGACCA GGGGAGGAC AGTGGCTGG GTGCAGAGCG TGGCCCGGAT GTCGCCGAGG ACTCGCGCCCC GGGGAGGAC AGGTGCGCGG GCGCGGGGG CGGCGCGGG AGGAGAGCA GGTCACGCC CCTTCCCACC ACCTCCCGCC GCCACGGGG CGGCGCGCG AGGAGACGCA GGTCACGCC CCTTCCCACC ACCTCCCGCC GCCTCCCCC GGCGGAGTC CCTTCTTCGC GGCCTCTGCC GCCCCCTGCG TCCCCTCGG AGGCGAGAA GAATTACAG AGTTGCAGGG GCACGGCTAA TGGGCTCTAA TAACCCACCC CCGCTGTCAT CCCCGGCGCT CCGCGGGCT GGGCCACGC GCCGTAATTA AGACCCCGC CCCCGTCCC GGAACCTCC CTTCGCCACC CCCCACCAC CCACCTCCGG GACCCGCTA AGGCCTACT GGGGCCAGGA CTTCGGCAGC CCCTCCACCAC CCACCTCCGG GACCCTCTAACC AGGCCTCACT GGGGCCAGGA CTTCGGCAGA CCCAACTCCC GAACCTCCC GAACCTCCT GCGCGCGTTAATTA AGACGCGGCT TACAGTCCTG GAAGCTCTC CTTGGCAAC CCACTCCGC GCACCTCCCAC GAGACCTG TACAGTCCTG GAAGCTCTC GCTGGAAGAA CTGGGAGGA TGCGCAGGAC ATTCGTTAA CAGAAACAT GAGGTCTAT GGAAGCTGA TGGGAGGG CCAGGACCT AAAGGCACC AGGAACCTC CCAGACCCG TCCTTTAACCA GGGACGGACA AGTCCCCCA GCCAGAACTC CCAGACCCG TCCTTTAACA GTGGCTTTAT GAGGACGACA AGCGACCCA GCCAGAACTC CCAGACCCG TCCTTTAACA GTGGCTTTAT GAGGACGGA AGCGCCA GCCAGAACTC CCAGACCCG TCCTTTAACA GTGGCTTTAT GAGGACGACA AGGACCCAC CCCACTCCGCG GGGAAATTAC CTTCTGCCAC AGAAAGGGAA CAGGAACGGA AGCGCCAG CCCAGACCTC CCAGACCCGC TCCTTTAACA GTGGCTTTAT GAGGACGAC ACGACCTCC TCCCCTGCG GGGAAATTAC CTTCTGCCAC AGAAAGGGAA CAGGAACGGA AGCGACCCACCAC CCAGACCCGC TCCTTTAACA GTGGCTTTAT GAGGACAGA ACGAACCGG AGACCTC CCAGACCCGC TCCTTTAACA GTGGCTTTAT GAGGACAGACACGC ACGAACCAGA AGAAAGGTGA CATCCCCGCC ACAGACCAGA AGCACACCGC TCCTTTAACACAGCCCC CTATAGGGAA CATCCCCCCCC ACAGACCAGA AGACACACACACACACACACACCACC CCACACCCCCCCC	300 360 420 480 540 600 660 720 780 840 900 960 1020 1140 1200 1260
55	ACAGGCAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAG AGGACACCCC CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGGCGACCAC GGGGAGGAGA AGGGGGGGGGG	300 360 420 480 540 600 660 720 780 840 900 900 900 1020 1140 1220 1320 1340
55	ACAGGCAAGA ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAG AGGACACCCC CTCCACCCCA GACATAGGAA AGGAGTCCAC CTGGCGCACA GGGGAGGAG AGGGGGGGGGG	300 360 420 480 540 600 660 720 840 900 1020 1020 1140 1200 1320 1380 1440
55	ACAGGCAAG ATCTGGTAAC CCTAGGTGC TCCAGTTTGA GGGAGGAGAG AGGACACCCC TCCACCCCA GACATAGGAA AGCAGTCCAC CCTGCGCACCA GGGGAGGAC AGTGGCTGG GTGCAGAGCG TGGCCCGAG GTCGCCGAGG ACTGCGCGCG CGGTAGAGG CGGGGGGGG GCGGGGGGG CGGGCGCGG AGGAGAGCA GGTCACGCC CCTTCCCACC ACCTCCCGCC GCCACGGGG CGGCGCGCG AGGAGACGCA GGTCACGCC CCTTCCCACC ACCTCCCGC GCCTCCCCC GGCGGGAGTC CCTTCTTCGC GGCCTCTGCC GCCCCTCGG TCCCCTCGG AGGCGAGAA GAATTACAG AGTTGCAGGG GCACGGCTAA TGGGCTCTAA TTACCCACCG CCGCTGTCAT CCCCGGCGCT CCGCGGGCT GGGCCACGC CCCTCTCAA ACAACCCCG CCGCTGCAT CCCCGGGCCT CCTCGCCACC CCCCACCAC CCACCTCCGG GACCCGTAA AGGCCTCACT GGGGCCAGAA CTTGGCCAC CCCCACCAC CCACCTCCGG GACCCTATA AGGCCTCACT GGGGCCAGGA CTTGGGAGAG ACTGGCAGG CCCTTCCACT CCCCTAAACC ATTCGTTCA CAGAAACAT GAGGTCTTT GGAAGTTAG CCTTCAGTG GAGGATGGC AGGCCCCA GGGCAGCAC TCCCCACCAC CCACCTCCGC CAGGAACCCG ACGGAACCT CCACACACCAC CCACTCCCAC CCACTCCCCG AAGGCCAC AGGACACCC CCACACACCC CCACTCCCAC CCACTCCCCG GAGGCTTAA ATTCGTTGA CAGAAACAT GAGGTCTAT GGAAGCTGA CCGCAGGAA ACGGAAGCGA AGTCCGCCA GCGAGAACT CCAGACCGC TCCTTAACACGC CCACTAGGGGA CCTAAGCCGC CCAGGACCT CCCCACACCCC TCCTCTCACCAC CCACCCCCCCC	300 360 420 480 540 600 660 720 840 900 1020 1080 1140 1260 1320 1380 1440 1560
55 60 65	ACAGGCAAGA ATCTGGTAAC CCTAGGTGCC TCCACTTTGA GGGAGGAGAG AGGACACCCC CTCCACCCCA GACATAGGAA AGCACTCCCA CTCCACCCCA GGGCAGGAG ACGTGGCTGG GTGCAGGAGG CGGGGGGGG GTGCAGGAGG CGGGGGGGG GGGGGGGGG GGGGGGGGG GGGGGGG	300 360 420 480 540 600 650 720 780 840 900 1020 1080 1140 1260 1320 1380 1500 1500
55	ACAGGCAAGA ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAGA AGGACACCCC CTCACCCCA GACATAGGAA AGCAGTCCAC CCTGCGCACCA GGGGAGGAC AGTGGCTGG GTGCAGAGGC TGGCCCGGAT GTCGCGGAGG ACTGCGCGCGC GGGGAGGAC AGTGGCTGG GCGCGGGGG CGGGCGCGG AGGAGAGCA GGTCACGCC CCTTCCCACC ACCTCCCGCC GCCACGGG CGGCGCGCG AGGAGACCGC GGTCAGCGC CCTTCCCACC ACCTCCCGCC GCCTCCCCC GGCGGGAGTC CCTTCTTCGC GGCCTCTGCC GCCCCTGCG TCCCCTCGC GGCTTCCAGA GATTTACAG AGTTGCAGGG GCACGGCTAA TGGGCTTACA ACACACCCCG CCGCTGTCAT CCCCGGCGCT CCGCGGGGCT GGGCCAACGC GCCGTAAATTA AGACGCCGCT CCCCGGTCCC GGAACCCTCC CTTCGCCACC CCACCCAC CCACCTCCGG GTCCCCAGGA CCACTGGCTG GGAACCTTCC CTTCGCCACC CCACCCAC CCACCTCCGG GTCCCCAGGA AGGCCACTGCT GGAGCCTTC GCTCGAAGGA AGTTCGTTGA CAGAAACAT GCGCCTTTT GGAAGCCG CCCTTCACT CCCCTAAACC AATTCGTTGA CAGAAACAT GAGGTCTAT TGGGATTAG GGCACGGAGA AGGGAAGGGA	300 360 420 480 540 650 660 720 780 840 900 960 1080 1140 1200 1320 1440 1550 1620 1620 1740
55 60 65	ACAGACAMA ATCTGATANC CCTAGGTECC TCCAGTTTGA GGAGGAGAG AGGACACCCC CTCCACCCCA GACATAGGAA AGCAGCTCCAC CTCCACCCCA GGGCAGGAG AGGAGGAGGA GGTGGAGGAG GGGCAGGAG GGGCAGGAG GGCCAGGAG GGCCAGGAG AGCAGCACCAC CCCACCCA	300 360 420 480 540 600 660 720 780 840 900 1020 1140 1220 1320 1350 1440 1500 1680 1680
55 60 65	ACAGGACAGA ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGA AGGACACCCC CTCACCCCA GACATAGAA AGCAGTCCAC CTGCGCACCA GGGGAGGAC AGTGGCTGG GTGCAGAGCC TGCCCGGAG GTCCAGGCC GGGCAGGAC AGTGCCGGCG GGGAGAGGAC GGGCAGGCGC GGCGAGGGGC GGCGAGGGCG GGCGAGGGCG GGCAGGGGCG GGCAGGGGCG CGCCACCGCC GGCCGCGCGCG	300 360 420 480 540 600 660 720 840 900 1020 1020 1140 1220 1380 1440 1550 1560 1680 1740 1860
55 60 65 70	ACAGGCAAGA ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAGA AGGACACCCC CTCCACCCCA GACATAGGAA AGCAGTCCAC CCTGCGCACCA GGGGAGGAC AGTGGCTGG GTGCAGAGGC TGGCCCGGAT GTCGCGGAGG ACTGGCGCACC GGGGAGGAC AGGTGCGGGG GCGGGGGG CGGGCGCGG AGGAGAGCCA GGTCACGCCC CCTTCCCACC ACCTCCCGCC GCCACGGGC CGGCGCGCG CAGGAGACCCTC GGCCACGGC CCCCCTCCGC GCCCACGGC CGCGCGCGCG CAGGAGCCCTC GGCCACGGC CCCCCTCCCCC CGCCGCTGCT CCCCTCCCCC GCCTGTCAT CCCCGGCCCC CGCCGCGCG GCACAGCCC GCCCTACAC ACACACCCCC CCCCGTCCAT CCCCGGCCCT CCGCCGCCCT GGCCAACGC GCCGTAAATA AGACACCCCC CCCCGGTCCC GGAACCCTC CTTCGCCACC CTCCACCAC CCACCTCCGG GTCCCCAGGA CCCACTGGCT GCAACTCCT CGCCCCTCC GGACTGCCC TCAGTCCCAC AGGCCTCACT GGGGCAACGC GCCGTAATA AGACGCGCT TACAGTCCTG GAACACTCT GCCCCCTCC GGACTGCCC TCAGTCCCAC AGGCCTCACT GGGGCAACAC CTCGCACCAC CCACCTCCGG GACGCCTAAACC TACAGTCCTG GAACACTC GCTGGAAGAG ACTGGGAGG CCCTTCACT CCCCTAAACC TATCCTTGA CAGAACACT GAGGTCTAT GGAAAGTTAG CCTTCAGTG GAGGAGCAC AATCCGCCCA GCGGAACCT CCAGACCCC TCGTTAACA GTGCCTTAT GAGGAGGAC AATCCGCCCA GCGAACACT CCAGACCCC TCGTTAACA GTGCCTTAT GGAAGGTGG CACGGAGCCCCC CCCCACCCC TCGTTAACA GTGCCTTAT GAGGAGGGG CAGGACCCCCC CCCCACCCC TCGTTAACA GTGCCTTAT GAGGAGGGG CCAGGACCCCCCC CCCCACCCC TCGTTAACA GTGCCTTAT GAGGAGGGG CCAGGACCTC CCCCACCCC TCGTTAACA GTGCCTTAT GAGGAGGGG CCAGGACCTC CCCCACCCC TCGTTAACA GTGCTTAT GAGGACGGG CCAGGACCTC CCCCACCCC TCGTTAACA GTGCCTTAT GAGGACGGG CAGGACCTC CCCCTCCCCC CATCTCAGGA AGAAAGGTGA CACCCCCCCC CCCAACCCC CCCCCCCCCCCCC CCCAGACCCC CTTCCCCCCC CAGGACACCC CCAAACCAG GCCAGGAG GCCCAGCC TCCCAGACCAC TCCCCCCCC CAAACCAG GCTCAGAGCT CCCCTCTAT AGGAATTA AGGGGTAGG AGGCCCTAAGGGA AGCAAGACAG GCCTAGAGCT CCCCCCCCC TCCAGGACA TCCCCCCCCCC	300 360 360 420 480 540 600 660 720 780 840 900 900 1080 1140 1260 1320 1480 1560 1620 1680 1740 1800 1800
55 60 65	ACAGGACAGA ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGAGGAGAGA AGGACACCCC CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGAGGAC AGTGGGTGG GTGCAGAGGC TGCCCGGAT GTGCCGGAG ACTCGCGCCC CGGGAGAGA AGGAGCGGG GCGGGGGG CGGCGCGGG AGGAGAGGCA GGTCACGCCC CCTTCCCACC ACCTCCCGC GCCCACGGGG CGGCGCGCG AGGAGAGCCA GGTCACGCCC CCTTCCCACC ACCTCCCGC GCCCACGGGG CGGCGCGCG AGGAGACCCC GGACAGGTGA CTCCTAGAGG ACTGCGTCT GGCTTCCCAC GGCGGGAGTC CCTTCTTCGC GGCCTCTGCC GCCCCCTGCG TCCCCTCCC GGCTGCAAA GAAATTACAG GATTGCAGGG GCACGGGTAA TGGGCTCTAA ACACACCCG ACGCGTGCAT CCGCGGGGCT CCGCGGGGCT GGGCCACGG GCCCATAATTA AGACGCGGC CCCCTGCCC GGAACCCCC CTTCGCCACC CTCCACCAC CCACTCCGG GTCCCCAGA ACACCCCG ACACTCCTG GGAACCCTCC CTTCGCCACC CTCCACCAC CCACTCCGG GTCCCCAGA AGCGCACACT GGGGCCAGAA CTTCGGCAGA CTCCAGAGCGG CCTTCCATC ACAGCCCG GAACCCTCC GCTGGAAGAA ACTGGCAGAG TGGGGGGGC CCAGGGACT ATTCGTTGA CAGAAACACT GCTGGAAGAA ACTGGCAGAG TGGGGGGG CCAGGGACT AAAGGCACG AGGAACTC CCAGACCCG TCCTTAAACA AGGCCCCAC ACCAGAACTC GCTGGAAGAA ACTGGCAGAG TGGGGAGGG CCAGGGACT AGGCCCCAC ACCAGAACTC CAGACCCG TCCTTTAACA GTGGCTTTAT GAGAGGCACA AGGCACCCA GCCAGAACTC CCAGACCCG TCCTTTAACA GTGGCTTTAT GAGAGGCACA AGGCACCCA GCCAGAACTC CCAGACCCG TCCTTTAACA GTGGCTTTAT GAGAGCACA AGGCACCCA GCCAGAACTC CCAGACCCG TCCTTCACAC GCCCTCAAACCAG AGGCCCCAGA GGGCCCGCCC TCCTTCACCC TCCTTCACCC CAACCCACC ACAGACACGA AGGCCCGCCC TCCTCCACCCC TCCTTCACC CCAAACCAG AGGCCCCAAACCAG AGGCCCAGAATTA AAGGGGAAC TTCCTGCCAC CATAGGGAA CATCCCCGC ACAGACAGA GCCCAGAATTA AAGGGAACA TGCGCCACCAC CATAGGGAA CATCCCCGC ACGCCCAAACA AGGCCCAGACT TCCTCTTATC ACCAATCTT TCCTGAGAC AGGCCTAAA AGTAGAAGCC ACGCCCAAACCAG GCCCAGACTT ACCCCCACCCC TCCTCTAACCAG GCTCAGAGCT TCCTCTTATC ACCAATCTT TCCTGAGGT CAGGGTGC CAAACCAG GCTCAGAGCT TCCTCTTATC ACCAATCTT TCCTGAGGT CAGGGTGC TCCAACCAG GCCCAGAACTA ATGCAGCCC TCCTCTATC CCCAACCAC CCAACCAGA TCCCCCACC TCCCCACCC TTCCTCCC CCAACCAG GCCCAGTAAA ATGCAGCCC TTCCTCCCC TTCCTCCC CCAACCAG CTCAAGCCCC TGATTTACC TCCCCAGCC TTCCTCCCC TTCCTCCC CCAACCAG CCAGTTCAA GTCCCCCAC TTCCTCCCC TTCCCCCCCCCC	300 360 360 420 480 540 660 660 720 780 840 900 1020 1120 1120 11320 1150 1550 1660 1740 1860 1920 1920
55 60 65 70	ACAGGAAAAA ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGAAGAAAA AGGACACCCC CTCCACCCCA GACATAGGAA AGCAGTCCAC CCTGCGCACCA GGGGAGGAC AGTGGCTGG GTGCAGAGGC TGGCCCGGAT GTCGCGAGGA GTCACGGCC GTGCAGAGGC CGGCGCGCG AGGAGAGGCA GGTCACGCCC CCTTCCCACC ACCTCCCGCC GCCACGGGC CGGCGCGCGC GAGGAGACGCA GGTCACGCCC CCTTCCCACC ACCTCCCGCC GCCACGGGC CGGCGCGCGC GAGGAGCCCCG GGACAGGTGA CCCTTAGAGA ACTGCGCTG GGCTTCCCAC GGGGGAGTC CCTTCTTCGC GGCCTCTGC GCCCCTCGC TCCCCTCTG GGCTTCCAGA AGTCTGACTC AGCCAAGCCC GCATCGCTT GCCTTCACA ACACACCCCC CCGCTGTCAT CCCCGGCGCT CCGCGGGCT GGGCCAACGC GCCGTAAATTA AGACGCGCT CCCCGGTCCC GGAACCCTC CTTCGCCACC CTCCACCCAC CCACCTCCGG GTCCCCAGGA CCACTGGCT GCAACTCCT CGCCCCTCTG GGACTGCCCC TCACTCCACG GAGAGCTACT AGGCCTCACT GGGGCAGAA CTTCGGCAGAA CCCAACCCCC CCACCTCCGG GTCCCCAGGA AGGCCTCACT GGGGCAGAAC CTTCGGCAGAA CCGAACCCC CCACTCCAC GAGAGCTCAT TACAGTCCTG GAAGGTCTCT GCTGGAAGAA CCGAACCCC CCACTCAGC GAGAGCTCAT AAAGGCACC AGGGCAGAACT GAGGTCTATT GGAAAGTTAG CCTTCAGTGA GAGGAGCTAA AATTCCGTCCA GCGAAACACT GAGGTCTATT GGAAAGTTAG CCTTCAGTGA GAGGAGCTAA AAGGCACCC AGGGCAGAACT CCAGACCCC TCGTTAAACA GTGGCTTAAT AGGGAAGGTGA AAGGCACCC AGGGCAGAACT CCAGACCCC TCGTTAAACA GTGGCTTAT GAGGAAGGTGA ACGACTCCC TCCCCTGGG GGGAAATTAC CTTCTGCGA AGAAGGTGA CATCCCCCCC ACGAACCCC CCCCTCTGGG GGGAAATTAC CTTCCTGCAA AGAAGGTGA CATCCCCCCC ACGAACCCC CCCCTCCAGG GGGAAATTAC CTTCCTGCAA AGAAGGTGA CATCCCCGCC ACGAACTCC TCCCCTGGG GGGAAATTAC CTTCCTGCAA AGAAGGTGA CATCCCCGCC ACGACGCCGC TCCTCTATC AGCAACTCT TCGCCACTCAA GATAGAGGCA AGGCCCGAAG CCCAGAATTA AAGGGGTAGT TTCGCCACA AGAAACGTGA CCCCCCCCCC	300 360 360 420 480 540 600 660 720 780 840 1020 1080 1140 1200 1320 1320 1440 1550 1620 1620 1620 1680 1740 1890 1990 2100
55 60 65 70	ACAGGCAAGA ATCTGGTAAC CCTAGGTGCC TCCACTTTGA GGGAGGAGA AGGACACCCC CTCCACCCCA GACATAGGAA AGCACCCCC CTCCACCCCA GGGCAGGAG AGGAGGAGGA GGGCGGGGGGGG	300 360 360 420 480 540 600 660 720 780 840 900 1080 1140 1200 1320 1380 1440 1500 1680 1740 1680 1740 1860 1980 1980 1980 1980 1980 1980 1980 198
55 60 65 70 75	ACAGGACAGA ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGAGGAGAG AGGACACCCC CTCACCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGAGGAC AGTGGCTGG GTGCAGAGGC TGCCCGGAT GTGCCGGAG ACTCGCGCCC CGGGAGAGAC AGGGCGGGG GCGGGGGG CGGGCGCGG AGGAGAGGCA GGTCACGCCC CCTTCCCACC ACCTCCCGCC GCCCACGGGG CGGCGCGCG AGGAGACGCA GGTCACGCCC CCTTCCCACC ACCTCCCGCC GCCCACGGGG CGGCGCGCG AGGAGACGCA GGTCACGCCC CCTTCCCACC ACCTCCCGCC GCCCACGGGG CGGCGCGCG AGGAGACGCA GGTCACGCTC CCCCCTCCGC GCCTCCCCC GGCGGGAGTC CCTTCTTCCC GCCCCTCTGC TCCCCTCCG GCCTTCCAC GCGGGGATC CCTCCACCCC CCCCCTCCACC CCCCTCCACA AGGCCAGAAA GAAATTACAG GATTGCAGGG GCACGGCTAA TGGCCTCTAA TTACCCACCG CCGCTGTCAT CCCCGGCGCCT CCGCGGGGCT GGGCCACGG GCCCAATATA AGACCCCGG CCCCTGCTC GGAACCCTCC CTTCGCCACC CCCCACCAC CCACCTCCGG GTCCCAGGA CCACTGGCTG CCAACTCCTG CTCGCACC CCCCACCAC CCACCTCCACG GTCCCAGGA AGGCCTCACT GGGGGCAGAA CTTCGGCAGA CTCGGAGGAG CCCAAGGCGG CCCTTCAATC AGAGCCTCA GCAGAAACTC GCTGGAAGAG ACTGGAGAG TGGGGAGGGG CCAGGGACT ATTCGTTGA CAGAAACAT GAGTCTTT GGAAAGTTAG CCTTCAATCA AGTCCCCCA GCCAGAACTC CCAGACCCG TCCTTAAACCA AGTCCCCCA GCCAGAACTC CCACACCCGC TCCTTCACAC GCACGGAGA AGGAGAGCAG AGTCCCCCA GCCAGAACTC CCAGACCCG TCCTTTAAC GGCACGGAGA AGGAGACGA AGGACCCGA GCCAGAACTC CCAGACCCG TCCTTTAAC GGCACGGAG CATCCCCGC ACAGACCGA GCCAGAACTC CCAGACCCG TCCTTTAAC GTGGCTTTAT GGCACGCAA AGGACCCGA GCCAGAACTT CCAGACCAC TCCTTCACAC GCCCCGCC ACAGACCGA GCCAGAACTA AGGGGAGAA TCCCCGCTC ACAGACCCG GCCAGAACTT CCCCTCATCA GCTCCCCCAACCAC ACGACCCGA GCCAGAACTA AGGGGAGAA TCCCCGCC ACAGACCAG AGCCCCGCC TCCTCTACACCAC CCCTCCACCAC ACGCCCGAAG GCCACGAATCT CCCCTACACCAC CCCTCTCCCCCAA GATAGAAGCC AGGCCCCAACCAG GCCACGACACA TCTCGCCCCCCCAA GATAGAACAG GCTCAGAGCT TCCCTCTATC AGCAATCTT TCCTGAGGT CCCCATAACCAG GCTCAGAGCT TCCCTCTATC AGCAATCTT TCCTGAGGT CCCCACTAC GCCCCCCCCC TTCATGTCTC CCCCATGAC TTCACTCAGCT TCCTCCAGCT TTTAGGTTAA GTCCCCCATA TTCCCCCCCCCCCCCCCC	300 360 360 420 480 540 600 660 720 1020 1020 1140 1220 1380 1440 1550 1560 1680 1740 1880 1920 1920 1980 1920 198
55 60 65 70	ACAGGCAAGA ATCTGGTAAC CCTAGGTGCC TCCACTTTGA GGAAGGAGA AGGACACCCC CTCCACCCCA GACATAGGAA AGCACCCCC CTCCACCCCA GGGCAGGAC AGGGCTGGCTGG GTGCAGAGGC TGGCCGCGGA GGGCAGGGC GGCGGGGGG GGGGGGGGG GGGGGGGG	300 360 360 420 480 540 600 660 720 780 840 900 1080 1140 1200 1320 1380 1440 1500 1680 1740 1680 1740 1980 1980 1980 1980 1980 1980 1980 198
55 60 65 70 75	ACAGGACAGA ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGAGGAGAGA AGGACACCCC CTCACCCCA GACATAGGAA AGCAGTCCAC CTGGCGACCA GGGGAGGAC AGTGGCTGG GTGCAGAGGC TGGCCCGAG GTCGCCGAGG ACTCGCGCCC GTGCAGAGGC TGGCCCGAG GTCGCCGAGG ACTCGCGCCC GCGCAGGGG CGGCGCGCG AGGAGAGCCA GGTCACGCCC CCTTCCCACC ACCTCCCGCC GCCACAGGGG CGGCGCGCG AGGAGACGCA GGTCACGCCC CCTTCCCACC ACCTCCCGCC GCCACAGGGG CGGCGCGCG AGGAGACGCA GGTCACGCCC CCTCCCACC GCCACAGGGG CGGCGCGCC AGGAGACCCG GCACAGGTAC CTCCTAAGGG ACTCGCCTG GGCTTCCAG AGTCTGACTC AGCCAACCCG GCACCGCTAA TGGCCTCTACA ACACACCCG ACGCGAGAAA GAAATTACAG GATTGCAGGG GCACGGCTAA TGGCCTCTAA TTACCCACCG CCGCTGTCAT CCCCGGCGCCT CCGCGGGGT GGGCCACGC GCCTCATACA ACACACCCG CCCCTGCTC GGAACCCCC CTTCGCCACC CCCCCACC CCACCTCCGG GTCCCCAGGA CCACTGGCTG CCAACTCCT CTTCGCCACC CCCCACCAC CCACCTCCGG GTCCCCAGGA CCACTGGCTG GGAACCCTCC CTTCGCACC CCCCACCAC CCACCTCCAG GAGGCCTAT AGGCCTCACT GGGGGCAGAA CTTCGGCAGA CTTGGGAGA CCCAACTCGG GGACCTCAGA AGGCCTCACT GGAGGCTCTC GCTGGAAGAC CCCAAGCCGG CCCTTCCACT AAAGGCACGA AGGAACACT GAGGTCTAT GGAAACCTG GCCTTAAACCA AGTCCCCCA AGGAACACT CCCGACACCC CTCCTCACAC CCCTTCACT AAAGGCACGA AGGAACACT GAGGTCTAT GGAAACTTAG GCCACGAACCC ACGAACCCG AGGAACTC CCCACACCCC TCCTTCACAC GCCACGACCAC ACGAACCCG AGCCAGACTC CCCACACCCG TCCTTCAGTGA GAGAGGGAA AGGACCCAC GCCAGAACTC CCCACACCCG TCCTTTAAC GTGGCTTTAT GAGGACGGA AGGCCCAGA GGCCCCGCC TCCTCACACCC TCCTTCACAC GCCCCGCA ACGACCCGA GCCAGAACTC CCAGACCCG TCTTCTGCCAC AGAAAGGGA CATCCCCGC ACAGACCGA GCCAGAATTA AAGGGTAAC CTCCTCTGCC CATAAGGGAG CTCGTGAGGG CTCAGAGCT CTCCCTCATC ACCACCACC TTCTTCTCCCAA AGAAAGGGA CATCCCCGC AGGCCCCAACACTC TCCCTCTATC AGCAACACA TGGGTCTAGA GAGCCCTGAA GATAGAAGCC AGGCCCAAGACT CTCCTCTATC AGCAATTCT TCCTGAGGT CCCACTCAC CCAACCAC CCCCCTGCC AGCTTTTACC TCCAGGACAA TGTGGGTTTC CCCACTGAA GATAGAAGCC CCCACTGAACCAG GCCCCCCCC TTCTCTTCCC CCAACCAGC CTCCCCTCAACCAG GGCCCCCCC TTCCAGGTT CCCAACCAGC CTCCCCTCAACCAG GGCCCCCCC TTCCTCTCC CAACCAGCC CTCCCCTCAGACT AGGCCCCCCC TTCCCCATGAC TTCCCCCAACCACC CTCCCCTCAGACCAG GGCCCCCCC TTCCCCCTCAACCAGCC CTCCCAGTTCC CCCACTTCC CTCAGACCTG GGCCCCCCC TTCCCCAAGAC GGGCCCCTC TCCCACTGCC TCCCA	300 360 360 420 480 540 600 660 720 780 840 1020 1080 1140 1200 1320 1440 1500 1620 1620 1620 1620 1620 1620 1620 16
55 60 65 70 75	ACAGGCAAGA ATCTGGTAAC CCTAGGTGCC TCCACTTTGA GGAAGGAGA AGGACACCCC CTCCACCCCA GACATAGGAA AGCACCCCC CTCCACCCCA GGGCAGGAC AGGGCTGGCTGG GTGCAGAGGC TGGCCGCGGA GGGCAGGGC GGCGGGGGG GGGGGGGGG GGGGGGGG	300 360 360 420 480 540 600 660 720 780 840 900 1020 1080 1140 1200 1320 1320 1380 1440 1500 1560 1740 1500 1620 1680 1740 1920 1980 2160 22160 22160 22160 2280 2340

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	Seq ID NO: 93 D	NA Compance				
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		ACTICACC TOTT				

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45 50	Nucleic Acid Acid Acid Sequence 1 11 11 11 1 1 1 1 1 1 1 1 1 1 1 1 1	Accession ce: 527. GGGTGGGG AGAGCCCT	#: NM_134	31 AGGCGATCCG CGACCCGCAC TTAAAATGAG	CTCGTTCCTC CGCGACCTGG GACAGCTCCT	CCAGGGCCAT GCCAGACGCG CCCTTGGGGG	
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	Nucleic Acid a Coding sequent 1 11 AGCTTCTGCC AA GCGGCACGA GG CCACCTTCCC CG CTGTGGTGAC AG ACAGGCCATG GT	Accession ce: 527. GGGTGGGG GGGAGCCCT GTCGCGGT GGTGAAATG GCTAGTGGC	8: NM_134- 1108 21 5 GCCCACGCGG GGCCTCCCCG TTGCTTCTCT AGAACGCACT CCAGTCAGGA TGGTCTCTGG	31 AGGCGATCCG CGACCCGCAGG TTAAAATGAG GAAGACAGCT CGCGGAACCA GTTGGCTGTT	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CTTGGTCCAA CTCCCTGGAG CCAGCTCCAA	CCAGGGCCAT GCCAGACGCG CCCTTGGGGG AGCCCCGCAC GTTCTGACCC AGAGAAGGAG	120 180 240 300 360
50	Nucleic Acid / Coding sequent 1 11	Accession ce: 527 GGGTGGGG AGAGCCCT GTCGCGGT GCTGAAATG CCTCGGCC TCTGCAGC	E B: NM_134- 1108 21 5 GCCCACGCGG GGCCTCCCCG TTGCTTCTCT AGAACGCACT CCAGTCAGGA TGGTCTCTGG	31 AGGCGATCCG CGACCCGCAC TTAAAATGAG GAAGACAGCT CGCGGAAAC GTTGGCTGTT CAGCTCCATT	CTCGTTCCTC CGCGACCTGG GACAGCTCCAA CTCCCTGGAG CCAGCTCCAA	CCAGGGCCAT GCCAGACGCG CCCTTGGGGG AGCCCGCAC GTTCTGACCC AGAGAAGGAG GGTCAGACCT	120 180 240 300
	Nucleic Acid / Coding sequent 1	ACCESSION CE: 527. GGGTCGCG IAGAGCCCT GTCGCGGT GTGAAATG CTAGTGGC ICCTCCGCC TTCTGCAGC	# 8: NM_134- 1108 21 	31	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CTTGGTCCAA CTCCCTGGAG CCAGCTCCAA CCTTAGCTGG	CCAGGGCCAT GCCAGACGCG CCCTTGGGGG AGCCCCGCA GGTCTGACCC AGAGAAGGAG GGTCAGACCT CTGCTGAAAA	120 180 240 300 360 420 480
50	Nucleic Acid / Coding sequent 1 11	ACCESSION CE: 527. GGGTGGGG AGAGCCCT AGTGGGGT AGTGAAATG CCTCCGCC TCTGCAGC TCTGCAGC TCGCAGCTGG	I #: NM_134- 1108 21 	31 AGGCGATCCG CGACCCGCAC TTAAAATGAG GAAGACAGCT CGCGGGAACA GTTGGCTGTT CAGCTCCATT CGTTCTCAGG GCCGCCGCCCCCCCCCC	CTCGTTCCTC CCGGACCTGG GGCAGCTCCAA CCTCCCTGGAG CCAGCTCCAA CCTTAGCTCCAA CCTTAGCTGG CCAGCCATGG	CCAGGGCCAT GCCAGACGCG CCCTTGGGGG AGCCCCGCAC GTTCTGACCC AGAGAAGAGGAG GGTCAGACCT CTGCTGAAAA TCACCGACCA	120 180 240 300 360 420 480 540 600
50	Nucleic Acid / Coding sequent 1	ACCEBBION CE: 527 GGGTCGCG INGAGCCCT IGTGAAATG ICTAGTGGC ICTCGCCC ICTCGCCC ICCAGCTCGC ICCAGCTCGC ICCAGCTCGC ICCAGCTCGC ICCAGCG ICCAGCTCGAGC ICCAGCTCGAGC	1 #: RM_134: 1108 21	31 	CTAGCTCCAA CTCCTTGGTCCAA CTCCTTGGTCCAA CTTCGTCCAA CTTAGCTCCAA CTTAGCTGGG CTAGCCCCAC GCACCCCATGGGC CTAGCCCCATGGCCCCACCCCCACCCCCATGCCCCATGCCCCATGCCCCACCCCCCCC	CCAGGGCCAT GCCAGACGCG CCCTTGGGGG AGCCCCGCAC GTTCTGACCC AGAGAAGAGGG GGTCAGACCT CTGCTGAAAA GCAAACAGAA TCACCGACCA	120 180 240 300 360 420 480 540 600 660
50 55	Nucleic Acid / Coding sequent 1 11 11 ACTTCTGCC AAN GGGGCGACGA GG CCACCTTCCC CG CTGTGGTGAC AG ACAGGGCATG GT ACTCCCTCT AG GAACCTTTC AC GAGAACCGTC GC CAGCAGCTGCAG GA GGAGTTGCAG GA GGAGTTGCAG GA GGAGTTGCAG GA GGAGTTGCAG GA	ACCEBBION CE: 527 GGGTGGGG IAGAGCCTT IGTGGCGGT ICTAGTGGC ICCTCGGC ICCTCGGC IGCAGCTGG IGGACTCAC IGGCCGAGG IGGCCGAGG IGGAGTAC	1 #: MM_134· 1108 121	31 AGGCGATCCG CGACCCGCAC TTAAAATGAG GAAGACAGCT GCTGGCGGAAACA GCTCCATT CAGCTCCATT CAGCTCCATC CCTGCGGGAC CCAGGACGCC CCTGCGGGAC CAAGGACTGC CTTCCCCTAC CTTCCCCTAC CTCCCCTAC CTCCCCTAC CTCCCCCTAC CAAGGACTGC CTTCCCCTAC CTTCCCCTAC	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CTTGGTCCAA CCTCCTGGAG CCAGCTCCAA CCTTAGCTGAG CTTAGCTGCA GCCGCATGG AACACGGAG CCCACCGGC	CCAGGGCCAT CCCAGGGCCAT CCCAGACGCG CCCTTGGGG AGCCCCGCAC AGAGAAGGAG GGTCAGACCT CTGCTGAAA GCAAACAGAA TCACCGACCA ACCTGACCGT CCAAGTTCGC	120 180 240 300 360 420 480 540 600 660 720
50	Nucleic Acid / Coding sequent 1	Accession ce: 527 	I #: RM_134- 1108 21 	31 AGGCGATCCG GACCCGCAC GACGCACCCCCCCCCCCCC	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CTTGGTCCAA CCTCCTGGAC CCAGCTCCAGCGC CAGCCCTCG AACACGAGG AACACGAGGC CGGCACGCCTCGACGCCTCGACGCCTCGCCCCCGCCCGCC	CCAGGGCCAT GCAGAGCGG GCCTTGGGGG AGCCCGCAC GTTCTGACCC AGAGAAGGAG GGTCAGACCT CTGCTGAAAA CCAAACAGAA TCACCGACCA ACCTGACCGT CCAAGTTCGC TCCGGAGTT	120 180 240 300 360 420 480 540 600 660 720 780
50 55	Nucleic Acid / Coding sequent 1	Accession ce: 527 GGGTGGG AGAGCCT AGTGAAATG CTTAGTGG CCTCCGC CTCTGCAGC GCACCTGAGG AGAGTTACA AGAGATCT CCGCACCTGAGG AGAGATCT CCGCACCTGA	1 #: RM_134· 1108 21	31 AGGCGATCCC CGACCCGCAC TTAAAATGAG GAAGACAGCT CGGCGAAACA GTTGCTCTTCAGC GCCGCCCCC CCTGCGGGAG CAAGGACTCCAT CGACGCACCGC CAGCGCCCCCAC CAGCGCCCCCAC CAGCGCCCCCAC CAGCGCACCGC CAGCGCACCGC CAGCGCACCGC CAGCGCACCGC CAGCGCACCGC	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CTCGTCCAA CTCCCTGGAC CCAGCTCCAA CTCCCTGGAC CCAGCTCCAA CCAGCTCCAA CCAGCCCATGG CCAACCGAGC CCCACCGGCC GCGCACGCT CCACCAGCC CCACCAGCC CGCGACGCTT CACCATCGACT CACCATCGACT	CCAGGGCCAT GCCAGGGCCAT GCCAGAGCGC CCTTGGGG AGCCCCCAC GCCAGAGAGCGG GGTCAGACCT CTGCTGAAAA GCAAACAGAA TCACCGACCA ACCTGACCGACCA ACCTGACCGACA ACCTGACGACT AGTGGGCCT AGTGGGCCT AGTGGGCCT AGTGGGCCT	120 180 240 300 360 420 480 540 600 660 720
50 55	Nucleic Acid / Coding sequent 1	ACCESSION CC: 527 GGGTGGGG GAGAGCCCT GTGGGGGT CCTAGTGGC GCTCAGC GGCCCAGG GGGACTCA GAGAGTCAC GGAGAGTCAC GGAGATCAC GGAGAGTCAC GAGAGATCAC GAGACAC GAGAGATCAC GAGAGATCAC GAGAGATCAC GAGAGATCAC GAGAGATCAC GAGACAC GAC	1 #: MM_134- 1108 21	31 AGGCGATCCC CGACCCGCAC TTAAATGAG GAAGACAGCT CGCGAAACA GTTGGCTGTTCAGC GCGCGCGCC CCTGCGGAC CAAGGACTGAG CAAGGACTGAC CAAGGACTGAC CAAGGACTGAC CAAGGACTGAC CAAGGACTGAC CAAGGACTGAC CAAGGACTGAC CAAGGACTGAC CAAGGACTGAC CAAGGACAG CAAGAGAAGATCGACGACGG CAAGGACAG CAAGAGAAGATCGAAGAAGAATCGACGGACGAAGAAGAATCGACGC CATGAAGAATCGACGGATGAAGATCGAAGAATCGACGGATGAAGATCGAAGAATCGACGCGATGAAGAATCGACGCGATGAAGATCGAAGAATCGACGCGATGAAGATCGAAGAATCGACGCGATGAAGAATCGACGCAAGAAGAATCGAACAATCGACCGCAAGAAGAATCGAACAATCGACCGCAAGAAGAATCGAACAATCAACACGCAAGAACAATCAAAAAAAA	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CGCGACCTGGAG CCCGGCACCGG CCTAGCTGGA CCCTAGCTGGAG CCCACGGCCTCG ACACGGAGTCC ACCACGGAGTCC ACCACGAGC CACAGGAGTCC ACGAGGAGTCC ACGAGGAGTCC ACGAGGAGTCC ACGAGGAGTCC ACGAGGAGGAGTCC ACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	CCAGGGCCAT GCCAGGGCCAT GCCAGGACGCG GCCTTGGGGG AGCCCCGCAC GTTCTGACC AGAGAAGAGG GGTCAGAACCCAA ACCTGAAAA CGCAAACAGAA ACCTGACCGT CCCAGGACTA AGTGGCCTT AGTGGGCCTT AGTGGGCCTT AGTGGACTACCT AGTGGACTACCCG AGTCCACCCG AGTCCACCCG AGTCCACCCG AGTCCACCCC	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55 60	Nucleic Acid / Coding sequent 1	ACCESSION CC: 527 GGGTGGGG GAGAGCCCT GTGGCGGT GTGAATG CTTAGTGGC GCCTCCGCC GCCCCCCCCCC	I #: RM_134· 1108 1108 21	31 AGGCGATCCG GGACCGCGCG TTAAAATGAG GAAGACAGCT GGGGAAACA GTTGGCTGTT CAGCTCCATT CATCTTCAGC GCCGCGCCC CCTGCGGGAG CAAGGACTCG CATCAGCGG CAAGGACTGGA CAAGGACTGGA CAATGAGACAT GATGAAGAT GATGAAGAT GATGAAGACAC GATGAACACAC GATCACACAC GATGAACACAC CACACAC C	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CTCGTCCAA CTCCTGGAC CTCGTGCAA CTCCTGGAC CCAGCCCTCCA GCCGCCATGG ACAACGGAGT ACAACGAGT ACCAGCGCC ACCAGCAC ACCAGCAC ACCAGCAC ACCAGCAC ACCAGCAC ACCAGCAC ACCAGCACAC ACCAGCACATGAC ACCAGAGATAC ACCAGAGATAC ACCAGAGATAC ACCAGAGATAC	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCCCCAC GCCTTGGGGG AGCCCCCAC GCCAGAGAGGAG GGTCAGACCT CTGCTGAAAA GCAAACAGAA TCACCGACCA ACCTGACCGACCA ACCTGACCGACT AGTGGGCCT TCGGGGAGTT AGTGGCCT TGGGAACACGC GGAACTGCC GCAAACTGCC	120 180 240 300 360 420 480 540 600 720 780 840 900 900
50 55	Nucleic Acid / Coding sequent 1 11	ACCESSION CC: 527 CCGTCCCC CCGCCCCCCCCCCCCCCCCCCCCCCCC	1 #: MM_134- 1108 21	31 AGGCGATCCG CGACCCGCAC TTANATGAG GAAGACAGCT CGCGGAAACA CGTTCCTAGC CGTTCCTAGC CGTTCCTAGC CCTCCCTAC CGCGCGCCC CTTCCCGGAA CAACACAGCTGGAA CATCAGCCGAC CATCAGCCGAC CGATGAAAAACAC CGATGAAAACAC CGATGAAACAC CGACCCCTAC CGCACACCCGACCGCCCCCCCCCC	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CTTGGTCCAA CCCTTAGCTGG CCAGCCCTCA CCCTAGCTGG ACACCGGCG GACAGCGCCT GACAGGGCCT GACAGGACGCT CACATGAGCT ACATGAGCT CACATGAGCT CAACAATGACC	CCAGGGCCAT GCCAGGGCCAT GCCAGAGCCGC CCCTTGGGGG AGCCCCCAC AGAGAAGGAG GGTCTGACC AGAGAAGGAG GCAAACAGAA CCAACGACCA ACCTGACCAC CCAGGTTCGC TCCAGGACTT AGTGGGCCTT TGGAGATCGC GAGTCCACCCC GGCAAACTGCC TCCAGCTCCCCC TCCAGCTCCCCCCCCC	120 180 240 360 420 480 660 720 840 900 960 1020
50 55 60	Nucleic Acid / Coding sequent 1	ACCESSION CC: 527 GGGTCGGG GAGAGCCCT GTGGGGGT GGTGAAATG CCTAAGTGGC GGCAGCTGG GGAGCTGG GGAGCTGA GGAGCTGA GAGAGATCAC GGCAGCTGA GAGAGATCAC GAGAGAAGA CCTGGAGC CAGACAAGA CCAGACAAGA CCAGACAAGA CCAGACAAGA CCAGACAAGA CCAGACAAGA	I #: MM_134- 1108 21	31 AGGGGATCCG GGACCGGAC TTAAATGAG GAAGAACAGCT CGGGAAACA GTTGGCTGTT CAGCTCCATT CAGCTCCATT CAGCTCCATC CCTGCGGAC CAAGGACTGAC CAAGGACTGAC CAAGGACTGAC CAAGGACTGAC CAAGGACTGAC CAAGGACTGAC CAAGGACTGAC CAAGGACTGAC CAAGGACTGAC CAAGGACTGAC CAAGGACTGAC CAAGGACGCCCTC CGACGCCCTC CGAGCGCCCCTC CGAGCGCCCCCC CGAGCGCCCCCC CGAGCGCCCCCCCC	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CTTGGTCCAA CTCCCTGGAG CCAGCCCTCG GCGCCATGG AACACGAGT CCACGGCG CCGGGAGGCT ACCACGGGG CCGAGGAGT CACATGACT CACAGGAGT CACAGGAGT CACAGGAGT CACAGGAGT CACAGGAGT CACAGGAGT CACAGGAGT CACAGGAGT CACAGGAGT CACAGGAGT CACAGGAGGAT CACAGGAGAT CACAGGAGGAT CACAGGA	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGCCGCAC GTTCTGACCC AGAGAAGAG GCTACAGCC TCGCTGAAAA GCAAACAGAA ACCTGACCGT CCCAGGAGTTA AGTGGCCTT AGTGGCCTT AGTGGCCTT AGTGGCCTT CCGAACTTCGC GCAAACTGGC GCAAACTGGC TCCGGGAGTT AGTGGCCTT TCCGGAGTG GGAAACAGAACA GCAAACTGGC GCAAACTGGC GGCAAACTGGC GCAGAAACAACA	120 180 240 300 360 480 540 660 720 780 840 900 960 1020 1080
50 55 60	Nucleic Acid / Coding sequent 1	ACCESSION CC: 527 GGGTGGGG GAGAGCCCT GTGGGGGT GTGAAATG CTTAGTGGC GGCAACTGAGCGGG GGGAACTGAGCGGGGGGAGCGAGCAGCAGCAGCACCT GAGAGCAGCAACAGAAGAAGACTCATCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA	I #: RM_134- 1108 1108 21	AGGCGAACCA GATGAGATCA GAGCGGAACCA GAGCACCGCAC TTAAAATGAG GAAGCAGCT CAGCTCCATT CAGCTCCATT CAGCTCCATC CATCTCAGG CAAGGACCC CATCGCGGAC CAAGGACTGAA CAATCAGCCG GAAGGACTGAA GATGAGACAT GATGAGCACC GAGCGCCCCC GGAAGCGCCCC GGAAGCGCCCC GGCAAGGCGCCC	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CTCGTCCAA CTCCCTGGAC CCAGCTCCAA CTCCCTGGAC CCAGCTCCAA CCCACCATGG CCAGCCATGG CCACCGGCC CGCGACGCT CACCATGGACT CACCAGCGC CACCAGCGC CACCAGCGC CACCAGCGC CACCAGCGC CACCAGCGC CACCAGCACT CACCAGCGC CACCAGCACT CACCAGCGC CACCAGCACT CACCAGCACT CACCAGCACT CACCAGCACT CACCAGCACT CACCAGCACT CCGCCCCCC CTGGACAGTAC CACCAGCACT CACCAGCACT CACCAGCACT CCGCCCCCC CTGGACAGTAC CACCACCACC CTGGACAGTAC CACCACCCCCC CTGGACAGTAC CTGGCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCC CTGCCCCCCC CTCCCCCCCC	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCCCCAC GCCTTGGGGG AGCCCCCAC GCAGAAGAGGG GGTCAGACCT TCAGCGACAA ACCTGACCGACA ACCTGACCGACA ACTGACCGACA AGTGACCT TCAGCGACT AGTGAGATCGC TCCGGGAGTT AGTGGCCT TGGGAACACT CGCAACTCGC GCAACTCGC GCAACTCGC GCAACTCGC GCAACTCGC TCCGGGAGT TGGGAGAACA ATCGTTCCGACAC ATCGTTCCACCC TGCTGCACTG GCAACTCTC TGCTGCACTG CGCAACTTCCC TGCTGCACTG CGCAACTTCCC TGCTGCACTG CGCAACTTCCT CTGCTGCACTG CGCAACTTCCT CTGCACTG CAGAGAACA ATCGTTCCT	120 180 240 300 360 420 660 660 720 780 840 900 960 1020 1040
50 55 60 65	Nucleic Acid / Coding sequent 1 11	ACCESSION CC: 527 CGGTCGGG CAGAGCCCT CGTCGCGGT CCTAGTGGC CCTCCGCC TCTGGGGT CGGACTGG CGGACTGG CGGACTGG CGGACTGG CGGACTGG CGGACTGG CGGACTGG CGGACTGG CGGACTGG CGGACTGG CGGACTGA CGGACTGA CAGAGATGG CAGAGATGG CAGAGATGG CAGACAGG CTGACCGGACCT CAGGCCTGAGG CAGCAGCAGT CCCGGGCCTTTA CCCGGGCCTTTA	I #: MM_134- 1108 21	31	CTCGTTCCTC CGCGACCTGG GGCACCTGGG GGCACCTGGAG CCTGGAGGCCTCGA CCTAGCTCCA GCCGCCATGG GCACGCCGCGCGCGCGCGCGCGCGCGCGGGGGGGGGG	CCAGGGCCAT GCCAGGGCCAT GCCAGAGCGCG CCCTTGGGGG AGCCCCCAC AGAGAAGGAG GGTAGACCT AGAGAACAGAA TCACCGACCA ACCTGACCAT CCAAGTTCGC TCCAGGACT TCAGGACT TCAGGACT TCAGGACT TCAGGACT TCAGGACT TCAGACT TCCCAGT TCACACCC TCAGAGAAACA ATCGTTCCT TGCTCCACT TGCTCACT 120 180 240 300 360 420 640 660 720 780 840 900 960 1020 1080 1140 1260	
50 55 60	Nucleic Acid / Coding sequent 1	ACCEBBION CE: 527 GGGTGGGG GAGAGCCT GTGGGGT GTGAAATG CTTAGTGGC GGTGAAATG TCTGGAGC GGCAACTGAGC GGAACTGAGC GGAACTGAGC GGAACTGAGC GGAACTGAGC ACCAGGAGC I #: MM_134* 1108 21 1 GCCCACGGG GGCCTCCCCG GGCCTCCCCA CCAGTCAGGA TGGTCTCTG CCAGTCAGGA AGGTGTAGTC TCTGCAGGA AGGGCTTCCT AGGCCACTT TCGCAGCA TGTGCTGCAGGA AGGGCTTCCT AGGCCAACTT TCGCAGGA CCTCCGCGGGG GCAACGGCT TCTTCTGCTGG GGAACGA AGGTTAGTC TCTTCAGGC GGAACGAATTC TCTTCAGGC AGGTTAGTC TCTTCAGGC TGTCCAGGAACA TGTTCTTCTGAGGC TGTCTTTGAGGC TGTCAAGAACA TGTTGCAAGAA TGTTGCAAGAA TGTTGCAAGAA TGTGCAAGAATTC TGGAACATTC TGGAACATTC TGGAACATTC	AGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CGCGACCTGGAC CCAGCTCCAA CTCCCTGGAC CCAGCTCCAA CCCACCCACC CCCACCCACC CCCACCCACC CCCACCA	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGGCCCCAC GCCTTGGGGG AGCCCCCAC GCCAGAGAGGGG GGTCAGACCT TCAGCGACAA ACCTGACCAC ACCTGACCAC ACCTGACCAC ACCTGACCAC ACCTGACCAC ACCTGACCAC ACCTGACCAC ACCTGAC ACCTGACAC ACCTGAC ACCTGACAC ACCTGAC ACCTCA	120 180 240 300 360 420 480 540 660 720 840 900 1020 1080 1140 1260 1380	
50 55 60 65	Nucleic Acid / Coding sequent 1 11	ACCESSION CC: 527 GGGTCGGG GAGAGCCCT GTGGGGGT GTGAGCGGT GTGAGTGG GGGAGCTGA GGAGCTGA GGAGCTGA GGAGCTGA GGAGCTGA GGAGCTGA GGAGCTGA GGAGCTGA GGAGCTGA GGAGCTGA GGGAGCTGA GGGGAGCTGA GGGGGGGGGG	I #: MM_134- 1108 21	AGGGGGATCCG GGACCGCAG TTAAATGAG GAAGACAGCT GCGGAAACA GTTGGCTGTT CAGCTCCATT CAGCTCCATT CAGCTCCATG CAGCACAG CAAGGACTGA CAAGGACTGA CAAGCACGC CAAGCACGC CAAGCACGC CAAGCACGC CAAGCACGC CAAGCACGC CAAGCACGC CAAGCACGC CAAGCACGC CAAGCACGC CAAGCACGC CAAGCACGC CAAGCACCCTC CAAGACATGC CTCCCCTCACC CTCCCCTCACC CTCCCCTCACC CTCCCCTCACC CTCCCCTCACC CTCCCCTCACC CTCCCCTCACC CTCCCCTCACC CTCCCCTCACC CTCCCCTCACC CTCCCCTCACC CTCCCCTCACC CTCCCTCACC CTCCTCACC CC CTCCTCACC CTCCTCCTCACC CTCCTCTCACC CTCCTCCTCACC CTCTCTCT	CTCGTTCCTC CGCGACCTGG GGCACCTGG GGCACCTGGAG CCGGCATGG CCTAGCCTCC GCGCCATGG GCACCCGGC GCGCATGG ACCACGGAG CCACGGAG CCCGGCCGG	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGGCAGCC GCCTTGGGGG AGCCCCCAC GCCAGACCAC CTGCTGAAA GCAAACAGAA ACCAGACT TCCCGAGCCT TCCGGACT AGTGGCCTT TGCGGACT AGTCGCCCC GCAAACTGC GCAAACTGC GCAAACTGC GCAAACTGC GCAAACTGC GCAAACTGC GCAAACTGC GCAGGCCT TCCCGAGGC TCCCTCCAGGCC TCCCCAGGCC CCAGGGCCCC	120 180 240 300 360 420 480 660 660 720 780 840 1020 1080 1140 1200 1320 1344
50 55 60 65	Nucleic Acid / Coding sequent 1	ACCESSION GGGTCGGG GGGCCCATG GGGTCGGGT GTGGAATG CTAAGTGGC GGCAGCTGG GGAGCTGG GGAGCTGA ACCTGGAG ACCTGGAG ACCTGGAG ACCTGGAG ACCAGAG ACCTGAG ACCAGATGAG ACCTGAG ACCAGATGAG I #: MM_134* 1108 21 GCCCACGCG GGCCTCCCCG TTGCTTCTCT AGACGCACT CCAGTCAGGA GGGTTAGTC CCTCTGGCAG AGGTTAGTC TCCTCGCAGC AGGCCTCCT ACGCCACT TCGCCAGC CCTCTGCGGGG GCAACGCCT TCTTCAGGA CCTCCCAGC CCTCTGCGGGG GCAACGCT TCTTCAGGA CCTCTGCGGGG GCAACGCT TCTTCAGGG GGAACGCT TCTTCAGGG AGGTTTCT TCTTCAGGG AGGTTTCT TCTTCAGGG AGGTTTCCT TCTTCAGGG AGGTTTCCT TCTTCAGGG AGGTTTCCT TCTTCAGGG AGGTTTCCT TGAATCAT TGTGATCAT GAT TGT	BI AGGCGATCCC GAACACCCCCACCCCACCCCACCCCACC	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CGCGACCTGGAG CCCAGCTCCAA CCCCCGCACGGC CCCAGCGCCCGGCCCG	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGCCGCAC GTTCTGACCC AGAGAAGAGG GGTCAGACCT CTGCTGAAAA GCAAACAGAA ACCTGACCGT CTGAGCCAT AGTGGCCTT AGTGGCCTT AGTGGCCTT CTGAGATCGC GCAAACTTGCC GCAAACTTGCC GCAAACTGCC GCAAACTGCC GCAAACTGCC GCAAACTGCC GCAAACTGCC GCAAACTGCC GCAAACTGCC GCAAACTGCC GCAAACTGCC GCAGGATCAC ATCGTTCCAGTG GCAGGACTCAC GCAGGCACTC CCCCGGCCT CTCCCAGGCC CTCCCAGGCT AGGGCACTC AGGGCACTCC AGGGCACTCC AGGGCACTCC AGGGCACTC AGGGCACTCC AGGGCACTC AGGGCACTCC AGGGCACTC AGGGCACTC AGGGCACTCC AGGGCACTCC AGGGCACTCC AGGGCACTCC AGGGCACTCC AGGGCACTC AGGGCACTCC AGGGCACTCC AGGGCACTCC AGGGCACTCC AGGGCACTCC AGGGCACTCC AGGGCACTCC AGGGCACTCC AGGGCACTCC AGGGCACTCC AGGGCACTCC AGGCACTCC AGGGCACTCC AGGGCACTCC AGGGCACTCC AGGGCACTCC AGGGCACTCC AGGCACTCC AGGGCACTCC GGGCACTCC AGGGCACCC AGGGCACCC AGGGCACTCC AGGGCACTCC AGGGCA	120 180 240 300 360 420 480 540 660 720 840 900 1020 1080 1200 1200 1200 1320 1380 1380	
50 55 60 65	Nucleic Acid / Coding sequent 1 11	ACCESSION CE: 527 GGGTGGGG AGAGCCCT KITGGCGGT KITGGCGGT KITGAATGGC KITGAATGGC KITGAATGGC KITGACTGGC KITGACTGGC KITGACTGGC KITGACTGGC KITGACTGGC KITGACTGGC KITGACTGAC KITGACACTGAC KITGACACTGAC KITGACACTGAC KITGACACTGAC KITGACACTGAC KITGACAC KITGACACTGAC KITGACACTGAC KITGACACTGAC KITGACACTGAC KITGACACTGAC KITGACACTGAC KITGACACTGAC KITGACACTCAC KITGACACTCAC KITGACACTCAC KITGACACTCAC KITGACACTCAC KITGACACTCAC KITGACACTCAC KITGACACTCAC KITGACACTCAC KITGACACTCAC KITGACACTCAC KITGACACTCAC KITGACAC KITGACACTCAC	I #: MM_134- 1108 1108 21	AGGEGAACCA CGACCCGCAC TTAAAATGAG GAAGACAGCT CAGGCACCCT CAGCCCCCCCCCC	CTCGTTCCTC CGCGACCTGG GACAGCTCCA CTCGTTCCAA CTCCCTGGAC CCAGCTCCAA CTCCCTGGAC CCAGCTCCAA CCAGCTCCAA CCAGCTCCAA CCAGCTCCAA CCAGCACTGC CCACCGGCC CGCGACGCTC ACCATCGACT CACCAACGACTC ACCAACGACTC CACCAACGACTC CACCAGCCCGC CCGGCCCGG CTGGACAGTA CACCAGCCCGC CCGGCCCGG CTCTGGCCCG CTCTGGCCCG CTCTGGCCCG CTCTGGGCCCG CTCTGGCCCC CTCTGGGCCCC CTCTGGCCCC CTCTGCCCC CTCTCTGCCCC CTCTCTGCCCC CTCTGCCCC CTCTCTGCCCC CTCTCTCT	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAC GCCTTGGGGG AGCCCCCAC AGAGAAGAG GCTAGAGAC TCACCGACA ACCTGACCAC AGAGACGAC AGCTGACCAC ACCTGACCAC ACCTGACCAC ACCTGACCAC ACCTGACCAC ACCTGACCAC ACCTGACCAC ACCTGACCAC ACCTGACCAC ACCTGACCAC CCGACACTCCC CCGACGCC CCGACCCC CCCGTCCACC CCCGTCCACT CCCGGGCT CCCGGGCC CCCGTCCATT	120 180 240 300 420 480 540 660 720 840 900 1020 1080 1140 1260 1380 1440 1560
50 55 60 65 70	Nucleic Acid / Coding sequent 1 11 11 ACTTCTGCC AN GGGGCGACAGA GG CCACCTTCCC CG CTGGGTGAC AG ACAGGGCATT CT GGGGTCCTCA CT GAGAACCGT GG CAGCAAGGT GG CAGCAAGGT GC CAGCAAGGT CA CAGCAAGGT CA CAGCAAGGT CA CAGCAAGGT CA CAGCAAGGT CA CAGCAAGGT CA CAGCAAGGT CA CAGCATTTC CA CAGCATTTC CA CAGCATTTC CA CAGCATTTC CA CAGCATTTC CA CAGCATTTC CA CAGCATTTC CA CAGCATTCCAGC CCCCCTCCCAC CCGGCTCCCC CCGGCTCCCC CCGGCTCCCC CCGGCTCCCC CCGGCCCCCCC CCGGCCCCCCC CCGCCCCCCCC	ACCESSION CC: 527 GGGTGGGG GAGAGCCT GTGGGGGT GTGGGGGT GTGGGGT GTGAGTGG GGGAGTCAC GGGAGTCAC GGGAGTCAC GGGAGTCAC GGGGTGAAGAGATCAC GGGAGTCAC GGGGAGTCAC GGGAGTCAC GGGAGTCAC GGGAGTCAC GGGAGTCAC GGGAGTCAC GGGAGTCAC GGGAGTCAC	I #: MM_134- 1108 21	AGGGGGAACA CGACCGGGA TTAAATGAG GAAGACAGCT CGCGGAACA GTTGGCTGTT CAGCTCCATT CAGCTCCATT CAGCTCCATT CAGCTCCATT CAGCTCCATT CAGCTCCATT CAGCTCCATT CAGCTCGAC CAAGGACTCC CAAGCACC CAAGCACC CAAGACTCC CAAGACTCC CAAGACTCC CTCCCCTCAC CGAGGAGAC CCCAAGTCA CCCCATCCACCC CCCAAGCTCC CCCAAGCTCC CCCAAGCTCC CCCAAGCTCC CCCAAGCTCC CCCAAGCTCC CCCAAGCTCC CCCAAGCTCC CCCAAGCTCC CCCAAGCTCC CCCCATCCC CCCCTCCCC CCCAAGCTCC CCCCTCCCCT	CTCGTTCCTC CGCGACCTGG GGCACCTGG GGCACCTGGA CTCGCTGGAG CCAGCCCTGGAG CCAGCCCTGG GCGCATGG ACCACGGCG CGGCATGG CGGAGGCT ACCACGGGG GCGGAGGT ACCACGGGG CGGGAGGAT CACAGGAGT CACAGGAGT CACAGGGGG CCGGCAGGGG CCGGCCGG CCGGCCGG CCGGCCGG	CCAGGGCCAT GCCAGGGCCAT GCCAGAGCGC GCCTTGGGGG AGCCCCGCAC GTTCTGACC AGAGAAGGAG GGTCAGACT CTGCTGAAA GCAAACAGAA ACCAAGTTCGC TCCGGACT AGTGGCCT TCGGGACT AGTGGCCT TCGGGATT AGTGGCCT TGCGGATGA CCAAGTTCGC GCAAACTGC GCAAACTGC GCAAACTGC GCAGGGCGCT TCCCGGGGCT TCCCTCCAGG CTCCCCCC CCGTTCATCAG CCCCCCC CCGTTCATCAT AGTGTCCTG CCCGGGCT CCCCGGGGCT CCCCTTCCAG CCCCTTCATT	120 180 240 300 360 420 480 660 660 720 780 840 1020 1080 1140 1200 1320 1320 1440 1500
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80						AGGAGCGGCC	120 180
						CGGACTCGGG ACGAGGCATT	240
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	TGAAAGTACA GCCGCCCCC CCCAAGTCAG CCTCGACACA TAAATCAGCA CGCGGCCGGA GAACCCCGCA ATCTCTGCGC CCACAAAATA CACCGACGAT GCCCGATCTA CTTTAAGGGC	240
65	TGAAACCCAC GGGCCTGAGA GACTATAAGA GCGTTCCCTA CCGCCATGGA ACAACGGGGA	300
	CAGAACGCCC CGGCCGCTTC GGGGGCCCGG AAAAGGCACG GCCCAGGACC CAGGGAGGCG	360
	CGGGGAGCCA GGCCTGGGCT CCGGGTCCCC AAGACCCTTG TGCTCGTTGT CGCCGCGGTC	420
	CTGCTGTTGG TCTCAGCTGA GTCTGCTCTG ATCACCCAAC AAGACCTAGC TCCCCAGCAG	480 540
70	AGACCGGCC CACAACAAAA GAGGTCCAGC CCCTCAGAGG GATTGTGTCC ACCTGGACAC CATATCTCAG AAGACGGTAG AGATTGCATC TCCTGCAAAT ATGGACAGGA CTATAGCACT	600
,,	CACTGGAATG ACCTCCTTTT CTGCTTGCGC TGCACCAGGT GTGATTCAGG TGAAGTGGAG	660
	CTAAGTCCCT GCACCACGAC CAGAAACACA GTGTGTCAGT GCGAAGAAGG CACCTTCCGG	720
	GAAGAAGATT CTCCTGAGAT GTGCCGGAAG TGCCGCACAG GGTGTCCCAG AGGGATGGTC	780 840
75	AAGGTCGGTG ATTGTACACC CTGGAGTGAC ATCGAATGTG TCCACAAAGA ATCAGGTACA	
13	AAGCACAGTG GGGAAGCCCC AGCTUTGGAG GAGACGGTGA CCTCCAGCCC AGGGACTCCT GCCTCTCCCT GTTCTCTCT AGGCATCATC ATAGGAGTCA CAGTTGCAGC CGTAGTCTTG	
	ATTGTGGCTG TGTTTGTTTG CAAGTCTTTA CTGTGGAAGA AAGTCCTTCC TTACCTGAAA	1020
	GGCATCTGCT CAGGTGGTGG TGGGGACCCT GAGCGTGTGG ACAGAAGCTC ACAACGACCT	1080
00	GGGGCTGAGG ACAATGTCCT CAATGAGATC GTGAGTATCT TGCAGCCCAC CCAGGTCCCT	1140
80	GAGCAGGAAA TGGAAGTCCA GGAGCCAGCA GAGCCAACAG GTGTCAACAT GTTGTCCCCC	1200 1260
	GGGGAGTCAG AGCATCTGCT GGAACCGGCA GAAGCTGAAA GGTCTCAGAG GAGGAGGCTG CTGGTTCCAG CAAATGAAGG TGATCCCACT GAGACTCTGA GACAGTGCTT CGATGACTTT	
	GCAGACTTGG TGCCCTTTGA CTCCTGGGAG CCGCTCATGA GGAAGTTGGG CCTCATGGAC	1380
	AATGAGATAA AGGTGGCTAA AGCTGAGGCA GCGGGCCACA GGGACACCTT GTACACGATG	1440

	CTGATAAAGT GO			C120000000000		·CTCCATCCC	1500
	TTGGAGACGC TO	SGICAACAA	AACCOGGCGA	CALGUCTUTE 1	CCACACCCI	TTCACCTCT	1560
							1620
	GGAAAGTTCA TO	STATCTAGA	AGGTAATGCA	GACTUIGUUA	GICCIAMGI (TOCACTOCA	1680
5	TCAGGAAGTC AC	JACCTTCCC	TGGTTTACCT	CLOCCOTAGE (CANGLECON (TOSTOTA	1740
,							1800
	ACATCACCCA G	IGGATGGAA	CATCCIGIAA	CITITCACIG C	ACTIGGCAL	MILLINIA	1860
	AGCTGAATGT G	ATAATAAGG	ACACTATUGA	AATGTCTGGA	CATICOGII	GIGCGIACI .	
	TTGAGATTTG G	TTTGGGATG	TCATTGTTTT	CACAGCACTT	ITTTAICCIA A	AIGIAAAIGC	1920
10	TITATTTATT T	ATTTGGGCT	ACATTGTAAG	ATCCATCTAC A	ACAGTCGTTG	rcogactica	1980
10	CTTGATACTA T	ATGATATGA	ACCITITIG	GGTGGGGGGT (GCGGGGCAGT '	CACTCTGTC	2040
	TCCCAGGCTG G						2100
	AAGCGATTCT C	CCACCTCAG	CCATCCAAAT	AGCTGGGACC	ACAGGTGTGC	ACCACCACGC	2160
	CCGGCTAATT T	TITGTATTT	TGTCTAGATA	TAGGGGCTCT	CTATGTTGCT	CAGGGTGGTC	2220
	TCGAATTCCT G						2280
15	GCGTGAGCCC C	CATGCTTGG	CCTTACCTTT	CTACTTTTAT .	AATTCTGTAT	GTTATTATTT	2340
	TATGAACATG A	AGAAACTTT	AGTAAATGTA	CTTGTTTACA	TAGTTATGTG	AATAGATTAG	2400
	ATAAACATAA A	AGGAGGAGA	CATACAATGG	GGGAAGAAGA	AGAAGTCCCC	TGTAAGATGT	2460
	CACTGTCTGG G	TTCCAGCCC	TCCCTCAGAT	GTACTITGGC '	TTCAATGATT	CGCAACTTCT	2520
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20	GTTGTTTACA T	ATGAGTCGG	GACCAAAGAG	AACTGGATCC .	ACGTGAAGTC	CTGTGTGTGG	2640
	CTGGTCCCTA C	CTGGGCAGT	CTCATTTGCA	CCCATAGCCC	CCATCTATCG	ACAGGCTGGG	2700
	ACAGAGGCAG A	TOGGTTAGA	TCACACATAA	CAATAGGGTC	TATGTCATAT	CCCAAGTGAA	2760
	CTTGAGCCCT G	TTTGGGCTC	AGGAGATAGA	AGACAAAATC	TGTCTCCCAC	GTCTGCCATG	2820
	GCATCAAGGG G						2680
25	AGTAGATGGC C						2940
45	GGGTACAGAT I	COCTACTO	accaertice	COCCTOTOTA	AGCATCTGAC	TCATCTCAGA	3000
	AATGTCAATT C		CTCCCAACAG	CACCTAGAAT	CCCTCACCCA	TTAAGGTTTT	3060
	CTTCTTGTGT	,11 000000 1	TATOCONOM	AGACCTCAGT	AACCATTTCA	CCTCTTTCC	3120
	AGCAAACCCT T						3180
30	CAGGAGTTTT	CICCATAGI	ATTICAGICA	COMMOGNIC	MITTATOCAG	CINCICATIC	3240
30	CAGGAGTTTT	GGICTITIC	TGTCTCAAGG	CALIGIGIGI	CACTOTTCTC	CACIOGITIC	3300
	GGTGGGACAA A	AGTTAGAATT	GCCTGAAGAT	CACACATICA	CACIGITOTO	ICIGIOGNOI	3360
				TTGCACTTCC			
	GGCATCCCAC (CGTTGTCCC	CTGCACTTCT	GGAAGGCACA	GGGTGCTGCT	GCCTCCTGGT	3420
25	CTTTGCCTTT (CTGGGCCTT	CTGTGCAGGA	CGCTCAGCCT	CAGGGCTCAG	AAGGTGCCAG	3480
35	TCCGGTCCCA (GTCCCTTGT	CCCTTCCACA	GAGGCCTTCC	TAGAAGATGC	ATCTAGAGIG	3540
				AATTTTTATT '			3600
	ACTCTCTCGC (CCAGGCTGGA	GTGCAACGG1	ACGATCTTGG	CTCAGTGCAA	CCTCCGCCTC	3660
				CTCCGGAGTAG			3720
	CACCACGCCT (GGCTAATTTT	TGTATTTT#	GTAGAGACGG	GGTTTCACCA	TGTTGGTCAG	3780
40	GCTGGTCTCG	AACTCCTGAC	CTCAGGTGA1	CCACCTTGGC	CTCCGAAAGT	GCTGGGATTA	3840
	CAGGCGTGAG (CCACCAGCCA	GGCCAAGCTA	TTCTTTTAAA	CTABCCTTCC	TGACGACATG	3900
					GIAGGIICC		
	AAATAATTGG (GGGTTTTGTT	GTTTAGTTAG	ATTAGGCTTT	GCTATATCCC	CAGGCCAAAT	3960
	AAATAATTGG (GGGTTTTGTT	GTTTAGTTAG	ATTAGGCTTT	GCTATATCCC	CAGGCCAAAT	3960 4020
	AGCATGTGAC	GGGTTTTGTT ACAGGACAGC	CATAGTATA	ATTAGGCTTT TGTGTCACTC	GCTATATCCC GTGGTTGGTG	CAGGCCAAAT TCCTTTCATG	
45	AGCATGTGAC A	GGGTTTTGTT ACAGGACAGC GTCAAAGGTC	GTTTAGTTAG CATAGTATAG CCTATTTGAJ	ATTAGGCTTT TGTGTCACTC ATGTGTTATA	GCTATATCCC GTGGTTGGTG ATACAAACAA	CAGGCCAAAT TCCTTTCATG GGAAGCACAT	4020
45	AGCATGTGAC (CTTCTGCCCT (TGTGTACAAA	GGGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT	GTTTAGTTAG CATAGTATAG CCTATTTGAA ATTTATGAA	ATTAGGCTTT TGTGTCACTC	GCTATATCCC GTGGTTGGTG ATACAAACAA	CAGGCCAAAT TCCTTTCATG GGAAGCACAT	4020 4080
45	AGCATGTGAC A	GGGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT	GTTTAGTTAG CATAGTATAG CCTATTTGAA ATTTATGAA	ATTAGGCTTT TGTGTCACTC ATGTGTTATA	GCTATATCCC GTGGTTGGTG ATACAAACAA	CAGGCCAAAT TCCTTTCATG GGAAGCACAT	4020 4080 4140
45	AGCATGTGAC AGCTTCTGCCCT CTGTGTACAAA TAAAAAAAAA	GGGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAA	CATAGTATAC CATAGTATAC CCTATTTGAA ATTTATGAA	ATTAGGCTTT TGTGTCACTC ATGTGTTATA	GCTATATCCC GTGGTTGGTG ATACAAACAA	CAGGCCAAAT TCCTTTCATG GGAAGCACAT	4020 4080 4140
45	AGCATGTGAC CTTCTGCCCT TGTGTACAAA TAAAAAAAAA Seq ID NO:	GGGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAAA	GTTTAGTTAG CATAGTATAG CCTATTTGAA ATTTATGAA Quence	ATTAGGCTTT TGTGTCACTC ATGTGTTATA CCATGACCAA	GCTATATCCC GTGGTTGGTG ATACAAACAA	CAGGCCAAAT TCCTTTCATG GGAAGCACAT	4020 4080 4140
	AGCATGTGAC CTTCTGCCCT TGTGTACAAA TAAAAAAAAA Seq ID NO: Nucleic Aci	GGGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAA 112 DNA Se d Accessic	GTTTAGTTAG CATAGTATAG CCTATTTGAM ATTTATGAM equence	ATTAGGCTTT TGTGTCACTC ATGTGTTATA CCATGACCAA	GCTATATCCC GTGGTTGGTG ATACAAACAA	CAGGCCAAAT TCCTTTCATG GGAAGCACAT	4020 4080 4140
45 50	AGCATGTGAC (CTTCTGCCCT (TGTGTACAAA TAAAAAAAAA Seq ID NO: Nucleic Acitoding sequ	GGGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAA 112 DNA Se d Accessic ence: 286.	GTTTAGTTAC CATAGTATAC CCTATTTGAA ATTTATGAA quence n #: NM_14 .1521	TATTAGGCTTT TOTTGTCACTC A ATGTGTTATA T CCATGACCAA	GCTATATCCC GTGGTTGGTG ATACAAACAA ATTAAATATG	CAGGCCAAAT TCCTTTCATG GGAAGCACAT AAACCTTATA	4020 4080 4140
	AGCATGTGAC (CTTCTGCCCT (TGTGTACAAA TAAAAAAAAA Seq ID NO: Nucleic Acitoding sequ	GGGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAA 112 DNA Se d Accessic	GTTTAGTTAC CATAGTATAC CCTATTTGAA ATTTATGAA quence n #: NM_14 .1521	ATTAGGCTTT TGTGTCACTC ATGTGTTATA CCATGACCAA	GCTATATCCC GTGGTTGGTG ATACAAACAA	CAGGCCAAAT TCCTTTCATG GGAAGCACAT	4020 4080 4140
	AGCATGTGAC (CTTCTGCCCT (TGTGTACAAA) TAAAAAAAAA Seq ID NO: Nucleic Aci Coding sequ 1	GGGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAAA	GTTTAGTTAC CATAGTATAC CCTATTTGAA ATTTATGAA equence in #: NM_14' .1521 21	ATTAGGCTTT G TGTGTCACTC A ATGTGTTATA C CCATGACCAA	GCTATATCCC GTGGTTGGTG ATACAAACAA ATTAAATATG	CAGGCCAAAT TCCTTTCATG GGAAGCACAT AAACCTTATA	4020 4080 4140 4160
	AGCATGTGAC ACTITCTGCCCT GTGTACAAA TAAAAAAAAA Seq ID NO: Nucleic Aci Coding sequ	GGGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAAA	GTTTAGTTAG CATAGTTAGA ATTTATGAA Quence m #: NM_14 .1521 21	TATTAGGCTTT G TGTGTCACTC A ATGTGTTATA CCATGACCAA 7187.1 31 T CTTATTTATT	GCTATATCCC GTGGTTGGTG ATACAAACAA ATTAAATATG 41 GTCACCAACC	CAGGCCAAAT TCCTTTCATG GGAAGCACAT AAACCTTATA 51 TGTGGTGGAA	4020 4080 4140 4160
50	AGCATGTGAC CTTCTGCCCT TGTGTACAAA TAAAAAAAAA Seq ID NO: Nucleic Aci Coding sequ 1 GCGCTTGCGG TTTGCAGTTG	GGGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATCT AAAAAAAAA 112 DNA Se d ACCESSIC ence: 286. 11 i AGGATTGCGT CACATTGGAT	GTTTAGTTAG CATAGTATAG ATTTATGAA: ATTTATGAA: .1521 21 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TITAGGCTTT TGTGTCACTC ATGTGTTATA CCATGACCAA 7187.1 31 1 CCTTATTTATT CCGGCCCGAA	GCTATATCCC GTGGTTGGTG ATACAAACAA ATTAAATATG 41 GTCACCAACC TGACGCCTGC	CAGGCCAAAT TCCTTTCATG GGAAGCACAT AAACCTTATA 51 TGTGGTGGAA CCGGAGGCAG	4020 4080 4140 4160
	AGCATGTGAC CTICTGCCCT TGTGTACANA TAANAANAAA Seq ID NO: Nucleic Aci Coding sequ 1 GCGCTTGCGG TTTGCAGTTG TGAAAGTACA	GGGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAAA	GTTTAGTTAG CATAGTATAG CATAGTATAGA ATTTATGAA GQUENCE on #: NM_14' .1521 21 TAGAGAGAC CTGAGTCAG CCCCAGTCAG CCCCAGTCAG CATAGTCAG CATAGTCAG CCCCAGTCAG CATAGTCAG CATAGTCAG CCCCAGTCAG CATAGTCAG CATAGTCAG CCCCAGTCAG CATAGTCAG CATAGTCAG CATAGTCAG CATAGTCAG CCCAAGTCAG CATAGTCAG CAT	ATTAGGETT TG TGTGTCACTC A ATGTGTTATA CCATGACCAA 7187.1 31 T CTTATTTATT CCGCCCCGAC CGACCCCAC	GCTATATCCC GTGGTTGGTG ATACAAACAA ATTAAATATG 41 GTCACCAACC TGACGCCTGC TAAATCAGCA	CAGGCCAAAT TCCTTTCATG GGAAGCACAT AAACCTTATA 51 TGTGGTGGAA CCGGAGCCAG CGCGGCCGGA	4020 4080 4140 4160
50	AGCATGTGAC CTTCTGCCCT TGTGTACAAA TAAAAAAAA Seq ID NO: Nucleic Aci Coding sequ 1 GGGCTTGCGG TTTGCAGTTG TGAAAGTACA GAACCCCGCA	GGGTTTTGTT ACAGGACAGG GTCAAAGGTC ATACTTATGT AAAAAAAAA 112 DNA Se d Accessic ence: 286. 11 j AGGATTGCGT CACATTGGAT GGCCGCCGCCG	GTITAGTIAG CATAGTATA CATAGTATA ATTITAGA ATTITAGA 1521 1 TGACGAGAC CCCAAGTCA CCCAAGACA CCACAAAAT	ATTAGGCTTT S TGTGTCACTC A ATGTGTATA T CCATGACCAA 7187.1 31 T CTTATTTATT C CCGCCCGAA A CACCGACGAT A CACCGACGAC	GCTATATCCC GTGGTTGGTG ATACANACAA ATTANATATG 41 GTCACCAACC TGACGCTGC TANATCAGCA GCCCCGATCTA	CAGGCCAAAT TCCTTTCATG GGAAGCACAT AAACCTTATA 51 I TGTGGTGGAA CCGGAGGCAG GGCGGCCGGA CTTTAAGGGC CTTTAAGGGC	4020 4080 4140 4160 60 120 180 240
50	AGCATGTGAC CTTCTGCCCT TGTGTACANA TANANANAN Seq ID NO: Nucleic Aci Coding sequ 1 GCGCTTGCGG TTTGCAGTTG TGANAGTACA GAACCCCGCA TGANAGCCACCAC	GGGTTTTGTT ACAGGACAGG GTCAAAGGTC ATACTTATGT AAAAAAAAA 112 DNA Se d Accessic ence: 286. 11 AAGAATTGCGT CACATTGGAT GCCGGCCGG GGGCCTGAGG	GTTAGTTAG CATAGTATA ATTTATGAA ATTTATGAA ATTTATGAA 1521 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ATTAGGCTTT TO THAT THAT THAT THAT THAT THAT THAT TH	GCTATATCCC GTGGTTGGTG ATACAAACAA ATTAAATATG 41 GTCACCAACC TGACGCCTGC TAAATCAGCA GCCCGATCTA	CAGGCCAAAT TCCTTTCATG GGAAGCACAT AAACCTTATA 51 TGTGGTGGAA CCGGAGGCAG CGCGGCGGA CTTTAAGGGC ACAACGGGGA ACAACGGGGA	4020 4080 4140 4160 60 120 180 240 300
50	AGCATGTGAC CTICTGCCCT TGTGTACANA TAANAANAAA Seq ID NO: Nucleic Aci Coding sequ 1 GCGCTTGCGG TTTGCAGTTG TGAAAGTACA GAACCCCCA CAGAACCCCC CAGAACCCCC	GGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAA 112 DNA Se ence: 286. 11 AGGATTGCGT CACATTGGAT GCCGCCGCCG GGGCCTGAGG GGGCCTGAGG CGGCCGCTTTGGAT	GTITAGTIAG CCTATTIGAM ATTIATGAM GUENCE ON #: NM_14* .1521 21 1 TGACGAGAC CCCCAGTCA CCCCAGTCA CCCCAGTCA CCGGGGCCCC CGGGGCCCC	ATTAGGETTT TOTAL TOTA	GCTATATCCC GTGGTTGGTG ATACANACAA ATTANATATG 41	CAGGCCAAT TCCTTTCATG GGAAGCACT AAACCTTATA 51 TGTGGTGGAA CCGGAGGCAG CGCGCCGGA CTTTAAGGGC ACAGGGGAA CAGGGGGAC CAGGGGGGCAC CAGGGAGGCAG CAGGGAGGCAG CAGGGAGGCAG CAGGGAGGCAG	4020 4080 4140 4160 60 120 180 240 300 360
50 55	AGCATGTGAC CTTCTGCCCT TGTGTACAAA TAAAAAAAA Seq ID NO: Nucleic Aci Coding sequ 1 GGGCTTGCGG TTTGCAGTTG TGAAAGTACA ACACCCCGCA TGAAACCCAC CAGAACGCCC CGGGGGGCA	GGGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAA 112 DNA Se d Accessic ence: 286. 11 AGGATTGCG7 CACATTGGAT GCCGCCGCG GGGCCTGAG CGGCCGCGTT	GTITAGTIAG CATAGTATA CATAGTATA ATTITAGA ATTITAGA 1521 21 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ATTAGGCTTT A MODITIATA CCATGACCAA 187.1 31 CCATGACCAA CCATGACCAA CCATGACCAA CCATGACCAA A CACCGACGAA A CACCGACGAA A CACCGACGAA A CACCGACGAC A CACCACCAT A GAAAAGCACCC C AAGAACCATC C AAGACCCTTC C AAGACCCTTC C AAGACCCTTC	GCTATATCCC GTGGTTGGTG ATACANACAA ATTANATATG 41 GTCACCAACC TGACGCTGG GCCCATGTA CCCCAGGACC TGCTCGTTGTT	CAGGCCAAAT TCCTTTCATG GGAAGCACT AAACCTTATA 51 TGTGGTGGAA CCGGAGCAG CGCGCCGGA CTTTAAGGC ACAACGGGGA CAGGGAGCCGG CGCGCCGGC CGCCCGGT CAGCCGGC	4020 4080 4140 4160 60 120 180 240 300 360 420
50	AGCATGTGAC CTICTGCCCT TGTGTACANA TANANANAA Seq ID NO: Nucleic Aci Coding sequ 1 1 GCGCTTGCGG TTTGCAGTTG TGANAGTACA GAACCCCGCA TGANACCCCAC CAGAACGCCC CCGGGAGCCA CTGCTGTTGG	GGOTTTTGTT ACAGAGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAA 1 DNA Se 14 ACCESSIC Ence: 286. 11 AGGATTGCGT CACATTGGAT GCCGCGCCG ATCTCTGCGG CGGCCTGGGC GGCCTGGGC TCTCAGGCTG	GTTTAGTTAG CCTATTTGAA ATTTATGAA: ATTTATGAA: ATTTATGAA: LQuence II #: NM_14' .1521 I TAGGAGAC CCCAAGTCA CCCCAAGTCA CCCACAGTCA CGGGGCCCG CCGGGTCCC CCGGGTCCC CCGGGTCCC CCGGGTCCC CCGGGTCCC CCGGTCCC CCGGGTCCC CCGGGTCCC CCGGGTCCC CCGGGTCCC CCGGGTCCC CCGGGTCCC CCGGGTCCC CCGGGTCCC CCGGGTCCC	ATTAGGETTT TOTAL TOTA	GCTATATCCC GTGGTTGGTG ATACANACAA ATTANATATG 41	CAGGCCAAT TCCTTTCATG GGAAGCACT AAACCTTATA 51 TGTGGTGGAA CCGGAGGCAG CGGGGCGGA CTTTAAGGGC ACAACGGGA CAGGGAGGCG CGCGCGGT CGCGCGGT TCCCCAGCAG	4020 4080 4140 4160 60 120 180 240 300 360 420 480
50 55	AGCATGTGAC CTICTGCCCT TGTGTACANA TAANAANAAA Seq ID NO: Nucleic Aci Coding sequ 1 GCGCTTGCGG TTTGCAGTTG TGANAGTACA GAACCCCCC CAGANACGCCC CGGGGAGCCA CTGCTGTTGA AGAGCGCCC	GGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAA 112 DNA Se cence: 286. 11 AGGATTGGGT CACATTGGAT GGCCGGCGCG ATCTCTGGGG GGGCCTGAGG GGCCTGAGGT TCTCAGCTGG TCTCAGCTGG CACAACAAA	GTTTAGTTAG CATAGTATAG CCTATTTGAG ATTTATGAG GUENCE ON #: NM_14' .1521 21 1 TGACGAGAC CCCAGAGAC CCCAGAGAC CCCAGAGAC CCGGGTCCC CGGGGTCCC AGGGGTCCAAAGAC AGACTTCAGC AGACTCCAG	ATTAGECTTE TO THE TOTAL TH	GCTATATCCC GTGGTTGGTG ATACANACAA ATTANATATG 41	CAGGCCAAT TCCTTTCATG GGAAGCACT AAACCTTATA 51 TGTGGTGGAA CCGAGGCAG CGCGCCGGA CTTTAAGGGC ACACCGGGA CAGGGAGGCAG CAGGAGGCAG CTTAAGGGC ACACCGGGA CAGGAGGAG CAGGAGGAG CAGGAGGAG CAGGAGGAG CAGGAGGAG CAGGAGGAG CAGGAGGAG CAGGAG	4020 4080 4140 4160 60 120 180 240 300 360 420 480 540
50 55	AGCATGTGAC CTTCTGCCCT TGTGTACAAA TAAAAAAAA Seq ID NO: Nucleic Aci Coding sequ 1 GCGCTTGCGG TTTGCAGTTG TGAAAGTACA GAACCCGCA GAACCCCAC CGGGGAGCA CTGCTGTTGG AGAGCGCCC CATATCTCAG	GGGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAA 112 DNA Se d Accessic ence: 286. 11 AGGATTGCG7 CACATTGGAT GCCGCCGC GGGCCTGAG CGGCCGGCTTT TCTCAGCTG CACACAACAAAA AAGACGGTA	GTTTAGTTAG CATAGTATAG CATAGTAGAG ATTTATGAG ATTTATGAG IS21 21 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ATTAGGCTTT A MODITATA CCATGACCAA 187.1 31 CCATGACCAA A CACCGACACA A CACCGACGAA A CACCGACGAC A GAAAGGCACG C AAGACCCTTG G ATCACCAAC C CCCTCAGAGC C TCCTGCAAC C TCCTCCAAC C T	GCTATATCCC GTGGTTGGTG ATACANACAA ATTANATATG 41 GTCACCAACC TGACGCTGG GCCCATGGA GCCCATGGA GCCCATGGA TGCTCGTTGT AAGACTAGC GATTGTGTCC ATGGACAGGACC ATGGACAGAGAC ATGGACAGGAC ATGGACAGGAC ATGGACAGGAC ATGGACAGGAC ATGGACAGGA	CAGGCCAAAT TCCTTTCATG GGAAGCACT AAACCTTATA 51 TGTGGTGGAA CCGGAGCAG CGCGGCCGGA CTTTAAGGGC ACAACGGGGA CAGCGGGA CAGCAGGAGCAG CAGCAGGAGCAG CAGCGGAGCAG CAGCGGAGCAG CAGCGGAGCAG CAGCGGAGCAG CAGCGAGGAGCAG CAGCGGAGCAG CACTGGACAC	4020 4080 4140 4160 60 120 180 240 300 420 480 540 600
50 55	AGCATGTGAC CTICTGCCCT TGTGTTACANA TANAANANA Seq ID NO: Nucleic Aci Coding sequ 1 GCGCTTGCGG TTTGCAGTTG TGANAGTACA GANACCCCAC CAGANCGCCC CGGGAGCCA AGAGGCGCCC CATATCTCAG CACTGTTTCA	GGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT ANAAAAAAA 112 DNA Se ence: 286. 11 AGGATTGCGT CACATTGGAT ACCTCTGGGCGCCGCTGGGCCGTTGGGCCGCTGGGCCCGCTGACAAAAAAAA	GTTTAGTTAG CATAGTATAG CATAGTAGAG ATTTATGAG GQUENCE IN #: NM_14' .1521 21 1 TAAGAGAGAC C CCCAAGTCAG C CCCAAGTCAG G GGGGGCCCG C CCGGGTCCC A GACGTCAG A GACTTATAGG G GAGGCCCG C CCGGGTCCC A GTCTGCTCT A GAGGTCCAG G AGATTGCAT	ATTAGGETTT TOTAL TOTA	GCTATATCCC GTGGTTGGTG ATACANACAA ATTANATATG 41	CAGGCCAAT TCCTTTCATG GGAAGCACT AAACCTTATA 51 TGTGGTGGAA CCGGAGGCAG CCGGAGCAG CACAGGGAGCAG CAGGGAGGAG CAGGGAGGG	4020 4080 4140 4160 60 120 180 240 300 360 420 480 540 600 660
50 55 60	AGCATGTGAC CTTCTGCCCT TGTGTACAAA TAAAAAAAA Seq ID NO: Nucleic Aci Coding sequ 1 GCGCTTGCGG TTTGCAGTTG TGAAACTACA GAACCCCGCA TGAAACCCAC CAGAAACCCCC CAGGAGCCA CTGCTGTTGG AGAGCGCC CATATCTCAG CACTGGAAT CTTAGTCCCT CTTAGTCCCT	GGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAA 112 DNA Se cence: 286. 11 AGGATTGGGT CACATTGGAT GGCCGGCGCG ATCTCTGGGC GGCCTTAGGT GGCCTGAGCT TCTCAGCTGG TCTCAGCTGG TCTCAGCTGGT AACACAAA AAGACGGTM ACCTCCTTTT ACCACCACTA	GTTTAGTTAG CATAGTATAG CCTATTTGAG ATTTATGAG ATTTATGAG I I I I I I I I I I I I I I I I I I I	ATTAGECTTT A TOTATTATA T CCATGACCAA 107.1 31 T CTTATTTATT C CCGCCCGAA A CCCTCGACACA C CACCGACGAT A GCCTTCCCTA G AAAAGCACTC G AAAACCCTTC G ATCACCAAC C CCCTCGAAAT C CCCTGCAAAT C TGCACCAACA C TCTGCAAAT A GCTTTCAACAACAGT C TCTGCAAAT C TGCACCAACAACAGT A GTGTTCTCACTAACAACAGT A GTGTTCTCACTAACAACAGT A GTGTTCTCACTAACAACAGT A GTGTTCTCACTAACAACAGT A GTGTTCTCACT	GCTATATCCC GTGGTTGGTG ATACANACAA ATTANATATG 41 GTCACCANCC TGACGCTTGC TGACGCATGGA GCCCATGGA GCCCAGGACC TGCTCATTGTCC ATGGCAGGAC ATGGACAGGA GGTGATTCAGC GGGAAGAAGGA GGGAAGAAGAAGAAGAAGAAGAAGAAG	CAGGCCAAT TCCTTTCATG GGAAGCACT AAACCTTATA 51 TGTGGTGGAA CCGAGGCAG CGCGCCGGA CTTTAAGGGC ACAACGGGGA CAGGAGGCAG CAGGAGGCAG CAGGAGGCAG CAGGAGGCAG CAGGAGGCAG CAGGAGGCAG CAGGAGGCAG CAGGAGGCAG CAGGAGGCAG CAGGAGGCAG CAGGAGGCAG CAGGAGGCAG CAGGAGGCAG CAGGAGGCAG CAGGAGGCAG CAGGAGGCAG CAGGAGGCAG CAGGAGGCAG CACTTCCCGGCAG CACTTCCCGGCAG CACTTCCCGGCAG CACTTCCCGGCAG CACTTCCCGGCAG CACTTCCCGG	4020 4080 4140 4160 60 120 180 240 300 420 480 540 660 660 720
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50 55 60 65 70 75	AGCATGTGAC TTGTGCCT TGTGTACAAA TAAAAAAAA Seq ID NO: Nucleic Aci Coding sequ 1 GGGCTTGCGG TTTGCAGTTG TGAAAGTACA GAACCCGCA TGAAACCCAC CAGAACGCCT CAGACGCCC CAGAACCCC CAGAACCCC CAGAACCCC CAGAACCCC CAGAACCCC CAGAACCCC CAGAACCCC CAGAACCCC CAGAACCCC CAGAACCCC CAGAACCCC CCAGAACCCC CCAGAACCCC CAGAACCCC CCAGAACCCC CCACACACCC CCACACACCC CCACACACCC CCACACACCC CCACACACCC CCACACACCC CCACACACCC CCACACACCC CCACACACCC CCACACACC CCACACACC CCACACACC CCACACACC CCACACACC CCACACACC CCACACACC CCACACACC CCACACACC CACACC CCACACACC ACACACC CCACACC C	GGTTTTGTT AAAAAAAA 112 DNA Se d Accessic ence: 286. 11 j AGGATTGCAT AGGATGCG ATCTCTGCG GGCCTGAGCT GGCCTGAGCT CACACAAAAAAAAAA	GTTAGTTAG CTATAGTATA CCTATTGAA CTATAGTAGA CTATAGTAGA CTATAGTAGA CTATAGTAGA CTATAGTAGA CTAGTAGAG CTAGTAGTAGAG CTAGTAGTAGAG CTAGTAGTAGAG CTAGTAGTAGAG CTAGTAGTAGAG CTAGTAGTAGAG CTAGTAGTAGAGG CTAGTAGTAGAGG CTAGTAGTAGAGG CTAGTAGTAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGA	ATTAGGETT TOTAL	GCTATATCCC GTGGTTGGTG ATACANACAA ATTANATATG 41	CAGGCCAAT TCCTTTCATG GGAAGCACT AAACCTTATA 51 TGTGGTGGAA CCGAGGCAG CGCGCCGGA CTTTAAGGGC ACAACGGGA ACACGGGA CTTTAAGGCT CAGGGAGCAG CAGGAGCAG CAGGAGCAG CAGGAGCAG CAGGAGCAG CAGGAGCAG CAGGAGCAG CAGGAGCAG CAGGAGCAG CAGGAGCAG CACTTCCGG AGGAGCAG CTTAAGCAT CTGAAGTGT CTGAAGTGT CCTCAATGG CCTCAATGG CCTCAATGG CCAGGAGCCA TGCGGAACCG TGAACCTGG AAGGTGATCC TGAACTGGGA CCTTAAGCATCT TGCATCTGG AAGGAACTCTG TAGAACTGGG AAGGAACTGCC TAGAACCTGG TAGAACCTGG TAGAACCTGG AAGGAACTTGCC AAGGAACTCTC	60 120 180 240 300 180 240 300 540 600 660 720 780 840 1020 1140 1260 1320 1340 1560 1620 1620 1640
50 55 60 65 70 75	AGCATGTGAC TTGTGCCTT TGTGTACANA TANANANAA Seq ID NO: Nucleic Aci Coding sequ 1 GCGCTTGCGG TTTGCAGTTG TGANAGTACA GAACCCGCA GGACAGCCCC CGGGGGCA CTGCTGTTGG AGAGCGCCC CATATGTCAG CACTGGAATG CACTGGAATG CACTGGAATG CACTGGAATG CACTGGAATG CACTGGAATG CACTGGAATG CACTGGAATG CACTGGAATG ACTGAGCGTG ACTGAGCGTG ACTGAGCTG ACTGAGAGCAA GCAGAGCCAA GCAGAGCCAA GCAGAGCCCA CGGGGCC CAGAGTGCCT AAGCAGAAGA GCAGAGCCCC CAGAGTGCCT CAGAGAGCTCA GCAGAGACTCTG CCTTTTTTCC CATGACCGGT TAACTTTTCA GGAAATGTCT CATGACCGGT TAACTTTTCA GGAAATGTCT CATGACCGGT TAACTTTTCA GGAAATGTCT CATGACCGGT TAACTTTTCA GGAAATGTCT CATGACCGGT TAACTTTTCA GGAAATGTCT CATGACCGGT TAACTTTTCA GGAAATGTCT CATGACCGGT TAACTTTTCA GGAAATGTCT CATGACCGGT TAACTTTTCA GGAAATGTCT CATGACCGGT TAACTTTTCA GGAAATGTCT CATGACCGGT TAACTTTTCA GGAAATGTCT CATGACCGGT TAACTTTTCA GGAAATGTCT CATGACCGGT TAACTTTTCA GGAAATGTCT CATGACCGGT TAACTTTTCA GGAAATGTCT CATGACCGGT TAACTTTTCA GGAAATGTCT CATGACCGGT TAACTTTTCA GGAAATGTCT CATGACCGGT TAACTTTTCA GGAAATGTCT CATGACCGGT TAACTTTTCA GGAAATGTCT CATGACCGGT TAACTTTTCA CATGACCGGT TAACTTTTCA CATGACCGGT TAACTTTTCA CATGACCGGT TAACTTTTCA CATGACCGGT TAACTTTTCA CATGACCGGT TAACTTTTCA CATGACCGGT TAACTTTTCA CATGACCGGT TAACTTTTCA CATGACCGGT TAACTTTTCA CATGACCGGT TAACTTTTCA CATGACCGGT TAACTTTTCA CATGACCGGT TAACTTTTCA CATGACCGGT TAACTTTTCA CATGACCGGT TAACTTTTCA CATGACCGGT TAACTTTTCA CATGACCGGT TAACTTTTCA CATGACCGGT TAACTTTTCA CATGACCGGT TAACTTTTCA CATGACCGT TAACTTTTCA CATGACCGGT TAACTTTTCA CATGACCGT TAACTTTCA CATGACCGT TAACTTTCA CATGACCGT TAACTTTCA CATGACCGT TAACTTTCA CATGACCGT TAACTTCA CATGACCCG CATTTCA CATGACCCG CATTTCA CATGACCC CATGACCC CATGACCC CATTTTCA CATGACCC CATTTCA CATGACC CATTTCA CATGACC CATTTCA CATGACC CATTTCA CATGACC CATTTCA CATGACC CATTTCA CATGACC CATTTCA CATGACC CATTTCA CATGACC CATTTCA CATGACC CATTTCA CATCA	GGTTTTGTT ACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	GTTTAGTTAG CATAGTATAG CCTATTTGAG ATTTATGAG ATTTATGAG ATTTATGAG ATTTATGAG ATTTATGAG ATTTATGAG CAGAGAGAC CCCAGAGAG CCCCAGAGAG CCCAGAGAG CCGGGGCCCG CCGGCGCG CCGGGGCCCG CCGGCGC CCGGCGC CCGCGCGC CGCGCGC CCGCGCC CCGCGCC CCGCGCC CCGCGCC CCGCCG	ATTAGGETT TOTAL	GCTATATCCC GTGGTTGGTG GTGGTTGGTG ATACAAACA ATTAAATATG I I GTCACCAACC TGACGCTGC TAAATCAGCA GCCCGATCTA GCCCCGATCTA AGGACTAGC GTGTTTGT GGTAAGTGGC ATGGACAGA TCACAAAGA TCACAAAGA TCACAAAGA TCACAAAGA TCACAAAAGA TCACAAAAGA TCACAAAAGA TCACAAAAGA TCACAAAAGA TCACAAAAGA TCACAAAAGA TCACAAAAGA TTAAATGAAGT AAGACATC ATGAGACT ATGAGA	SAGGACCAAT TOCTTTATA GGAAGCACT AAACCTTATA S1 TGTGGTGGAA CCGGAGGCAG CGCGCCGGA CTTTAAGGGC CGCGCCGGA CTTAAGGCC TCCCCAGCAG CACACGGAGCAC CTATAGCACT TCCCCAGCAG ACACTGGACCA ACACTGGACCA ACACTGCACC ATCAGGCAT CTATAGGACT TTGCAGTCT TGTGGGGAC CCTATAGGACCA AGGATCATCG TGGTGGAACCG TGGTGGAACCG TGGTGGAACCG TGGTGGAACCG TGGTGGAACCG TGGTGGAACCG TGAACCGGGC TAAACCGGGG TGAAACCGGG TAAACCGGG 120 180 180 190 190 190 190 190 190 190 190 190 19	
50 55 60 65 70 75	AGCATGTGAC TTTTCTGCCCT TGTGTACAAA TAAAAAAAA Seq ID NO: Nucleic Aci Coding sequ 1 GCGCTTGCGG TTTGCAGTTG GAAACCCAGC CAGAACCCAGC CAGAACCCCGCA TGAAACCCAC CAGAACCCCC CAGAACCCCC CATATCTCAG CACTGGAGT TAAACTCAC CAGAACCCC CATATCTCAG CACTGGAGT ATCATAGGAG TTACTGTGGA CCTGAGACTC GAAGACCTC GCAGAGCCCA ACCAGAACCC CCGGAAGCCC CCGGAATGCCT ACCTGAGTC CCTTTTTCC CCTTATTTCC CCTTTTTCC CATCACCCGT TAACTTTTCA GCAGACCTC CCTTTTTCC CTTACCCGGT TAACTTTTCA GGAAATGTCT CTTTCACACCA TTTCACACCA	GGTTTTGTT ACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	GTTTAGTTAG CCTATTGAG GUERCE ON #: NM_14' .1521 21 1 TGACGAGAC CCTATTGAG CCGAGTCA CCGAGTCA CCGAGTCA CCGAGTCA CCGAGTCA CCGAGTCA CCGAGTCA CCGAGTCA CCGAGTCA CCGAGTCA CCGAGTCA CCGAGTCA CCGAGTCA CCGAGTCA CCGAGTCA CCGAGTCA CCGAGTCA CCGGGTCCC CCAGTCA CCGGGTCCC CCAGTCAGT CCGCAGT CCCGAGTCA CCGGGTCCC CCGCTGGG CCCCAGT A CTCTTACAC CCCTGCTGG CCCCAGTCA A CTCTTGACA CCCCTGTTGACA CCCTGTTGACA CCCTTTTACAC CCTTTTTACC CCCTTTTGACA CCCTTTTGACA CCCTTTTGACA CCCTTTTGACA CCCTTTTGACA CCCTTTTGACA CCCTTTTGACA CCCTTTTGACA CCCTTTTGACA CCCTTTTGACA CCCTTTTGACA CCCTTTTGACA CCCTTTTGACA CCCTTTTGACA CCCTTTTGACA CCCTTTTGACA CCCTTTTGACA CCCTTTTGACA CCCTTTTTGACA CCCTTTTTGACA CCCTTTTTGACA CCCTTTTTGACA CCCTTTTTGACA CCCTTTTTTGACA CCCTTTTTTGACA CCCTTTTTTGACA CCCTTTTTTGACA CCCTTTTTTGACA CCCTTTTTTTGACA CCCTTTTTTTGACA CCCTTTTTTTGACA CCCTTTTTTTGACA CCCTTTTTTTTGCCCCCTTTTTTTTCACCCCCTTTTTTTT	ATTAGGETT TOTAL	GCTATATCCC GTGGTTGGTG ATACANACAA ATTANATATG 41	CAGGCCAAT TCCTTTATAGG GGAAGCACT AAACCTTATA 51 TGTGTGGAA CCGAGGCAG CGCGCGGA CTTAAGGCAC ACCTGGACGC ACCTGGACGC ACCTGGACGC ACCTGGACGC ACCTGGACGC ACCTGGACGC ACCTGGACGC CTATAGCACT TTGCAGTCT TGCAGTCT GCAGTCT TGCAGTCT TGCAGTCT TGCAGTCT TGCAGTCT TGCAGTCT TGCAGTC	4020 4080 4140 4160 120 180 240 300 360 420 480 540 660 720 1080 1140 1200 1260 1320 1380 1440 1560 1680 1740 1860 1860

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	CTTGGCTCAC TATAGCCTTG ACCTCTCAGG CTCAAGCGAT TCTCCCACCT CAGCCATCCA	2040 2100
	AATAGCTGGG ACCACAGGTG TGCACCACCA CGCCCGGCTA ATTTTTTGTA TTTTGTCTAG ATATAGGGGC TCTCTATGTT GCTCAGGGTG GTCTCGAATT CCTGGACTCA AGCAGTCTGC	2160
5	CCACCTCAGA CTCCCAAAGC GGTGGAATTA GAGGCGTGAG CCCCCATGCT TGGCCTTACC	2220
,	TTTCTACTIT TATAATTCTG TATGTTATTA TTTTATGAAC ATGAAGAAAC TTTAGTAAAT	2280
	GTACTTGTTT ACATAGTTAT GTGAATAGAT TAGATAAACA TAAAAGGAGG AGACATACAA	2340
	TGGGGGAAGA AGAAGAAGTC CCCTGTAAGA TGTCACTGTC TGGGTTCCAG CCCTCCTCA	2400
	GATGTACTIT GGCTTCAATG ATTGGCAACT TCTACAGGGG CCAGTCTTTT GAACTGGACA	2460
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	GCACCCATAG CCCCCATCTA TGGACAGGCT GGGACAGAGG CAGATGGGTT AGATCACACA TAACAATAGG GTCTATGTCA TATCCCAAGT GAACTTGAGC CCTGTTTGGG CTCAGGAGAT	2640 2700
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20	TTAAGACCTC AGTAACCATT TCAGCCTCTT TCCAGCAAAC CCTTCTCCAT AGTATTTCAG	3060
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	TCTGGAAGGC ACAGGGTGCT GCTGCCTCCT GGTCTTTGCC TTTGCTGGGC CTTCTGTGCA	3360
25	GGACGCTCAG CCTCAGGGCT CAGAAGGTGC CAGTCCGGTC CCAGGTCCCT TGTCCCTTCC	3420
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	CTTTTATTIT TAATTITTIT GAGACAGAAT CTCACTCTCT CGCCCAGGCT GGAGTGCAAC	3540
	GGTACGATCT TGGCTCAGTG CAACCTCCGC CTCCTGGGTT CAAGCGATTC TCGTGCCTCA	3600 3660
30	GCCTCCGGAG TAGCTGGGAT TGCAGGCACC CGCCACCACG CCTGGCTAAT TTTTGTATTT TTAGTAGAGA CGGGGTTTCA CCATGTTGGT CAGGCTGGTC TCGAACTCCT GACCTCAGGT	3720
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35	GAAATGTGTT ATAATACAAA CAAGGAAGCA CATTGTGTAC AAAATACTTA TGTATTTATG	4020
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15	GCTGGGAGTG AGGCGGCGGA GGAGCCAGGT GAGGAGGAGC CAGGAAGGCA GTTGGTGGGA	120 180
45	AGTCCAGCTT GGGTCCCTGA GAGCTGTGAG AAGGAGATGC GGCTGCTGCT GGCCCTGTTG GGGGTCCTGC TGAGTGTGCC TGGGCCTCCA GTCTTGTCCC TGGAGGCCTC TGAGGAAGTG	240
	GAGCTTGAGC CCTGCCTGGC TCCCAGCCTG GAGCAGCAAG AGCAGGAGCT GACAGTAGCC	300
	CTTCCCCACC CTCTCCCCCT CTCCTGTGGG CGGGCTGAGC GTGGTGGCCA CTGGTACAAG	360
	CACCCCACTC CONTROL TOTAL TOTAL CTACCCCCT GGAGGGGGGG CCTAGAGATT	
50	GCCAGCTTCC TACCTGAGGA TGCTGGCCGC TACCTCTGCC TGGCACGAGG CTCCATGATC	420
	GCCAGCITCC IACCIGNAGA IOCIGGECG IACCIGIGE INCCIGIGE	480
	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA CGATGATGAG	480 540
	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA CGATGATGAG GACCCCAAGT CCCATAGGGA CCTCTCGAAT AGGCACAGTT ACCCCCAGCA AGCACCCTAC	480 540 600
	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA CGATGATGAG GACCCCAAGT CCCATAGGGA CCTCTCGAAT AGGCACAGTT ACCCCCAGCA AGCACCCTAC TGGACACAC CCCAGCTCAT GGAGAAGAAA CTGCATGCAG TACCTGCGGG GAACACCGTC	480 540 600 660
55	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA CGATGATGAG GACCCCAAGT CCCATAGGGA CCTCTCGAAT AGGCACAGTT ACCCCCAGCA AGCACCCTA TGGACACACC CCCAGCGCAT GGGGAAGAAA CTGCATGCAG TACCTGCGGG GAACACCGTC AAGTTCCGCT GTCCAGCTGC AGGCAACCCC ACGCCACCA TCCGCTGGCT TAAGGATGGA	480 540 600 660 720
55	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA CGATGATGAG GACCCCAAGT CCCATAGGGA CCTCTCGAAT AGGCACAGTT ACCCCCAGGCA AGGACCCTAC TGGACACAC CCCAGCGCAT GGAGAAGAAA CTGCATGCAG TACCTGCGGG GAACACCGTC AAGTTCCGCT GTCCAGCTGC AGGCAACCCC ACGCCACCA TCCGCTGGCT TAAGGATGGC CAGGCCTTTC ATGGGGAGAA CCGCATGGA GGCATCGGC TGCGCCATCA GCACTGGAGT	480 540 600 660
55	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA CGATGATGAG GACCCCAAGT CCCATAGGGA CCTCTCGAAT AGGCACAGTT ACCCCCAGCA AGCACCTAC TGGACACACC CCCAGCGCAT GGAGAAGAAA CTGCATGCAG TACCTGCGGG GAACACCGTC AAGTTCCGCT GTCCAGCTGC AGGCAACCCC ACGCCCACCA TCCGCTGGCT TAAGGATGGA CAGGCCTTTC ATGGGGAGAA CCGCATTGGA GGCATTCGGC TGCGCCATCA GCACTGCAG CTCTGTGATGG AGAGCGTGGT GCCCTCGGAC CGCGGCACAT ACACCTGCCT GGTAGAGAAC GCTTGTGGGCA GCATCCGCTA TAACTACCTG CTAGATGTGC TGGAGGGGTC CCCGCACCGG	480 540 600 660 720 780
55	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA CGATGATGAG GACCCAAGT CCCATAGGGA CCTCTCGAATA AGGACAGTT ACCCCCAGGCA AGGACCCTAC TGGACACACC CCCAGCGCAT GGAGAAGAAA CTGCATGCAG TACCTGCGG GAACACCGTC AAGTTCCGCT GTCCAGCTGC AGGCAACCCC ACGCCCACCA TCCGCTGGCT TAAGGATGGA CAGGCCTTTC ATGGGAGAA CCGCATGGA GGCATTCGG TGGCCCATCA GCACTGGAG CTCGTGATGG AGAGCGTGG GCCCTCGGAC CGCGCCACA TACACCTGCCT GGTAAGAAC GCTTTGGGCA GCATCGGCTA TAACTACCTG CTAGATGTGC TGGAGCGGTC CCCCCACCCG CCCATCCTGC AGGCCGGCAAC ACCACAGCGG TGGTGGGCAG GAGGTGC CCATCCTGC AGGCCGGCAAC ACCACAGCGG TGGTGGGCAG GAGGTGCGC	480 540 600 660 720 780 840 900 960
	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA GGATGATGAG GACCCCAAGT CCCATAGGGA CCTCTCGAAT AGGCACAGTT ACCCCCAGCGA AGGACCCTAC TGGACACACC CCCAGCGCAT GGAGAAGAAA CTGCATGCAG TACCTGCGG GAACACCGTC AAGTTCCGCT GTCCAGCTGC AGGCAACCCC ACGCCCACCA TCCGCTGGCT TAAGGATGGA CAGGCCTTTC ATGGGAGAA CCCCATTGGA GGCATTCGGC TGCGCCATCA GGACTGGGG CTCGTGATGG AGAGCGTGGT GCCCTCGGAC CCCGCACAT ACACCTGCCT GGTAGAGAAC GCTGTGGGCA GCATCCGCTA TAACTACCTG CTAGATGTGC TGGAGCGGTC CCCGCACCGC CCCATCCTGC AGGCCGGCCT CCCGGCCAAC ACCACAGCG TGGTGGGCAG CGACGTGGAG CTGCTGTGCA AGGTCTACAG GGATGCCCAC CCCCACATCC AGTGGCTGAA GCACATCTAC	480 540 600 660 720 780 840 900 960
55 60	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA CGATGATGAG GACCCAAGT CCCATAGGGA CCTCTCGAAT AGGCACAGTA ACCCCAGCA GGACCCTAC TGGACACACC CCCAGCGCAT GGAGAAGAAA CTGCATGCAG TACCTGCGGG GAACACCGTC AAGTTCCGCT GTCCAGCTGC AGGCAACCC ACGCCCACCA TCCGCTGGCT TAAGGATGGA CAGGCCTTTC ATGGGGAGAA CCGCATTGGA GGCATTCGGC TGCGCCATCA GCACTGAGT CTCGTGATGG AAGACGTGGT GCCCTCGGAC CGCGCACAT ACACCTGCCT GGTAGAGAAC GCTGTGGGCA GCATCCGCTA TAACTACCTG CTAGATGTGC TGGAGCGGTC CCCGCACCGG CCCATCCTGC AGGCCTGGCT CCCGGCCAAC ACCACAGCG TGGTGGCAG GAACGTGCAG CTGCTGTGCA AGGTGTACAG CGATGCCCAG CCCCACATCC AGTGGCTGAA GCACATCGTC ATCAACGGCA GCAGCTTCGG AGCCGACGGT TTCCCCCTATG TGCAAGTCCT AAAGACTGCA	480 540 600 660 720 780 840 900 960 1020
	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA CGATGATGAG GACCCAAGT CCCATAGGGA CCTCTCGAAT AGGACACTTA ACCCCCAGCA AGACCCTAC TGGACACACC CCCAGCGCAT GGAGAAGAAA CTGCATGCAG TACCTGCGG GAACACCGTC AAGTTCCGCT GTCCAGCTGC AGGCAACCCC ACGCCCACCA TCGCCTGGCT TAAGGATGGA CAGGCCTTTC ATGGGAGGA CGCATTGGA GGCATTGGC TGGCCCATCA GCACTGGAGT CTCGTGATGG AGAGCGTGGT GCCCTCGGAC CCCGGCCACA ACACCTGCCT GGTAGAGAAC GCTGTGGCGA GCATCCGCTA TAACTACCTG CTAGATGTGC TGGAGCGGTC CCCCCCCCCGCCACA ACCCACAGCG TGGTGGGAG GAGGTGGAG CCCATCCTGC AGGCGGGCT CCCGGCCAAC ACCCACAGCG TGGTGGGAG GAGGTGGAG CTGCTGTGCA AGGTGTACAG CGATGCCCAG CCCCATCCTAT TGCAAGTCCT AAAGATGCC ATCAACGGCA GCAGCTTCGG AGCCAGGGT TTCCCTTAT TGCAAGTCCT AAAGATGCC AGCATCAATA GCTGAGAGT GAGGGGTCT TACCTGCGGA ACCTGCAGC CGAGGGAGGCA	480 540 600 660 720 780 840 900 960 1020 1080 1140
	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA GGATGATGAG GACCCAAGT CCCATAGGGA CCTCTCGAAT AGGACAGCTT ACCCCCAGCA AGGACCCTAC TGGACACACC CCCAGCGCAT GGAGAAGAAA CTGCATGCAG TACCTGCGG GAACACCGTC AAGTTCCGCT GTCAGGTGC AGGCAACCCC ACGCCCACCA TCCGCTGGCT TAAGGATGGA CAGGCCTTTC ATGGGAGAA CCCCATTGGA GGCATCGGC TGGCCATCA GCACTGGAGT CTCGTGATGG AGAGCGTGGT GCCCTCGGAC CCCGCCACAT ACACCTGCCT GGTAGAGAAC GCTGTGGGGA GCATCCGCTA TAACTACCTG CTAGATGTGC TGGAGCGGTC CCCGCACCGG CCCATCCTGC AGGCCGGGCT CCCGGCCAAC ACCACACCG TGGTGGGAG CGACGTCGGAG CTGCTGTGCA AGGTCTTACAG CGATGCCCAA CCCCACATCC AGTGGCTGA GCACTCGTC ATCAACGGCA GCAGCTTCGG AGCGAGGTT TTCCCCTATG TGCAAGTCCT AAAGACTGCA GACATCAATA GCTCAGAGGT GGAGGTCCTG TACCTGCGGA ACGTGTCCAG CGCGAGATCA GGCGAGTACA CCTGCCTCGC AGGCAATTCC ATCGGCCTC CCTACCAGTC TGCCGGGTC GGCGAGTACA CCTGCCTCGC AGGCAATTCC ATCGGCCTCT CCTACCAGTC TGCCTGGGCTC	480 540 600 660 720 780 840 900 960 1020 1080 1140
60	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA CGATGATGAG GACCCAAGT CCCATAGGGA CCTCTCGAAT AGGCACAGTT ACCCCCAGCA AGCACCTAC TGGACACACC CCCAGCGCAT GGAGAAGAAA CTGCATGCAG TACCTGCGGG GAACACCTC AAGTTCCGCT GTCAGCTGC AGGCAACCC ACGCCCACCA TCCGCTGGCT TAAGGATGGA CAGCCTTTC ATGGGGAGAA CCCCATTGGA GGCATTCGGC TGCGCCATCA GCACTGGAGT CTCCTGATGG AGAGCATGGT GCCCTCGGAC CGCGCACAT ACACCTGCCT GGTAGAGAAC GCTGTGGGCA GCATCCGCTA TAACTACCTG CTAGATGTGC TGGAGCGGTC CCCCACCGG CCCATCCTGC AGGCTGACAG CGATGCCCAG ACCACAGCG TGGTGGGCAG CGACGTGGAG CTGCTGTGCA AGGTGTACAG CGATGCCCAG CCCCACATCC AGTGGCTGAA GCACTGCTG ATCAACGGCA GCAGCTTCGG AGCCGACGGT TTCCCCTATG TGCAAGTCCT AAAGACTGCA GACATCAATA GCTCAGAGGT GAAGTCCTT TACCTGCGGA ACCTGTCAGC CGAGGAGGGC GGCGAGTAC CCTGCCTCGC AGGCAATTCC ATCGGCCCAC CGACGAGGCC CACGTGTCGC CAGAGGAGGA CCCCACATGG ACCGCAGCAG CGCCCAGGCC CAGGTTATACG	480 540 600 660 720 780 840 900 960 1020 1080 1140 1200
	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA GGATGATGAG GACCCAAGT CCCATAGGGA CCTCTCGAAT AGGACACTTA ACGCCCAGTT ACCCCCAGCA AGGACCCTAC TGGACACACC CCCAGCGCAT GGAGAAGAAA CTGCATGCAG TACCTGCGG GAACACCGTC AAGTTCCGCT GTCAGGTGC AGGCAACCCC ACGCCCACCA TCCGCTGGCT TAAGGATGGA CAGGCCTTTC ATGGGAGAA CCCCATTGGA GGCATCGGC TGGCCATCA GCACTGGAGT CTCGTGATGG AGAGCGTGGT GCCCTCGGAC CCCGCCACAT ACACCTGCCT GGTAGAGAAC GCTGTGGGCA GCATCCGCTA TAACTACCTG CTAGATGTGC TGGAGCGGTC CCCGCACCGC CCCATCCTGC AGGCCGGGCT CCCGGCCAAC ACCACACCG TGGTGGGCAG CGACGTCGGAG CTGCTGTGCA AGGTCTACAG GGATGCCCAC CCCCACATCC AGTGGGCAG CGACGTCGGAG GACATCAATA GCTCAGAGGT GGAGGTCCTG TACCTGCGGA ACGTGTCAG GACATCAATA CCTGCCTCGC AGGCAATTCC ATCGGCCTC CTACCAGTC TGCTGCGGA ACGTGCTGC CAGAGGAGA CCCCACATGC ACGCGAGGA CGCCCAGGC CAGGTATACG GACACTCATC TGTAGCGCTC GGGCTCCTG TGCTGCTG TGCTCCTGCT CTTACCAGGTC CAGGGAGCAC CCCCACATGC ACCGCCAGCG CCCCCACCAC CAGGTATACG GACATCATC TGTAGCGCTC CGGCTCCTG TGCTCTGCTG TGCTCCTGCT CTTATCCAGTC CCAGGGCCCT CCACGGCCCG CCCCCCCCCC	480 540 600 660 720 780 840 900 1020 1080 1140 1200 1220 1380
60	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA GGATGATGAG GACCCAAGT CCCATAGGGA CCTCTCGAATA AGGCACAGTA ACACCCGAC AGACCCTAC TGGACACAC CCCAGCGCAT GGAGAAGAAA CTGCATGCAG TACCTGCAGGA AGCACCCTAC AGTTCCGCT GTCAGGTGC AGGCAACCCC ACGCCACCA TCCGCTGGCT TAAGGATGGA CAGGCCTTTC ATGGGAGGAGA CCGCATGGA GGACTTCGC TCGCTGGCT TAAGGATGGA CTCGTGATGG AGAGGAGGAG CCCGCACCAT ACACCTGCCT GGTAGAGAGC CTCTGGGCA GCATCCGCTA TAACTACCTG CTAGATGTGC TGGGCAGG CGACCGG CCCATCCTGC AGGCCGAGGT CCCGGCCACA CACACAGCG TGGTGGCAG GACGTGCAG ATCAACGGCA GCAGCTTCGG AGCCGACGAT TTCCCCTATA TGGACTGAA GCACTCAGAG GAGGTTCCG AGCCACAGTC TTCCCCTATA TGCATGGCT ATCAACGGCA GCAGCTTCGG AGCCGACGT TTCCCCTATA TGCAACGTCC AGACCTGCA GGCGAGTACA CCTCCCCCCC AGGCAATTC ATCGCCCTG ACCGCAGGG CACCCCACAGC GACATCATC TGTACCGCTC GGCCTCGCTG CCCCACATGC ACCGCCAGG CACCCCCCC CTGACAGGT CGCCGAGGG CACCCCCCCC CGCCCACCCCC TGTCCAGCC CGTGCAGAG GACATCATC TGTACCGCTC CAGGCCCGC CACCCCCCCC CGCCCCACC CTTGCCAGGC CTCTCCCCCT TCCCTCTGGC CCGACAGTC TCCCTGGGT GCCCCCCACC CTTGCCAGGC CTCTCCCCCT TCCCTCTGGC CCGACAGTC TCCCTCGGT CCCCCCCCC CGCCCCCCC TGTCCAGAG CTCTCCCCCCT TCCCTCTGGC CCGACAGTC TCCCCTCGGT CACCCCCCCC CGCCCCCCC CTGCCAAGAC CTCTCCCCCCT TCCCTCTGGC CCGACAGTC CACCCCCCCC CGCCCCCCC TGTCCAGAGC CTCTCCCCCT TCCCTCTGGC CCGACAGTC CACCCCCCCC CGCCCCCCC CTGCCAGAGC CTCTCCCCCTT TCCCTTCTGCC CCGACAGTC TCCCTGGGT CACCCCCCCCC CGCCCCCCCC CTGCCCAATCC	480 540 660 720 780 840 960 1020 1140 1200 1260 1320 1380
60	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA GATGATGAGGACCACAGT CCCATAGGGA CCTCTCAGATA AGGACACTAC TGGACACAGT CCCATAGGGA CCTCTCCAGATA AGGACACTAC TGGACACACC CCCAGCGCAT GAGCAAGAAA CTGCATGCAG TACCTGCAGG GAACACCGTC AGGCCACCA TCCGCTGGCT TAAGGATGGA CAGGCCATTCA AGGGGAGAGAAA CTGCATGCAG TGGCCCATCA GACTGGAGT CCCTGGATGG AGAGCGTGGT GCCCATCAG CACTGGAGT GCCCTTCGATGG AGAGCGTGGT GCCCATCAGACACTCAGACACTCAGACACTCAGACACTAGAACACACAGACAG	480 540 600 660 720 780 900 960 1020 1140 1200 1326 1320 1380 1440
60	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA GGATGATGAG GACCCAAGT CCCATAGGGA CCTCTCGAAT AGGACACTTA ACGCCCAGTT ACCCCCAGCA AGACCCTAC TGGACACACC CCCAGCGCAT GGAGAAGAAA CTGCATGCAG TACCTGCGG GAACACCGTC AAGTTCCGCT GTCAGGTGC AGGCAACCCC ACGCCCACCA TCCGCTGGCT TAAGGATGGA CAGGCCTTTC ATGGGAGAA CCCCATTGGA GCCATCGCT GGACGCATC GGACTGGAGC CTCGTGATGG AGAGCGTGGT GCCCTCGGAC CCCGGCCACA ACACCTGCCT GGTAGAGAAC GCTGTGGGCA GCATCCGCTA TAACTACCTG CTAGATGTGC TGGAGCGGTC CCCGCACCGC CCCATCCTGC AGGCCGGGCT CCCGGCCAAC ACCACACGC TGGTGGGCAG GACGTGGAG CTGCTGTGCA AGGTCTACAG GGATGCCCAC CCCCACACC TGGTGGCGAG GACGTGGAG ATCAACGGCA GCAGCTTCCG AGCCGACGT TTCCCCTATG TGCAAGTCCT AAAGACTGCA AGCATCAATA GCTCAGAGGT GGAGGTCCTT ATCCTGCGGA ACGTGTCAGC CAGGAGAGCA GACATCAATA CCTGCCTCGC AGGCAATTC ATCGGCCTC CTACCAGTC TGCCTGGCTC ACGTGCTGC CAGAGAGAGA CCCCACATGG ACCGCACAGC CCCCCAGGGC CAGGTATACG GACATCATCC TGTACGCGTC CCAGGGCCGC CCCCCCCCC CCCCCCCCC CTGTGCTGCGCA ACGTTATCGAG GGCAGGCGCT CCAGGGCCGC CACCCCCCC CGCCCCCCCC TTGCAAGTAA ACGTCATCC TGTACGAGG CGCGCTCCTCCTGGCTG TGCTCCTGCT CCTGCCGGA ACGTCATCC TGGTACGAGG CGCCCCCCCC CCCCCCCCCC	480 540 600 660 720 780 900 960 1020 1140 1200 1320 1380 1440 1500
60	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA GGATGATGAG GACCCAAGT CCCATAGGGA CCTCTCGAATA AGGCACAGTA ACACCCTAC TGGACACAC CCCAGCGCAT GGAGAAGAAA CTGCATGCAG TACCTGCAGGA AGCACCCTAC AGTTCCGCT GTCAGGTGC AGGCAACCCC ACGCCCACCA TCGCTGGCT TAAGGATGGA CAGGCCTTTC ATGGGAGGAGA CCGCATGGA GGACCATCA CTCTGTGATGG AGGCGGGAGA CCCCACATGCG TGCGCCATCA GCACTGGAGG CTCTGTGATGG AGGCGGGCT CCCGGCCACA CACACAGCG TGGTGGCAG GGAGGGTC CCCATCCTGC AGGCCGGCT CCCGGCCACA CACACACGC TGGTGGCAG GACGTGCAG CTCATCCTGC AGGCCGTC AGCCGACGGT TCCCCCACTCC ATCAACGGCA GCAGCTTCGG AGCCGACGGT TTCCCCTTATG ATCAACGGCA GCAGCTTCGG AGCCGACGGT TTCCCCTTATG ACACGCAG GCAGCTCCC AGGCATTCC ATCCTGCATCC GGCGGAGTACA CCTCACTGC AGGCATTCC ATCCTGCAGC CGAGGAGGC GACTCATCC TGTACGACGT CCCCACATGC ACCCCCCCCC CCAAGGC CAGTTACAG GACATCATCC TGTACGCGC CCCCACATGC ACCCCCCGCC CCCACAGCC CGCTATACAGCC CGAGTATACA CTCTCCCCCT TCCCTCTGCC CGGCCCCC CCCCCCCCC	480 540 600 660 720 780 840 900 1020 1080 1120 1260 1120 1120 11500 1500 1620
60	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA GGATGATGAG GACCCAAGT CCCATAGGGA CCTCTCGAATA AGGCACAGTA CCACCCAGCA AGACCCTAC TGGACACACC CCCAGCGCAT GAGAAGAAA CTGCATGCAG TACCTGCAGGA AGACCCTAC AGGTTCCGCT GTCCAGCTGC AGGCAACCCC AGGCCACCA TACCTGCGCG GAACACCGTC CAGGGCTTTC ATGGGAGGA CGCATCGGA GGCCATCAC TCCGCTGGCT TAAGGATGGA CTCGTGATGG AGAGCGTGGT GCCCTCGGAC CGCAGCACA ACACCTGCCT GGTAGAGAAC CCCATCCTGC AGGCGGGCT CCCGGCCAAC ACCCACAGCG TGGGGCGAC GAGGTGGAG CTGCTGTGCA AGGTGTACAG CGATGCCAG ACCCACAGCG TGGTGGGGAG GAGGTGGAG CTGCTGTGCA AGGTGTACAG CGATGCCAG CCCCATCCTAG ACCCAGGCAG GAGGTGGAG CTGCTGCCAACGC AGGCGACTC TACCTGCTGA ACCCACAGCG TGGTGGGCAG GAGGTGGAG CACATCAATA GCTGAGAGT GAGGGTCTT TACCTGCGA ACCGTCAGCG GACATCAATA GCTGAGAGT GAGGGTCCTT TACCTGCGA ACCGTCACGC CACATCATC CTGACAGCT AGGCGATCC TCCCCACAGC CAGGGAGCGCA CACATCATCC TGTACCAGCT CCCCACATG ACCGCAGCAG CAGGCACCG CACATCATCC TGTACCAGCT CACAGCCGC CACCCCGCC CGCCCACACC CTGTATCCAG GGCAGCGCT CACAGCCGG CACCCCCGC CGCCCACCAC TGTGCAGAGC CTCTCCCCCT TCCCTCTGGC CGCACAGTC TCCCTGGAGT TCCCCGGGA CTCTCCCCCT TCCCTCTGGC CGCACAGTC TCCCTCGGGT CACGCCCCCCC CTGTACCAGC CAGGCAGCGC CACCCCGCC CGCCCCCCCC TGTGCAGGAC CTCTGCAGCAC CTCCTGGGC CACCCCGCC CGCCCCCCCC TGCGCCAGC CTCTGGAGCC CAGGCAGCAC CTATGGGAGT TCCCCCGGGA CTCTGGAGCCC TACAGGCAG CGCCGCCCCCCC CGCCACCTC CCCCACAGCAC CTCTGGAAGC CCCTAGCCAC CGCGCGCCCCCCCCCCCC	480 540 600 660 720 840 900 1020 1140 1200 1200 1380 1440 1500 1560 1660
60	GECCEGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA GGATGATGAG GACCCAAGT CCCATAGGGA CCTCTCGAAT AGGACAGTT ACCCCCAGCA AGGACCTAC TGGACACAC CCCAGCGCAT GGAGAAGAAA CTGCATGCA TACCTGCGG GAACACCTC AAGTTCCGCT GTCAGGTGC AGGCAACCCC ACGCCCACA TCCGCTGGCT TAAGGATGGA CAGGCTTTC ATGGGAGAA CCCCATTGGA GCATTGGG TGGCCATCA GCACTGGAGT CTCTGAATG AGAGCGTGGT GCCCTCGGAC CCCGCCACAT ACACCTGCCT GGTAGAGAAC GCTGTGGGCA GCATCCGCTA TAACTACCTS CTAGATGTGC TGGAGCGTC CCCGCACCGC CCCATCCTGC AGGCCGGGCT CCCGGCCAAC ACCACACGC TGGTGGGGAG GAACTGGAG CTGCTGTGCA AGGTCTACAG GGATGCCCAC CCCCACACC TGGTGGGCAG GACATGGAG ATCAACGGCA GCAGCTTCCG AGCCGACGT TTCCCCTATG TGCAAGTCCT AAAGACTGCA AGCAGGATACA CCTGCCTCGC AGGCAATTC ATCGGCCTC CCTACCAGTC TGCAGGCGCA ACGGTGCTGC CAGAGGAGGA CCCCACATG ACCGCAGCAG CGCCCAGAGC CAGGTATACA GACATCAATC CTGCACCCGC CCCCACATG ACCGCAGCAG CGCCCAGAGC CAGGTATACG GAACTCATCC TGTACGCGTC CCAGGGCCGC CACCCCCCC CGCCCCACCAC CAGGTATACG CTCTCCCCGT TCCCTCTGGCG CCAGGAGCAGC CCCCCCCCC CGCCCCCCC CTGTGCAGGAG CCCTCTGCAGTC TCCCTCTGGCG CCACAGCCC CCCCCCCCC CGCCCCCCCC CGCCCCCCC CTGTATCCAG GGCAGCGCT CCAGGGCCG CACCCCCCCC CGCCCCCCCC TITGCAGAGA CCTCTCCCCTGTACCAG CGCCTCCTC TCCTCCAGGG CCCCCCCCCC	480 540 600 660 720 840 900 1020 1080 1140 1250 1320 1380 1440 1500 1620 1620
60	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA GGATGATGAG GACCCAAGT CCCATAGGGA CCTCTCGAATA AGGCACAGTA CACCCCTAC TGGACACAC CCCAGCGCAT GAGAAGAAA CTGCATGCAG TACCTGCAGGA AGACCCTAC AGGTTCCGCT GTCAGGTGC AGGCAACCCC AGGCCACACA TCGCTGGCT TAAGGATGGA CAGGCCTTTC ATGGGAGGAGA CGCCACCACACA TCGCTGGCT TAAGGATGGA CTGTGATGG AGAGGTGGT GCCCTCGGAC CGCCACACAT ACACCTGCCT GGTAGGAGC CCCATCCTGC AGGCCAGGCT CCCGGCCAAC ACCCACAGCG TGGTGGGGGC GGAGTGGAG CCCATCCTGC AGGCGGGCT CCCGGCCAAC ACCCACAGCG TGGTGGGGAG GAGGTGGAG CTGCTGTGCA AGGTTTCAG AGCCGACGGT TCCCTATG TGCAGTCCT AAAGACTGCA ATCAACGGCA GCAGCTTCAG AGCCGACGGT TCCCCTATG TGCAGTCCT AAAGACTGCA AGCATCAATA GCTGAGAGT GAGGGTCCTT ACCTGCGGA ACCTGCAGC CAGGAGGAGC GACATCATC CTGTCAGGGT GAGGGTCCTT ACCTGCGGA ACCTGCAGC CAGGAGGCC CTGTATCAG GGAGGAGGAC CCCCACATG ACCGCACAGC CAGCTACACC CTGTATCAG GGAGGAGGA CCCCACATG ACCGCACAGC CAGCTACACA CTCTCCCCCT TCCCTCTGGC CGACAGCGC CACCCCGCC GCCCCACACC CTGTATCAGG GGAGGCGCT CACCGCCAC CACCCCGCC CTCTGAGCA TACTCTGGCC CTGTACAGCC TCCTCTGGC CGACAGGTC TCCCTGGAGT CAGCCCACACC CTCTGGAGC TAGACTACAC CTGCGCACAG CCCCGCCCAC TTTGCAGAG CTCTCCCCCT TCCCTCTGGC CGACAGCAC CACTCACAGG CTCTTGGGAAGC CCCTAGGCGA GGCTCCTT CCCCCGGGA CTCTTGGGAAGC CCCACACGCAC CTATGGGAGT TCCCCCGGGA CTCTTGGCAGAG CCCTAGCCAC CTGCGCTCC TCCCCCGGC CTCTGGAGC CCCACACCCCC CGCCACCT TCCCCCGGG CTCTGGAGC CCCACACGCAC CTATGGGAGT TCCCCCGGGA CCCCCCCCCAC TAGCCAGCACCCCCCC CCCCACCTT CCCCCCGGG CTCTGGAGCC CCCACACCCCC CCACACCCCCC CCCACACCCCCCC	480 540 600 660 720 840 900 1020 1140 1200 1320 1380 1440 1500 1560 1680 1740 1860
60 65 70	GECCEGEAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA GATGATGAGGA GACCCCAACT CCCATAGGGA CCTCTCCAGATA AGGCACCTAC TGGACACCAC CCCAGCGCAT GAGAAGAAA CTGCATGCAT ACCCCCAGCA AGACCCCTAC AGGTCACCCAC CCCAGCGCAT GAGAAGAAA CTGCATGCAT TACCTGCGGG GAACACCGTC AGGCCTTCC AGGGGAGAGAAA CCGCATGGAG GCCATCAGCACCACA TCCGCTGGCT TAAGGATGGA CCCATGGAGT GCCTCGAGTGAG GCCTTGGAGGGCTT CACGGGGAGACACCTA GCCCTGGACCGG CCCATCCTGC AGGCCGGCACA ACACCTGCCT GGTAGAGAAC CCCCATCCTGC AGGCCGGCCACA ACACCTGCCT GGTAGAGAAC CCCCACTCCTGC AGGCCGGCCACA ACACCACGCG TGGTGGGGGC CCCCACCCGG CCCCACCTCC ACCGCCACA ACACCACGCC TGGTGGGAG CACGTGGAG CCCCACATCC AGTGGCTGAA GCACTGAGAG CCCCACATCC AGTGGCTGAA GCACTGCAGC GAGCTGCAG CACCCCCACATC AGTGGCTGAA GCACTGAGAG CACACCACCGC TGCACAGCA GCACCTCCACATC AGGCAGGAGACACACACACCACCC CCCCACATCC AGGCAGTACA CCTGCCTCCC AGGCAATCA CCTGCCTCCC CAGGCACATC ACCGCCAGAG CCCCCACATC AGGCAGCACACACCACCCC CAGGGAGACCAACCACCCCC CAGGCACACCCCCC CAGGCACACCACCCC CAGGCACACCACCCC CAGGCACACCACCCCC CAGCCCACCCC CAGGCACCCCCC CAGGCACACCACCCCC CAGCCCACCCC CAGCCACACCACCCC CAGCCCACCCC CAGCCCACCCC CAGCCCACCCC CAGCCCACCCC CAGCCCACCCC CAGCCCACCCC CAGCCCACCCCC CAGCCCACCCCC CAGCCCACCCC CAGCCCACCCC CAGCCCACCCCC CAGCCCACCCC CAGCCCACCCC AGCCCACCC CAGCCCACCC CAGCCCACCC CAGCCCACCC CAGCCCACCC CAGCCCACCCC CAGCCCACCCC CAGCCCACCCC CAGCCCACCCC CAGCCCACCCC CAGCCCACCCC CAGCCCACCCCC CAGCCCACCCCC CAGCCCACCCCC CAGCCCACCCC CAGCCCACCCC CAGCCCACCCC CAGCCCACCCCC CAGCCCACCCCC CAGCCCACCCCC CAGCCCACCCCC CAGCCCACCCCC CAGCCCACCCCACCCCCCCC	480 540 660 720 840 960 1020 1140 1220 1280 1380 1440 1500 1620 1680 1740 1800 1800
60	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA GGATGATGAG GACCCAAGT CCCATAGGGA CCTCTCGAATA AGGCACAGTA CACCCCAGCA AGACCCTAC TGGACACAC CCCAGCGCAT GAGAAGAAA CTGCATGCAG TACCTGCGGG GAACACCGTC AAGTTCCGCT GTCCAGCTGC AGGCAACCCC ACGCCCACCA TCGCTGGCT TAAGGATGGA CAGGCCTTTC ATGGGAGGA CCGCATGGA GGCATTCGG TGCGCCGCT TAAGGATGGC CTGTGATGG AGAGCGTGG GCCCTCGGAC CCCGGCCACA TCACCTGCGC TAAGGAGAC CCCATCCTGC AGGCCGGCCTA TAACTACCT CTAGATGGC TGGGCGGC CCCCCCCTCCGAC CCCGGCCACA ACACCGCGC CCCATCCTGC AGGCCGGCCTA CACCACAGCG TGGTGGGCAG GACGTGCGA CCCATCCTGC AGGCCGGCTA CACCACAGCG TGGTGGGCAG GACGTCGGA ACTCACCGC GCAGCCACA ACCACAGCG TGGTGGGCAG GACGTCGAC ATCAACGGCA GCAGCTTCGG AGCCGACGGT TTCCCCTATG TGCAAGTCCT AAAGACTGCA GCAGTCAAA CCTGCCACCAC GAGCAATTCC ATCGGCCTC CCTACCAGTC TGCTGGCCA ACGGTGCTGC CAGAGGAGA CCCCACATCG ACCGCAGCAG GCCCCAGAC CAGGCAGGC CTCTCCCCGT TCCTTGGCC CGGCCCAC CCCCCCCCC CGCCCACATC TGCTGGCCG CTCTTCCCGT TCCTCTGGCC CGGACGTCT TCCCTGGAG CAGCCCACATCA AGCTCATCC TGTACGAGG CCGCACATCT TCCCTGGAG CAGCCCCCCCC CTCTGCACCT TCCTCTGGCC CGGACGTCT TCCCTGGAG CAGCCCCCCCC CTCTGGAGTC TAGACCAC CTCCGAGCCGC CACCCCCCCC CGCCCCCCC CTCTGGAGTC TAGACCAC CTCCGAGCCGC CACCCCCCCC CGCCCCCCC CTCTGGAGTC TAGACCAC CTCCGAGCCGC CACCCCCCCC CCCCCCCCC CTCTGGAGTC TAGACCAC CTCCGAGCCGC CACCCCCCCC CCCCCCCCCC	480 540 600 660 720 940 950 1080 1140 1260 1320 1380 1560 1680 1740 1860 1980
60 65 70	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA GGATGATGAG GACCCAAGT CCCATAGGGA CCTCTCGAATA AGGCACAGTA ACACCCTAC TGGACACAC CCCAGCGCAT GAGAAGAAA CTGCATGCAG TACCTCCAGCA AGACCCTAC AGTTCCGCT GTCAGGTGC AGGCAACCCC ACGCCCACA TACCTGCGG GAACACCGTC AGGTTCCGTTC ATGGGAGGAGA CCGCATGGA GGACCCACAC TCCGCTGGCT TAAGGATGGA CTGTGGATGG AGAGGGTGGT GCCCTCGGAC CCGCCACACA TCCGCTGGCT TAAGGAGAC CCCATCCTGC AGGCCGGCCTA CAACCACAGCG TGGGCCATA GCACTGGAG CCCATCCTGC AGGCCGGCCTA CAACCACAGCG TGGTGGGGAG GAAGTGGAG CTGCTGTGCA AGGTGTACAG CGATGCCAG CCCCACACTC ATCAACGGCA GCAGTTCAG AGCCGACGGT TCCCCCATG TGCAGTCCT AAAGACTGCA ACACAACAATA GCTGAGAGG AGGGGTCCT TACCTGCGGA ACTGGTCAGC GAAGTGGAG GACATCATC CTGACGGC CAACCACACGC CCCCCACACC CACATCATC CTGACAGGG GGCTCCTG ACCGCACAC ACGCCACAGC CAGGTCATAC CACATCATCC TGTACCGGTC CCACAGCAG GCCCCAGGC CAGGTCATAC CTCTCCCCCT TCCCTCGC CCGACAGTC TCCCTGGAGT TCCCCCGGC CTCGTGAGC CAGGCGCCA CCACCCCCC CCCCCCCCC CTCGTGAGC CAGGCCCCACACC CCACCACGC CCCCCACACC CTCTCCCCCT TCCCTCGCC CCGACAGTC TCCCTCGGGT TCCCCCGGC CTCGTGAGC CAGGCCCCAC CCACCCCCC CCCCCCCCC CTCGTGAGC CAGGCCCCAC CCACCCCCC CCCCCCCCC CTCGTGAGC CAGGCCCCACACCACACCACACACACACACACACA	480 540 600 660 720 840 900 1020 1140 1200 1380 1440 1500 1560 1680 1740 1800 1920 1980
60 65 70	GECCEGARA ATCICACCTT GATTACAGGT GACTCCTTGA CETCCAGCAA GATGATGAG GACCCAARG CCCTATAGGGA CCTCTCGAATA AGGCACAGTA CACCCCTAC TGGACACAC CCCAGGCCAT GAGAAGAAA CTGCATGCAG TACCTGCAGCA AGACCCTAC AGTTCCGCT GTCAGGTGC AGGCAACCCC AGGCACCACA TACCTGCGGG GAACACCGTC AGGTTCATTC ATGGGAGGAGA CGCCATGGA GGCATCGAG CTGGTGATGG AGACGGAGGAG GCCCACCACAT ACACCTGCCT GGTAGAGGAG CTCGTGAGGA GCATCCGCTA TAACTACCTG CTAGATTGCC TGGGCAGCC CCCGCACCAC CCCATCCTGC AGGCCGACC TACACTACCAC ACCCACACCC AGGCAGGCCT CCCGCACCGG CCCATCCTGC AGGCCGACGC CCCCACATCC AGTGGCTGAA GCACTCGGA ATCAACGGC GCAGCTTCGG AGCGACGAT TCCCCTATA TGCAAGGTCCT AGACTGCAG GCCGATCAACACCA GCCACACTCC AGGCACTCC AGTGGCTGAA GCACTCGTC ATCAACGGCA GCAGCTTCGG AGCGACGAT TCCCCTATA TGCAAGGACCA ACCACACCAC GCAGCACTCC AGGCAATTCC ATCCCCCCT CCCACATCC AGTGGCTGAA GCACTCATCC CTGAGAGGA CCCCCACATCC ACCCCCCCC CCCCACTGCA ACCGCACAGC CCCCACATCC AGTGCCTGAC GCCACTACGAC GCAGCAGGCAC CCCACTCGACCCCCCCCCC CGCCCCACTCC AGCACCCCCCCC CCCCACTCGACCACTCC ACCCCCCCC CCCCCCCCCC TCCCCCCCC CCCACATCC ACCCCCCCC	480 540 600 660 720 780 840 960 1020 1140 1220 1380 1560 1560 1620 1680 1740 1860 1980 2040 2100
60 65 70	GECCEGAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA GATGATGAG GACCCAAGT CCCATAGGGA CCTCTCGAATA AGGCACAGTA CACCCCAGCA AGACCCTAC TGGACACAC CCCAGCGCAT GAGAAGAAA CTGCATGCAG TACCTGCGGG GAACACCGTC AAGTTCCGCT GTCCAGCTGC AGGCAACCCC ACGCCCACCA TCCGCTGGCT TAAGGATGGA CAGGCCTTTC ATGGGAGGAGA CCCCTAGGAG GGCATTGGG TGGCCCATCA GCACTGGAG CTCTGTGATGG AGAGGAGGA CCCCCACGAC TCCGCTGGCT TAAGGAGGC CCCATCCTGC AGGCGGGCT CCCGGCCAAC ACACCTGCCT GGTAGAGAAC CCCATCCTGC AGGCGGGCT CCCGGCCAAC ACACCAGGCG TGGTGGGCAG GGAGGGGC CCCATCCTGC AGGCGGGCT ATACCTACCTG TAGAGTGGC TGGTGGCAG GGAGGGGC CTGCTGTGCA AGGTTTACAG GAATGCCAC CCCCACATCC AGTGGCTAGA GCACTCGCA ACTCACCGCA GCACTCTCG AGCCGACGGT TTCCCCTATG TGCAGGCGT GCCATCCACC CAGAGGAGGA CCCCACATCC TACAGTCC CAGAGGCGCA ACGTGCTGC CAGAGGAGGA CCCCACATCC ACCGCCACGC CGCCACATCC ACGTGCTGC CAGAGGAGGA CCCCACATCG ACCGCAGGAG GACCGAGGC CTCTCCCGCT TCCCTCTGCG CGGCCACATCC ACCCCCCCC CGCCCACATC AGCTCATCCC TGGTACGAGG CGGCACGTCT TCCCTCAGGGC CAGCCCGCCC CTCTCCCGCT TCCCTCTGCG CGGCACGTC TCCCTGCCCAC ACCTCACCCT TCCCTCTGCG CGGCACGTC TCCCTGCCCAC ACCCCCCCC TCCCTCTGCG CGGCACGTC TCCCTGCCCAC ACCCCCCCC TCCCTCTGCG CGGCACGTC TCCCTGGGCT CTCGGAGGC CAGCCCCCCC CGCCCCCCC CCCCGCCCAC TTGGCAAGTC AGCTCATCC TGGTACGAGG CGGCGCGCC CACCCCCCC CCCCCCCCC TCCCTCTGGC CGGCGCGCC CACCCCCCC CCCCGCCCAC TCCCTCTGGCC CCCTGGCCCGC CGCCCCCCCC CCCCCCCCC CCCCGCCCAC TCAGCCAC GGCTGCTTT TCCCCCGGG CCCCCCCCC CCCCGCCCCCC CCCCGCCCTGA CCAACCCAC CTATGGGAGT TCCCCCGGGA ATCGGACCACAC AGGCACGTC TCCGGACGCCC CCACACAGA ACACTACACA CCTGCTTGGT TGCCAGGAGT ACCGCCAGGAGGC CAGCCTTGGC CCCACACAGA ACACCTACCA CCACCCCCCCCC CCCCCCCCCC CCCCCCCCC CCCCCCCC	480 540 600 660 720 940 950 1080 1140 1260 1320 1380 1500 1560 1680 1740 1860 1920 1920 2040 2160
60 65 70	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA GGATGATGAG GACCCAAGT CCCATAGGGA CCTCTCGAATA AGGCACAGT ACCCCCAGCA AGACCCTAC TGGACACAC CCCAGCGCAT GAGAAGAAA CTGCATGCAG TACCTGCGGG GAACACCGTC AGGTTCGGCT GTCAGGTGC AGGCAACCC ACGCCACCA TCGCTGGGCT TAAGGATGGA CAGGCCTTTC ATGGGAGGAGA CCGCATGGA GGACCCACCA CTGGTGATGG AGACGGGGGACA CCGCATGGA GGACCATCA CTCTGTGATGG AGACGGGGT CCCGGCCACA TCACCTGCGC GGTAGGAGGG CCCATCCTGC AGGCCAGCT TAACTACCTG CTAGAATGGC TGGACGGTC CCCGCACCAC CCCATCCTGC AGGCCAGCCT ATACTACCTG CTAGAATGGC TGGTGGCAG GGACGTCCCC CTGCTGTGCA AGGTTACAG GGAGGCCCCACATCC AGTGGCTGAA GCACTCGGA ATCAACGGCA GCAGCTTCGG AGCCACGGT TTCCCCTATG TGCAAGTCCT AAACTGCA GCACACAAATA GCTCAGAGGT GGAGGTTCCT TACCTGCGA ACCTCACACTC CTACCAGTC TGCCTGGCA GGCAGTACA CCTGCCCCCC AGGCAATTCC ATCGGCTCC CTACCAGTC TGCCTGGCT GGCAGTCCC CAGAGGAGGA CCCCCACATCA ACCGCACAGC CAGGTACAC GACATCATCC TGTACGCGC GGCCCACATCA ACCGCACGGA GCCCCAAGC CAGGTATACA GACATCACCC TGTACGAGG CGCCCAATGC ACCCCCCCCC CGCCCCCCC TGCCAGGC CAGGTATACA GCCTCACCCGT CCCCTCTGGC CGCCACATCC TCCTCGGCAG CACCCCCCCC CTCTGACAGG CAGGTATACA AGCTCATCCC TGGTACGAGG CAGCCCCCCC CCCCCCCCC CTCTGACAGGC CAGGTATACA ACCTCATCCC TGGTACGAGG CAGCCCCGCC CACCCCCCCC CTCTGACAGC CAGGTATACA ACCTCATCCC TGGTACGAGG CAGCCCCGCC CACCCCCCCC CTCTGAGAGC CAGGTATACA CTCTCCCAGTT CCCTTGGGC CGCCAATGCA CAGGCTGGGC CAGGTATACA CTCTCCCAGT CCCCTCTGGC CGCACATTC TCCCTGGAG CAGGCCCGCC CTCTGGAAGC CCCTAGGCCG CACCCCCCCC CCCCCCCCCC CCCCACAGGAAGCAC CCTAGGCCGC CCCACATCT TCCCTGGAGG CACCCCCCCC CCCCCCCCCC CCCCACAGGAAGCAC ACCTAGCCCCACA CCCAATGCC CACCCCCCCC CCCCCCCCCCC CCCACACAAGA ACACTACCC CCCACATGCC CGCCCCCCCC CCCACACAAGA ACATCATCCA CCTGCTGTC TCCCGAGGA GAGGCCCCCCCCC CCCACACAAGA ACATCATCCAA CCTGCTTGTC TCCCGAGGATC CAGGCACTCC CACACAAGA ACATCATCCAA CCTGCTTGTC TCCGAGATGC AGGCCCCCCCC CCCACCCCCCCCCCCCCCCCCCCCC	480 540 600 660 720 900 900 1020 1140 1220 1320 1380 1500 1680 1740 1890 1920 1980 2040 2160 2160 2220
60 65 70 75	GECCEGAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA GGATGATGAG GACCCAAGT CCCATAGGGA CCTCTCGAAT AGGACAGTT ACCCCCAGCA AGACCCTAC TGGACACAC CCCAGCGCAT GAGAAGAAA CTGCATGCAG TACCTGCGGG GAACACCGTC AGGTTCGGT GTCAGGTGC AGGCAACCCC AGGCCACAT ACCCTGCGCT TAAGGATGGA CAGGCCTTTC ATGGGAGGA CCGCATGGA GGACCATCGC TCGCTGGCT TAAGGATGGA CTCTGTGATGG MAGACGTGGT GCCCTCGGAC CCCACAT TCCGCTGGCT TAAGGAGAC CTCTGTGATGG MAGACGTGGT GCCCTCGGAC CCCACATTCGC TGGGCCATA GACACTGCCT CTCTGTGATGG MAGACGTGGT CCCGGCCAAA ACCACAGCGG TGGGCGAT CCCCACATCGC CCCATCCTGC AGGCCGGCTA TAACTACCTG CTAGATGTGC TGGGCGAG GGACGTGCAC CCCATCCTGC AGGCCGGCTA CACCACAGCG TGTTGGGCAG GACATCGCA ACTCACACAAA AGGTGTACAG GGAGGGCT TTCCCCTATG TGCAGGCGT ACAACAATA GCTCAGAGGT GGAGGTCCTT TACCTGCGAA ACCTGCAGC GACATCAATA GCTCAGAGGT GGAGGTCCTT TACCTGCGAA ACCTGCAGTC ACGGGAGTACA CCTGCCTCCG AGGCAATTCC ATCGGCCTC CCTACCAGTC TGCCTGGGCA ACGGTGCTGC CAGAGGAGGA CCCCACATCG ACCGCAGCAG CCCCACATCG CTGTATCCAG GGAGGCGCT CACCGCCCCC CCCCACATCC CTCACCAGTC TGCTTACCAG GGAGGCGCT CACCGCCCCC CCCCCACATCC TCCCTCCCCCC CTCTCCCCCT TCCCTCTGGC CCGACAGTCT TCCCTCGAGT TCCCTCGGC CTCTCCCCCT TCCCTCTGGC CCGACAGTCT TCCCTCAGGG CACCCCCCC CTCTGGAGTC TACAGGCAG GGCTCCTT TCCCTCAGGG CACCCCCCC CTCTGGAGTC TACAGCCAG CTCCACATCG CCCACATCG CCCCCCCCC CTCTGGAGTC TACAGCCAG CGCCGCCTTT TCCCTCAGGG CACCCCCCCC CTCTGGAGTC TACAGCCAG CGCCTGCTT TCCCTCAGGG CACCCCCCCC CTCTGGAGTC TACAGCCAG CGCCTGCTT TCCCTCAGGG CACCCCCCCC CTCTGGAGTC TACAGCCAG CGCCTGCTT TCCCTCAGGG CACCCCCCCC CTCTGGAGT CACAGCCAG CACCTGGC CACCCCCCCC CTCTGGAGT CACAGCCAG CACCCCCCCCC CCCACACAGA ACAATCACAA CCTGCTTGGT TCCCCCAGGG CACCCCCCCC CCCACACAGA ACATCATCAA CCTGCTTGGT TCCCCCAGGG CACCCCCCCA ATCGTGGAGT CCCCCCCCAA GGGAACCTGC CCGACAGGAATCA AGGACCTAGC CCCACACAGA ACATCATCAA CCTGCTTGGT CTCGGAATCAG AGGTGATCAG CCCCCCCCCCAA GGGAACCTG CCGCACTGTC CTGGGAATGA AGCTGACGCC CCACACAGA ACATCATCAA CCTGCTTGGT CTGGACTG AGCAGGCC CTTTACGTACG CCCCCCCCCAAC CCCCCCCCCAA GGGAACCTG TCCGGAATGAA ACCACACCCCCCCCAACTCCCCCCCCCC	480 540 600 660 720 900 900 1080 1140 1200 1380 1440 1500 1680 1740 1800 1860 1920 2040 2100 2160 2220
60 65 70 75	GRICCIGEGAS ATCICACCTT GATTACAGGT GACTCCTTGA CCTCCAGCA GGACCCTAC TGGACACAGT CCCATAGGGA CCTCTCGAAT AGGACAGTA ACACCCTAC TGGACACACC CCCAGCGCAT GAGAAGAAA CTGCATGCAG TACCTCGCGAG AGACCCCTAC AGGTTCCGCT GTCCAGCTGC AGGCAACCCC AGGCCACCA TACCTCGCGG GAACACCGTC CAGGCCTTC ATGGGAGGAGA CGCCACCACCA TCCGCTGGCT TAAGGATGGA CCGGTGCTTC ATGGGAGGAGA CGCCACCACA TCCGCTGGCT TAAGGAGGC CTCGTGATGG AGAGGGTGGT GCCCTCGGAC GCCATCACCG TGGGCCATCA GCACTGGAG CCCATCCTGC AGGCCAGCAC ACCACAGGC TGGGCCATCA GCACTGGAG CCCATCCTGC AGGCCGGCCTA TAACTACCTG CTAGATGTGC TGGAGGGTC CCCCCACCGC CCCATCCTGC AGGCGGCTC CCGGCCAAC ACCACAGGC TGGTGGGGAG GAGGTGGAG CTGCTGTGCA AGGTTCAGG AGCCGACGGT TCCCCTATG TGCAGTCCT AAAGACTGCA ATCAACGGCA GCAGCTTCAG AGCCGACGGT TCCCCTATG TGCAGTCCT AAAGACTGCA ACACATCAATA GCTCAGAGGT GAGGGTCCTT TACCTGCGGA ACCTGCACG CAGGAGGCAC GACATCATC TGTAGAGGT GAGGGTCCTT TACCTGCGGA ACCTGCACG CAGGAGGCC CACATCATCC TGCAGCTGC CACGCCACA CCCCCACCAGC CCCCCACAGC CACATCATCC TGCAGCTGC CCACAGCAG CCCCCACAGC CAGCCACAGC CTCTTATCAG GGCAGGCGCT CCACGCCGC CACCCCCCC CGCCCACAC TTGCCAGGA CCTCTCCCCCT TCCCTCTGC CCGACAGTC TCCCTGGAGT TCCCCCGGC CTCGTGAGC TACGTCACCA CTATAGGAGT TCCCCCGGA CTCTTGGAAGC CCTAGCAGCA GCGTCCTT CCCTCTGGC CTCTGGAGC CAGACACAACA CCCTACCACCAC CCCACACCC CCCCCCCCCC	480 540 600 660 720 840 900 1020 1180 1220 1380 1440 1500 1560 1680 1740 1800 2040 2100 2160 2220 2380 2440
60 65 70 75	GECCEGAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA GGATGATGAG GACCCAAGT CCCATAGGGA CCTCTCGAAT AGGACAGTT ACCCCCAGCA AGACCCTAC TGGACACAC CCCAGCGCAT GAGAAGAAA CTGCATGCAG TACCTGCGGG GAACACCGTC AGGTTCGGT GTCAGGTGC AGGCAACCCC AGGCCACAT ACCCTGCGCT TAAGGATGGA CAGGCCTTTC ATGGGAGGA CCGCATGGA GGACCATCGC TCGCTGGCT TAAGGATGGA CTCTGTGATGG MAGACGTGGT GCCCTCGGAC CCCACAT TCCGCTGGCT TAAGGAGAC CTCTGTGATGG MAGACGTGGT GCCCTCGGAC CCCACATTCGC TGGGCCATA GACACTGCCT CTCTGTGATGG MAGACGTGGT CCCGGCCAAA ACCACAGCGG TGGGCGAT CCCCACATCGC CCCATCCTGC AGGCCGGCTA TAACTACCTG CTAGATGTGC TGGGCGAG GGACGTGCAC CCCATCCTGC AGGCCGGCTA CACCACAGCG TGTTGGGCAG GACATCGCA ACTCACACAAA AGGTGTACAG GGAGGGCT TTCCCCTATG TGCAGGCGT ACAACAATA GCTCAGAGGT GGAGGTCCTT TACCTGCGAA ACCTGCAGC GACATCAATA GCTCAGAGGT GGAGGTCCTT TACCTGCGAA ACCTGCAGTC ACGGGAGTACA CCTGCCTCCG AGGCAATTCC ATCGGCCTC CCTACCAGTC TGCCTGGGCA ACGGTGCTGC CAGAGGAGGA CCCCACATCG ACCGCAGCAG CCCCACATCG CTGTATCCAG GGAGGCGCT CACCGCCCCC CCCCACATCC CTCACCAGTC TGCTTACCAG GGAGGCGCT CACCGCCCCC CCCCCACATCC TCCCTCCCCCC CTCTCCCCCT TCCCTCTGGC CCGACAGTCT TCCCTCGAGT TCCCTCGGC CTCTCCCCCT TCCCTCTGGC CCGACAGTCT TCCCTCAGGG CACCCCCCC CTCTGGAGTC TACAGGCAG GGCTCCTT TCCCTCAGGG CACCCCCCC CTCTGGAGTC TACAGCCAG CTCCACATCG CCCACATCG CCCCCCCCC CTCTGGAGTC TACAGCCAG CGCCGCCTTT TCCCTCAGGG CACCCCCCCC CTCTGGAGTC TACAGCCAG CGCCTGCTT TCCCTCAGGG CACCCCCCCC CTCTGGAGTC TACAGCCAG CGCCTGCTT TCCCTCAGGG CACCCCCCCC CTCTGGAGTC TACAGCCAG CGCCTGCTT TCCCTCAGGG CACCCCCCCC CTCTGGAGT CACAGCCAG CACCTGGC CACCCCCCCC CTCTGGAGT CACAGCCAG CACCCCCCCCC CCCACACAGA ACAATCACAA CCTGCTTGGT TCCCCCAGGG CACCCCCCCC CCCACACAGA ACATCATCAA CCTGCTTGGT TCCCCCAGGG CACCCCCCCA ATCGTGGAGT CCCCCCCCAA GGGAACCTGC CCGACAGGAATCA AGGACCTAGC CCCACACAGA ACATCATCAA CCTGCTTGGT CTCGGAATCAG AGGTGATCAG CCCCCCCCCCAA GGGAACCTG CCGCACTGTC CTGGGAATGA AGCTGACGCC CCACACAGA ACATCATCAA CCTGCTTGGT CTGGACTG AGCAGGCC CTTTACGTACG CCCCCCCCCAAC CCCCCCCCCAA GGGAACCTG TCCGGAATGAA ACCACACCCCCCCCAACTCCCCCCCCCC	480 540 600 660 720 840 900 960 1020 1140 1200 1320 1380 1500 1680 1740 1920 2160 2200 22160 22460

						COTON ACCOM	2580
	TTGGGATCCA (GCTCCTTCCC ATAGGCTGGT	GCCTTGGGC (CTTGGGGCTC	AGCCACAGCC AGCCACAGCC	TGACACAGTG	2640
	CTCGACCTTG .	ATAGCATGGG	GCCCCTGGCC	CAGAGTTGCT	GTGCCGTGTC	CAAGGGCCGT	2700
5	GCCCTTGCCC 1	TTGGAGCTGC	CCTCCCTGTG '	TCCTGATGGC	CCAAATGTCA	GGGTTCTGCT TGGCTGGAGA	2760 2820
,	GCTGCTATGC	TARACCTCCT	GCCTCCCAAT	ACCAGCAGGA	GGTTCTGGGC	CTCTGAACCC	2880
	CCTTTCCCCA	CACCTCCCCC	TGCTGCTGCT	GCCCCAGCGT	CTTGACGGGA	GCATTGGCCC	2940
	CTGAGCCCAG	AGAAGCTGGA	AGCCTGCCGA	AAACAGGAGC	AAATGGCGTT	TTATAAATTA	3000 3015
10	TITITION	AIAAA					
	Seq ID NO:						
	Nucleic Aci Coding sequ		1 #: NM_0229	63.1			
	1	11		31	41	51	
15	1			1	1	(COCCOCCA)	60
	CCCAGGAGCG	AGGCGGGGGGA	CTGCGGACCC GGAGCCAGGT	CAGGAGGAGC	CAGGAAGGCA	GTTGGTGGGA	120
	AGTCCAGCTT	GGGTCCCTGA	GAGCTGTGAG	AAGGAGATGC	GCCTGCTGCT	GGCCCTGTTG	180
20	GGGGTCCTGC	TGAGTGTGCC	TGGGCCTCCA TCCCAGCCTG	GTCTTGTCCC	TGGAGGCCTC	TGAGGAAGTG	240 300
20	CTTGGGCAGC	CTGTGCGGGCT	GTGCTGTGGG	CGGGCTGAGC	GTGGTGGCCA	CTGGTACAAG	360
	GAGGGCAGTC	GCCTGGCACC	TGCTGGCCGT	GTACGGGGCT	GGAGGGGCCG	CCTAGAGATT	420
	GCCAGCTTCC	TACCTGAGGA	TGCTGGCCGC GATTACAGGT	CACTCTTCA	TGGCACGAGG	CTCCATGATC	480 540
25	GACCCCAAGT	CCCATAGGGA	CCTCTCGAAT	AGGCACAGTT	ACCCCCAGCA	AGCACCCTAC	600
	TGGACACACC	CCCAGCGCAT	GGAGAAGAAA	CTGCATGCAG	TACCTGCGGG	GAACACCGTC	660 720
	CAGGCCTTTC	ATGGGGAGAA	AGGCAACCCC	GCATTCGCC	TGCGCCATCA	GCACTGGAGT	780
	CTCGTGATGG	AGAGCGTGGT	GCCCTCGGAC	CGCGGCACAT	ACACCTGCCT	GGTAGAGAAC	840
30	GCTGTGGGCA	GCATCCGCTA	TAACTACCTG	CTAGATGTGC	TGGAGCGGTC	CCCGCACCGG CGACGTGGAG	900 960
	CTGCTGTGCA	AGGTGTACAG	CGATGCCCAG	CCCCACATCC	AGTGGCTGAA	GCACATCGTC	1020
	ATCAACGGCA	GCAGCTTCGC	AGCOGACGGT	TTCCCCTATO	TGCAAGTCCT	AAAGACTGCA	1080
35	GACATCAATA	GCTCAGAGGT	GGAGGTCCTG	ATCGCCCTCT	CCTACCAGTO	CGAGGACGCA TGCCTGGCTC	1140 1200
33	ACGGTGCTGC	CAGGTACTG	GCGCATCCCC	CACCTCACAT	GTGACAGCCT	GACTCCAGCA	1260
	GGCAGAACCA	AGTCTCCCAC	TTTGCAGTTC	TCCCTGGAG1	CAGGCTCTTC	CGGCAAGTCA	1320 1380
	AGCTCATCCC	TOGTACGAG	TOTOGACOCA	CTATGGGAG	TCCCCCGGG	CAGGCTGGTG	1440
40	CTTGGGAAGC	CCCTAGGCG	GGGCTGCTTT	GGCCAGGTAG	TACGTGCAGA	GCCTTTGGC	1500
	ATGGACCCTG	CCCGGCCTG	CCAAGCCAGC	ACTGTGGCC	S TCAAGATGCT	CAAAGACAAC GCTGATCGGC	1560 1620
	CGACACAAGA	ACATCATCA	CCTGCTTGGT	GTCTGCACC	AGGAAGGGC	CCTGTACGTG	1680
45	ATCGTGGAG1	GCGCCGCCA	GGGAAACCTG	CGGGAGTTC	TGCGGGCCCC	GCGCCCCCCA	1740
45	GGCCCCGACC	COCCUTACO	A CGGTCCTCGG	GCATGAG	GGCCGCTCTC	CTTCCCAGTC	1800 1860
	ATCCACCGGC	ACCTGGCTG	COGCAATGTO	CTGGTGACT	G AGGACAATG	CATGAAGATT	1920
	GCTGACTTTC	GGCTGGCCC	CGGCGTCCAC	CACATTGAC	I ACTATAAGA	AACCAGCAAC	1980 2040
50	CAGAGTGAC	TGTGGTCTT	TGGGATCCTC	CTATGGGAG	A TCTTCACCC	f GTACACACAC f CGGGGGCTCC	2100
	CCGTATCCTC	GCATCCCGG	T GGAGGAGCTC	TTCTCGCTG	C TGCGGGAGG	3 ACATCGGATG	2160
	GACCGACCCC	CACACTGCC	C CCCAGAGCTO	TACGGGCTG	A TGCGTGAGT	G CTGGCACGCA A GGTCCTGCTG	2220 2280
	GCCGTCTCTC	AGGAGTACC	T CGACCTCCGC	CTGACCTTC	G GACCCTATT	C CCCCTCTGGT	2340
55	GGGGACGCC	A GCAGCACCT	G CTCCTCCAGG	GATTCTGTC	T TCAGCCACG	A CCCCCTGCCA	2400 2460
	GTGCAGGCA	A GCTCCTTCC C ATAGGCTGG	T GGCCTTGGG	CTTGGGGCT	C AGCCACAGC	G GCTCAAGGCT C TGACACAGTG	2520
	CTCGACCTT	G ATAGCATGG	G GCCCCTGGC	CAGAGTTGC	T GTGCCGTGT	C CAAGGGCCGT	2580
60	GCCCTTGCC	C TIGGAGCTG	C CGTGCCTGT	TCCTGATGG	C CCAAATGTC	A GGGTTCTGCT C TGGCTGGAGA	2640 2700
00	GCTGCTATG	C TARACCTCC	T GCCTCCCAA	T ACCAGCAGG	A GGTTCTGGG	C CTCTGAACCC	2760
	CCTTTCCCC	A CACCTCCCC	C TGCTGCTGC	T GCCCCAGCG	T CTTGACGGG	A GCATTGGCCC	2820 2880
	TTTTTTTGA		A AGCCTGCCG	A AAACAGGAG	C AAA1GGCG1	T TTATAAATTA	2895
65							
		: 15 DNA Se	quence on #: NM_00	2045 2			
		quence: 1		2043.2			
70	1	11	21	31	41	51	
70	ATGAGGGGA	.C TTGGGACTT	CCTGGCGAC	T TTGGCCGG/	C TTTTGCTA	C TECGECGGC	60
	GAGACGTTC	T CAGGTGGC	G CCTCTTTGA	T GAGCCGTAT	TA GCACATGTO	G ATATAGTCAA	120
	TCTGAAGGT	G ATGACTTC	VA TTGGGAGCA	A GTGAACAC	T TGACTAAAC	C GACTTCTGAT	180
75	AGAGCCCAC	C TGCTCTTA	C CCAACTTAA	G GAAAATGA	CA CCCACTGC	CC TGAGGGGCAG AT CGATTTTCAC	300
	TATTTTGTG	T CCAGCAAG	G TAATTCTCC	T CCGGGGTT	AC TCAATGTCT	TA CGTGAAGGTC	360
	AATAACGGC	C CACTGGGG	A TOOTATOTO	G AATATATC	T TTTATCAC	AC ACGTACATGG ST GATTITTGAA	420 480
	GTGATAACT	T CTGGACAT	CA AGGCTATCT	C GCTATCGA	TG ACCTGAAG	T GTTAGGACAT	540
80	CCATGTACC	A GGACTCCT	CA CTTCCTGCC	G ATTCAGAA	TG TGGAAGTT	aa tgctggccag	600
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	ATGATTCG	LA CTGAAGGA	GG TGTTGGAA1	A TCAAACTA	TG CAGAGTTG	GT AGTTAAAGAA	840

	THE PROPERTY OF THE PROPERTY O	900
	CCACCOGTTC CTATTGCCCC ACCTCAGCTC GCCTCTGTAG GAGCCACCTA CCTGTGGATA CAGCTCAACG CCAACTCCAT CAATGGGGAT GGGCCCATTG TGGCCCGAGA GGTGGAGTAC	960
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		1080
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10		1020 1080
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	TTCGCCCAGC TAGGCAAGCT	GCGCTTCCTC	AACCTCTCTG	CCAACGAGCT	ACAGCCCTCC	900
	CTGCGCCACG CGGCCACCTT	CGCACCGCTG	CCCTCCCTCT	CCTCCCTCAT	CCTCTCGGCC	960
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50	CTGCGCGAGC TGCGCCTGGA					1140
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	TCACAGTGGT TATGGATTT					
	AGGCTGALAG TGGAATCTT	CIGITIAGG	or crimmere	- IONGGGTC	LI GOTOMCTONO	-320

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• •	CACTAATAGA						4933
	Cherran	un.					
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	Nucleic Act			792.2			
15	Coding sequ						
13	Course sede	11	21	31	41	51	
	†	†*			7	1	
		l COMPONENTED		GAGCGGAGAG	CACCCAACAA	CCCCCTCCCC	60
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5	Seq ID NO:	d Accession	#: NM_0169	41.1			
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40					TCAGTTCTAA		1920
		134 DNA Se id Accessio	n #: FGENES	H predictio	n		
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	1 ATGTGCCAGG CTGCAGCCAT CAGGCCCAGT AAAAGGTTGG AAAACATCTT GTAACTATCT CATGTAGAAG Seq ID NO:	11 CTTTCCTCTG ACCCACCTGA TACCACTTGG AAAGGAAGTA CTCTAGAGTT CGGAAAATCT GCATGGTTAA	21 GGTGCTAGGG ACATGCCCAA ATGGGTGAAG CCCCAGCTGT CCCTGCTGTT CATCTCCAAP	ACACTGTGGGG TCTTGCCTGF TGGCCCTTGG TGGATGGGGG GGATTCCATF	 TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG AAATTGAAGC CAGCTGATGG TCTGTCAACA	TGCCCGTTGT TAAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT	120 180 240 300 360
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50 55	1 ATGTGCCAGG CTGCAGCCAT CAGGCCAGT AAAAGATTG AAAACATCTT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq 1	11 CTTTCCTCTC ACCCACCTGA TACCACTGGA TACCACTGG TACCACTGGCAAATCT CCGAAAATCT 135 DNA Se id Accessic uence: 184. 11	21	ACACTGTGGC TCTTGCCTGG TGGCCCTTGG TGGATGGGG GGATTCAT GCCTCTTCTC	I TICTCAAAAA A TCTCAGAAGC C ACTTGAGGAG G AAATTGAAGC A CAGCTGATGG G CCAAATGTA	TGCCCGTTGT TAAGCAGGGT CTCACTGTCC ACAGATATGT TCCACTGAA GCAGGACTCT G	120 180 240 300 360 411
50	I I ATGTGCCAGG CTGCAGCCAT CAGGCCCAGT AAAAGTTTG AAAACATCTT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq I GAGAGGGCCC CGGGAGGGCCC	11 CTTTCCTCTG ACCCACCTGG ACCCACCTGG AAAGGAAGTC CCGAAAATCT CCGAAAATCT GCATGGTTA 115 DNA Se id Accessic uence: 184. 11	21	ACACTGTGGC TCTTGCCTGG TGGCCCTTGC TGGCCCTTGC TGGATCCATA GCCTCTTCTC 812.1 31	I TITCTCANANA TOTCTCAGAGG ACTTGAGGAGG ACTTGAGGAGG CACGCTGATGG CCANATGTP	TIGCCCGTTGT TANGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G	120 180 240 300 360 411
50 55	1 ATGTGCCAGG CTGCAGCCAGT CAGGCCCAGT AAAAGGTTGG AAAACATCTT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq 1 GAGAGGGCCC CCGGGAGCGGG GGGCTGAGCC	11	21	ACACTGTGGC TCTTGCCTGG TGGCCCTTGG TGGCCTTGG GATCTGGTGG GGATTCCATI GCCTCTTCTC 812.1 31 1 CCGCAGGAGC GCCCCCTTCCTGG AGCAGCAGC GCCCCTTCCTGG AGCAGCAGC	I TITCTARARA A TOTCAGRAGO A CHTCAGGAG A CAGCTGATGA A TOTGTARACA C CAGCTGATGA A TOTGTCARCA G GCCARATGTA 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TIGCCCGTTGT TAAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G 51 GCAGGGCGGGG TGCGCCTCCG GCGCCGCAGG	120 180 240 300 360 411
50 55 60	I ATGTGCCAGG CTGCAGCCAT CAGGCCCAT AAAAGTTGG AAAACATCTT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq I GAGAGGGCCC GAGAGGGCCC GGGCTGAGCC AGGATGGGCT	11 CTTTCCTCTG ACCCACTTGA ACCCACTTGA AAGGAAGTA CTCTAGAGTTA CGAAAATCT GCATGGTTA 135 DNA Se id Accessic uence: 184. 11 GGACTAGGGG GGGGCGGGATG GGCGCCGGGA	21	ACACTGTGGC TCTTGCCTTGG TGGCCCTTGG TGGCCCTTGG TGGATCGGTG GGATTCCATA GCCTCTTCTC 812.1 31 C CGCAGGAGC G CGCCTCTTGG AGCAGCCAGC GCCATCGAGC	I TITCTCAAAAA A TCTCAGAAGC C ACTTGAGGAG G AAATTGAAGC A CAGCTGATGA C CGCCAAATGTA 41 I CCCCGCGGGC C GGGCCGGGGC C GGGCCGGGGCC C CCCCCTACTI	TIGCCCGTTGT TAAGCAGGGT TAAGCAGGGT TCCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G 51 I GCAGCGCGCG TGCAGCGCCGCG CGCGCCAGG	120 180 240 300 360 411
50 55	I ATGTGCCAGG CTGCAGCCAT CAGGCCCAGT AAAACATCTT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq I GAGAGGGCCCGGGAGCGGG AGGGTGAGCC AGGATGGGCTAAGCC AGGATGGGCTAAGCC AGGATGGGCTAAGCC AGGATGGGCTAAGCCAGGATGGGCTAAGCCAGGATGGGCTAAGCC	11 CONTROL OF CONTRO	21	ACACTGTGGC ACACTGTGGCTGG TGGCCTTGG TGGCCTTGG GATCTGGTGG GATCTGTTG GCTCTTCTC 812.1 31	I TITCTCAAAAA A TCTCAGAAGG C ACTTGAGGAG A CAGCTGATGA A TCTGTCAACA C CAGCTGATGA A TCTGTCAACA C CCCGCGCGGCCC C GGGCCCGGGGCC C CGCCTACTI C CCGCGATGCT C CGGGATGCT C CGGGATGCT	TIGCCCGTTGT TAAGCAGGGT CTCACTGTCC TACAGTATGT TTCCACTGAA GCAGGACTCT G 51 GCAGGGCGCGG TGCCCCTCCG CGCAGGGCGCAGG CGCCAGCGCC TGGAAGCTGG TGCCGCCCCCC TGGAAGCTGG	120 180 240 300 360 411 60 120 180 240 360
50 55 60	I ATGTGCCAGG CTGCCCTCCAGGATGAGAGAGGCCCCTCCAGGAGGAGGGCCCCTCCAGGAGGAGGCCCCCCGGGAGCAGGGCCCCCCGGGAGCAGGAGG	11 CTTTCCTCTC ACCCACTTGA ACCCACTTGA AAGGAAGTA CTCTAGAGTT 135 DNA Se id Accessic uence: 184. 11 GGACTAGGGG GGGGGGGA GGGGGGGGA CGGGGGGGA CGGGGGGGA CAGGGGCGCA ACAGGGGCC ATGGTGTGGC	21	ACACTGTGGC TCTTGCCTTGG TGGCCCTTGG TGGCCCTTGG TGGCCCTTGG TGGCCCTTGG GATCCATA GCCTCTCTC 812.1 31 CCGCAGGAGC GCCTCCTTG TGCATCCAGGC TGCATCCAGG TGCATCCAGG TGCATCCAGG TGCATCCAGG TGCACTGCAC	I TITCTCAAAAA A TCTCAGAAGG A AATTGAGGAG A CAGCTGATGA A CAGCTGATGA A TCTGTCAACA G GCCAAATGTA 1	TIGCCCGTTGT TAAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G 51 I GCAGCGCGCG TGCAGCGCCCAG CGCAGCGCCCAGG CGCAGCGCCCAGG CGCAGCGCCCAGG CGCAGGGCCCAGG	120 180 240 300 360 411 60 120 180 240 300 360 420
50 55 60	I ATGTGCCAGG CTGCAGCCAGT AAAACGAACTATCT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq I GAGAGGGCCCGGGAGCGGG GGGGTGAGCC AGGATGGGCTAGCCAGGAGGAGGGCCCCGGAGAAAACAAAC	11 CONTROL OF CONTRO	21	ACACTGTGGC TCTTGCCTGG TGGCCTTGC TTGAATGGGC GATCTGGTGG GGATTCCAT/ GCCTCTTCTC 812.1 31	I TITCTAANAA A TOTCAGAAGG C ACTTGAGGAG A CAGCTGATGA A TOTGACACA C CAGCTGATGA A TOTGTCAACA C CCCGCGCGGCCC C CGCGCCGGGCCC C CGCGCCGCGGCT C CCCGCTACTI C CCCGCTACTI C CCGCGATGCC C CCGCTACTI C CCGCGATGCC C CCGCTACTI C CCGCCATGCCGCC C CCGCTACTI C CCGCCATGCCGCC C CCGCTACTI C CCGCCATGCCCGCC C CCAGCCCCCC C CCAGCCCCCC C CCAGCCCCCC C CCAGCCCCCC C CCAGCCCCCC C CCAGCCCCCC C CCAGCCCCCC C CCAGCCCCCC C CCAGCCCCCC C CCAGCCCCCC C CCAGCCCCCC C CCAGCCCCCC C CCACCCCCC C CCACCCCCCCCCC	TGCCCGTTGT TAAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G 51 GCAGGGCGCGG TGCCCTCCGA CGGAGGCTGCC GGAGGAGTGGA CCCACAGAAG CCCCTCTGACC AATGCCTGCA	120 180 240 300 360 411 60 120 180 240 300 360
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50 55 60	I ATGTGCCAGG CTGCAGCCAGT CAGGCCCAGT AAAAGGTTGG AAAACATCTT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq I GAGAGGGGCC CGGGAGCGGG GGCTGAGCC AGCATGGGGC ACCAGGGAAACACG ACACGGAACAGACT CAGAAACAGA AAAACAGAAACAACAAAAAAAAAA	11 CTTTCCTCTC ACCCACTTAG TACCAC	21	ACACTGTGGC TCTTGCCTGG TCTTGCCTGG TGGCCTTGG TGGATGGGG GATCTGGTGG GATCTGGTGG GGATCCATI 1 1 2 CGCAGGAGG GGCTCCTTGG AGCAGGAGG GGCTCCTTGG AGCAGCAGG GGCCTGCAC AGCCCAGGT CCCCAGGGG GGCTGCAC AGCCCAGGGG CCCAGGGG GCTAAAAGA ACCCAAG	I TITCTAANAA A TOTTCAGAAGG A CAGCTGATGG A CAGCTGATGG A CAGCTGATGG A TOTGTCAACA G GCCAAATGTA 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TIGCCGTTGT TRAGCAGGGT TAAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G S1 I GCAGGACTCT GGCGCGCGGG CGCGCGCAGG CGCCGCGCAGG CGCCAGGAGTGGA CCCCCTGACC GGAAGATGGA ACCCAGAGAAG CCCCTTGACC ATGCAGAGATGA TCGAAGAATG ATCGAAGAT	120 180 240 300 360 411 60 120 180 240 360 420 480 540 660
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50 55 60 65 70 75	I ATGTGCCAGG CTGCAGCCAT CAGGCCCAGT AAAAGGTTGG AAAACATCTT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq I GAGAGGGCCC GGGAGCGGG GGGTGAGCC AGGATGGGCT ACCCGGGAAG ACACGAGT CAGGAACAGA CCGGAAACAGA CCTGCATCCC CCGAATTCT TTGTTGGGAC ATTCTGTTTCT CTTACCAGGT TCAAGGTAC GGATCCAGTT AGCAGTCAT GGATCCAGTT AGCAGTCAT AGCAGT	11 CTTTCCTCTC ACCCACTTAG ACCCACTTAGAGTT TACACTTGC AAAGGAAATCT GCATAGAGTT 115 DNA Se id Accessic uence: 184. 11 GGACTAGGGG GAGGCGAGA GCGGCAGAG GCGGCAGAG GCGGCAGAG GCGGCAGAG CAGAATCA ATGGGCT GTGAGGCC ATGGGTTAAC GCACTGAAT ACTAGAACT CCTTCTGAGC ACTGCAAAT AGTAGTGAG GGGCAGAGT TACTGCAAAT AGTAGTGAG GGGCAGCT TACCCATGAAA AGGAAACTC TCCATGAAA AGGAAACTC TCCATGAAA AGGAAACTC TCCATGAAA AGGAAACTC TCCATGAAA AGGAAACTC TCCATGAAA AGGAAAACTC TCCATGAAA AGGAAACTC CCATGAAA AGGAAAACTC CCATGAAA AGGAAAACTC CCATGAAA AGGAAAACTC CCATGAAA AGGAAAACTC CCATGCAAC ACCCATGCAA ACCCATGCAAC ACCCATGCAAC ACCCATGCAAC ACCCATGCAC ACCCATGCAC ACCCATGCAC ACCCATGCAC ACCCATGCAC ACCCATGCAC ACCCATGCAC ACCCATGCAC ACCCATGCAC ACCCATGCAC ACCCATGCAC ACCCTCCTCCT	21	ACACTGTGGC TCTTGCCTGG TCTTGCCTGG TGGCCTTGG TGGATGGGG GATCTGGTGG GATCTGGTGG GATCCATI 1 1 2 CGCAGGAGG GCTCCTTGG AGCAGCAGG GCTCCTGG GCCACCAGG GCCACCAGG CCACCAGG I TITCTAANAA A TOTCAGAAGG A CAGCTGATGA A TOTGAGAGG A CAGCTGATGA A TOTGTCAACA B GCCANATGTA I I GGGCGGGGC C GGGCGGGGC C GGGCGGGGC C GGGCATGCT C GGGCATGCT C GGGCATGCT C GGGCATGCT C GGGCATGCT C GGGCATGCT C GGGCATGCT C GGGCATGCT C GGGCATGCT C GGGCATGCT C TGGGCATGCT C TGGGCATGCT C TGGGCATGCT C TGGGCATGCT C TGGGCATGCT C TGGACTGCT C TGGCT C	TIGCCCGTTGT TAAGCAGGGT TAAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G TTCCACTGAA GCAGGACTCT G TGCAGGACTCT GGCGCGCGGG CGCAGGAGCTCG GGCGCGCAGG CGCAGGAGTGGA CCAGAGAAGA CCAGAGAAGA CCACTGACC ATGCAGAGATCG ATGCAGAGATCG TGTAATACGGT TAATACGGT TAATACGGT TAATACGAT CATTACAAAT CATGATAAAAAA GAGACAGATCG GTCCTTGCG GTCTCTGGG TATTACAAAT TATGAAAAAA	120 180 240 300 360 411 120 180 240 300 360 420 480 540 600 660 720 780 840 900 1020 1080 1140 1200 1200 1200	
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	GTACACTGCC CCAGGACTGT CATTTTGGCA TCTGCAAAGG AATCACTTTA GAAAGCCAGC	1620
	ACCTGGTTGA TGTGTATTCA TACTGACATT AGATTGATGT GCACTGCATT AGAAATGAGG	1680
	TAGCTGACAC AGAAAAAGGA TGTTTTGATA GGAATAATTT TCTAGTATGT CTTGAAACAT	1740
5	GITCATCTGG AAGTATTTTC CTCCAAAGTA ATGTAGCATG ATTTTTCAAG GATTGTTAAC	1800
	ATGCCTGGGA TTGGGAAAGA TAGGACTAAA GTTGTGCCAA ACTATATCAA TAAATTCCAT	1860
	GTTTAGCAGA AATAGCAGC CTATTGGTGT TATGTTTATG TAACATAGTC CAGAGAACTG	1920
	GITTAGEAGA ARTAGEAGE CHATTEGIGI TATOTITATO TATOTITATO	1980
	ACATGCAGGT CAAAAGTCAG ATACGCAACC TCCTTATCTG CTAACTCTGT TATTCTTCAA	
	ACACAAGTGG GTAGTGTCAT TITTCCTTCC TICCTTCCAT TGGCAGATTG TATATTTATT	2040
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	IGCVIGATOR CONTCOLOGO		CONCROS ROUNDLIS		

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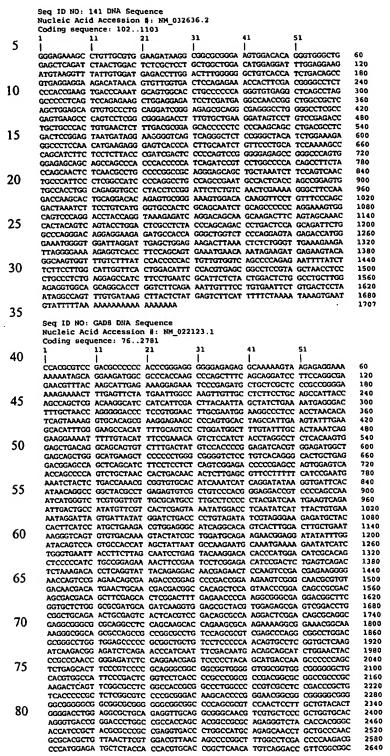
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	CELEMBRIC INTEGRECON CHIEFLEIN ONLOGISTON WHICHOUSE WEDNESTED	

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35	TCTAATCTGG AGGCAAGCTG CTGCTCTCGT ACTAACTGTG CCAGTGCCCA TGTTTACAGA	1620
33	AGTCAGGGGA AGGAAGGAGC CTGTGTCCCT GGGACGACAG TCAACTGGAG CTAGGTGTTG ACCTCAGAAC TGCATTTTAT TTATTAATTT ATAAGCAGAA CAGGCCAGAG TTCTAGGCTC	1680 1740
	TOTTTCTAGG TGCTGTTTTC AAAACCCCAG ATGACAGTCA TAGAAAATTT GGAACTTAGG	1800
	AAAATAGCTG GAATCATGAA TGACAATGAG ATAACATACA GATGTCAGTG GAGACAAAGT	1860
40	TGTGGGTTCC TCCTCCCACC TGGCTTTGAG GCTGTCGTCG ATATCATAGT ACTTTACATG	1920
40	GATTCACATG AACTGAAACG CCACCACTTG GCCCAGGATG TTGAAAGGGT GCAAATTCCT	1980
	TCTGGGTAGA TAAGAAATGA CTCTGGGAGA GGATTTCCCT TATGTGAATC TAGGTAAAAA	2040 2100
	GATGAAAAAA AATTGTATTA TGTGATCCTA AGGACAGGAA TAGCAGACCA GCCAACGGGA TGGCCTTGGG TACATCACTC AGCCTTTCTG GACCCAATTT TTCCCCAGTG AAAGCCAAGT	2160
	TGGACTGAAT TTCTGGAGTT CTCATCAGTG CACATTCCAT AGTTCTCCAG TGCTTGGCGA	2220
45	TCAGCCCAAT TGAAGGACTG GCTCTGTACT GACACTTATT ATCGGTACAG GCAAAGAGGA	2280
	GCCTGTTGTC TGTTAGGGAC CACTAAATCA ACAACCACAA ATGGATTTTT TTTTTAAGAG	2340
	GAGCTGTGCA CCTCAATTTG CTGTCTAGTT GAGAATAGAG ATTGTGTGCC TTCATTTCAT	2400
	TITCATTGCT TIGTAGTATT ITATIGTATG CATGTACCAT AATTTATTTA TCCAGTTGGA ATTTATCCTG GCAAAGATTT GCAGTAAGTC TCCAGCTGAA TTTCTTTTCA GGCGACTAGC	2460 2520
50	CAGTTGCACC AACAATATTT AGTGAGTAAT CCGTCTTTTC TCCACTAATG TAAATGCCAC	2580
	TITTATTATT TATTAAATGA CCTTAAATAT TGTGGTCTAC TTCCAGACTT GCTCTTCTGC	2640
	TCCATTCATC TITCTATTTC TGAATTIGCA ATGAACAGTT TATTATTGTC ACTITATAAT	2700
	ACACTTTAAG ATCTGGCAGA GTTTGTCTCC CGCATTTCTC TTTCTTTTTC AGAACTTTTC	2760
55	TTGATTTCCC TGCATGATCT TTGGAATCAG CTTGTCAAGA TCCAAAATAA TCCTGTTGGT ATGTTTGTTT GTATCCCATT AAAATTATAG ATGAAAAG	2820 2858
33	AIGHTGTTT GTATCCCATT AAAATTATAG AIGAAAAG	2030
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	Nucleic Acid Accession #: NM_021077.1	
60	Coding sequence: 37402	
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	CGCGCGCCCG AACGAAGCCG CGGCCCGGGC ACAGCCATCG CCCGGCGGGC GGGGGGCGCT	60
	COGATOTICG GCAGCCTCCT GCTCTTCGCC CTGCTCGCTG CCGGCGTCGC CCCGCTCAGC	120
	TGGGATCTCC CGGAGCCCCG CAGCCGAGCC AGCAAGATCC GAGTGCACTC GCGAGGCAAC	180
65	CTCTGGGCCA CCGGTCACTT CATGGGCAAG AAGAGTCTGG AGCCTTCCAG CCCATCCCAT	240
	TGGGGACAGC TCCCCACACC TCCCCTGAGG GACCAGCGAC TGCAGCTGAG TCATGATCTG CTCGGAATCC TCCTGCTAAA GAAGGCTCTG GGCGTGAGCC TCAGCCGCCC CGCACCCCAA	300 360
	ATCCAGTACA GGAGGCTGCT GGTACAAATA CTGCAGAAAT GACACCAATA ATAGGGGCAG	420
	ACACAACAGC GTGGCTTAGA TTGTGCCCAC CCAGGGAAGG TGCTGAATGG GACCCTGTTG	480
70	ATGGCCCCAT CTGGATGTAA ATCCTGAGCT CAAATCTCTG TTACTCCATT ACTGTGATTT	540
	CTGGCTGGGT CACCAGAAAT ATCGCTGATG CAGACACAGA TTATGTTCCT GCTGTATTTC	600
	CTGCTTCCCT GTTGAATTGG TGAATAAAAC CTTGCTCTT	639
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75	Nucleic Acid Accession #: NM_002055.1	
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80	AGAGCCAGAG CAGGATGGAG AGGAGACGCA TCACCTCCGC TGCTCGCCGC TCCTACGTCT	60 120
50	CCTCAGGGGA GATGATGGTG GGGGGCCTGG CTCCTGGCG CCGTCTGGGT CCTGGCACCC GCCTCTCCCT GGCTCGAATG CCCCCTCCAC TCCCGACCCG GGTGGATTTC TCCCTGGCTG	180
	GGGCACTCAA TGCTGGCTTC AAGGAGACCC GGGCCAGTGA GCGGGCAGAG ATGATGGAGC	240
	TCAATGACCG CTTTGCCAGC TACATCGAGA AGGTTCGCTT CCTGGAACAG CAAAACAAGG	300
	COCTGOCTGC TGAGCTGAAC CAGCTGCGGG CCAAGGAGCC CACCAAGCTG GCAGACGTCT	360

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TTCTAMAGGC CTCTTCCTTG CTGTGTCATA CCAGGCCCC CCAGCCTCTG AGCCCCTGGG ACTGCTGCTC CTTAMACCCAG GTAAGCCAT GGCACAGCTCT CACCCCATAG TGTACCCGGT CTTTTCCCTA AGCCAAGGC TCTTGCGTC CACCCCATAG ANGTARGCCA CTGGCTCATA TTCCTCAGC TTTTCAGTTC TAAACTGAG GCACGACAA ANGTARGCCAG CTGGCTCATA TTCCTCAGC CTGGAGGCG GCTCTCAGG GCTGACAGCT TGTGCCCAGC GATGGGACTG GGAGGGCCCA CTTCAGGTC GGTGGCAGGC TGTGCAGGCT TGTGCCCAGC GATGGGACTG GGAGGGCCCA CTTCAGGTC TCCTCTCCC CTCTAGGCC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGGGTT CTCCTCTCCC CTCTAGGCC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGGCTT CTCCTCTCCC CTCTAAGCC ACCTGCTGCT GCTGCTCGTC TAAACTTCA GGGCACTGCT TCCCTCCCC TCTTAGGCC ACCTGCTGCT GCTGCTCTC CCCCAAGACT TGGTGTGCTT TCCCTCCACT TCTTCCTGCC AACAAAATAAAG ACAAATGCTG CGCCCTTAAA AAA Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L79126.1 GAATTCGCC TCAACATGGC CAGGTCCTG GCCACATTGT CCCTCCAAC CTCCAGCCGG GCGCTGTTGG CGTGAGTGTA TCGAGCCGGC CCCCACAGCGCC CCCCACAGCCC CCCCACAGCCC CCCCACAGCCC CCCCACAGCCC CCCCACAGCCC CCCCCACACACCCC CCCCACACACCCC CCCCACACACCCC CCCCACACACCCC CCCCACACACCCC CCCCACACACCCC CCCCACACACCCC CCCCCACACACCCC CCCCCC	25	GACCAGTTGC ACTTGGCCTC TGGATTGTGG GAATTAAGGA AGTGACTCAT CCTCTTGAAG	
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TCCCTGGTTC GAAGGGCTGC CCTCACACAC AAGACAACC ACTTCAATTA TGAGAAGACA CACAACTTTA AGGTCCACAC GTTCCGAGGC CCACACTGGT GTGAATATTG TGCCAATTTC ATGTGGGGGC TCATCGCCCA AGGGGTCCGG TGCTCAGACT GTGAATATTG ACCTAACAAA 1200 CAGTGTTCCA AGCACGTTCC CAATGACTGC CAACCTGATC TCAAGAAGACT CAAGAAAGTG TACTGTTGTG ACCTCACACA ACTTGTGAAG GCTCACAACA CTCAGAGACC CATGGTGGTA TCTGGGTACA TTCGGGAAAT TGAAGCAAGA GGATTAAAAT CGGAAGGCCT TTACAGAGTC GCCGATATAT CTGCCAATGT CTATCCAGAC ATAAACATCA TCACTGAGGC CCTTAAACTG GCCGATATT CTGCCAATGT CCATCCAGC ATAAACATCA TCACTGAGGC CCTTAAACTG GCAGAAAAA TCTCCAATGT CCATCCAGC ATAAACATCA TCACTGAGGC CCTTAAACTG GCAGCAAAAA TCTCCCAATGC ACATCAGCAC ACAATATGATA CCCATTCCAA AATTTATAGAT 1560 CTGCCTCCTG CCCACTATGA AACCCTCCGG TACCTAATGA TCCACCTCAA AAAGGTTAACT CTGATGAGGC CCCCTGAGGA CAGCACCCTG ACCACCCTG GGATGGTGTT TGGGCCCACT 1740 CTGATGTGC AGATTTTAAT AGAAAACGAA GACGTTAATG ATAAACATT TCTTACCAC CAGGGAAATG AGGTGAATGC CCCAGCACA TCAAGTTACA ACAGCTAAGG ATAAAACATT TCTTACCAC TAGGGAAATG AGGTGAATGC CCCCCTGAGGA CAGCACCCTG ACCACCCTG CAGGGAATG CAGGGAAATG AGGTGAATGC CCCAGCACA TCAAGTTAC ACAGCTAAGG ATAAAACATT TCTTACCACT TGATTGTC AGATTTTAAT AGAAAACGAA GACGTTAAGG ATAAAACATT TCTTACCACT TGATTGTTT TCCAAGCAAG TGCTAGAATT TGCTGGACTG CAGGGAATG CTGAGGGGC TGATTGTTT TCCAAGCAAG TGCTAGAATT TGCTGGACTG CAGGGAATG CTGAGTGGGG 1980			
70 CACAACTTTA AGGTCCACAC GTTCCGAGGC CCACACTGGT GTGAATATTG TGCCAATTTC ATGTGGGGGC TCATCGCCCA AGGGGTCCGG TGCTCAGACT GTGGATTGAA GTACACAAA ATGTGGGGGGC TCATCGCCCA AGGGGTCCGG TGCTCAGACT GTGGATTGAA CGACACTGTTC CAGTGTTCCA AGCACGTTCC CAATGACTGC CAACCTGATC TCAAGAGGAT CAAGAAAGTG 1260 TACTGTTGTG ACCTCACACA ACTTGTGAAG GCTCACAACA CTCAGAGACC CATGGTGGTA 1320 GACATATGCA TTGGGAAAT TGAAGCAAGA GGATTAAAAT CGGAAGGCC TTACAGAGGT 1320 GCGATATAT CTGCCAATGT TGAAGAAGA ATAAACATCA TCACTGGAGC CCTTAAACTG GCGACAAAAA TCTCCCAATGC ACATGAACACA TTAAACATCA TCACTGGAGC CCTTAAACTG TATTTCAGAG ACTTACCCAT CCCTGTCATC ACATATGATA CCCATGTCAA ATTTATAGAT 1550 GCAGCAAAAA TCTCCCAATGC AGATGAAGAG CTGGAAGCCG TCCATAGAGT GCTGATGCTG CTGCCTTCCTG CCCACTATGA AACCCTCGG TACCTAATGA TCCACTCAAA AAAGGTTACT 1680 ATGAATGAAA AAGACAATT CATGAATGCA GAAAATCTG GGATCGTGT TGGGCCCACT 1740 CTGATTGGC CCCTTGAGGA CAGCACCCTG ACCACCCTGC ATGATATGCG TACCAAAAG 1860 CTGATTGGC AGATTTAAT AGAAAACCAA GACGCTTATT TCTAATCCAT CAGGGAAATG 1860 AGCTGAATGG CCCAGCACCA TCAAGATTGAC ACAGCTAAGG ATAAAACATT TCTTACCACT 1920 TGATTTGTTT TCCAAGCAAG TGCTAGAATT TGCTGGACTG CAGAGGATCG CTGAGTGGGG 1980		AATGAACCAA GAAAAACAAA CGTCACACAT GAAGAACACA CAGCGGTGGA AAAGATCTCC	
ATGTGGGGGC TCATCGCCCA AGGGGTCCGG TGCTCAGACT GTGGATTGAA CITACACAAA 1200 CAGTGTTCCA AGCAGGTTCC CAATGACTGC CAACCTGATC TCAAGAGGAT CAAGAAAGTG 1260 TACTGTTGTG ACCTCACACA CATTGTGAAG GCTCACAACA CTCAGAGGAC CATGGTGGTA 1320 GACATATGCA TTCGGGAAAT TGAAGCAAGA GGATTAAAAT CGGAAGGCCT TTACAGAGTC 1380 TCTTGGGTTCA CTGAACACAT TGAAGATGTC AAAATGGCAT TTGACAGAGA TGGTGAAAAG 1440 GCCGGATAATAT CTGCCAATGC TCATCACACA ATAAACATCA TCACTGGGC CCTTAAACTG 1500 TATTTCAGAG ACTTACCCAT CCCTGTCATC ACATATGATA CCTATTCCAA ATTTATAGAT 1550 GCAGCAAAAA TCTCCAATGC ACATGAGAG CTGGAAGCCG TCCATGAAGT GCTGATGCTG CTGCTCCTG CCCACTATGA AACCCTCAG TACCTAATGA TCCACTCCAA AAAGGTTACT CTGCTCCTG CCCACTATGA AACCCTCAG TACCTAATGA TCCACTCCAA AAAGGTTACT ATGAATGAAA AAGACAATT CATGAATGCA GAAAATCTG GGATCGTGT TGGGCCCACT CTGATGAGGC CCCCTGAGGA CAGCACCCTG ACCACCCTG ATGATATGCG GTACCAAAAG AGCTGATTGTG ACATTTTAAT ACAAAACGAA GACGTTATTA TCTAATCCAT CAGGGAAATG AGCTGAATGG CCCAGCACCA TCAAGTTGAC ACAGCTAAGG ATAAAACCAT TCTTACCACT 1920 TGATTTGTT TCCAAGCAAG TGCTAGAATT TGCTGGACTG CAGAGGATCG CTGAGTGGGG 1980	70	TCCCTGGTTC GAAGGGCTGC CCTCACACAC AACGACAACC ACTICAATTA TGAGAAGACA	
CAGTGTTCCA AGCACGTTCC CAATGACTGC CAACCTGATC TCAAGAGGAT CAAGAAAGTG TACTGTTGTG ACCTCACAAC ACTTGTGAAG GCTCACAACA CTCAGAGACC CATGGTGGTA 1320 75 TCTGGGTTCA CTGAACACAT TGAAGATGTC AAAATGGCAT TTGACAGAGCC TTACACAGGTC 1380 GCCGATATAT CTGCCAATGT CTATCCAGAC ATAAACATCA TCACTGGAGC CCTTAAACATG TATTTCAGAG ACTTACCCAT CCCTGTCATC ACAATGGTAAT CCCTATCCAA ATTTATAGAT 1560 GCAGCAAAAA TCTCCAATGC ACATCAGAGG CTGAAGCCG TCCATGAAGT GCTGATGCTG 1620 CTGCTCCTG CCCACTATGA AACCCTCCGG TACCATATGA TCCACCTCAA AAAGGTTACT 1680 ATGAATGAAA AAGACAATT CATGAATGCA GAAAATCTGG GGATCGTGTT TGGCCCCCT 1740 CTGATGAGGC CCCCTGAGGA CAGCACCCTG ACCACCCTG GATCGTGTT TGGCCCCCT 1740 CTGATGAGG CCCCCGGAGCA CAGCACCCTG ACCACCCTGC ATGATATGG GTACCAAAAG 1800 CTGATTGTG AGATTTTAAT AGAAAACGAA GACGTTAAG TCTAATCCAT CAGGGAAATG 1860 AGCTGAATGG CCCAGCACCA TCAAGTTAC ACAGCTAAGG ATAAAACATT TCTTACCACT 1920 TGATTTGTT TCCAAGCAAG TGCTAGAATT TGCTGGACTG CAGGGAATG CTGAGTGGGG 1980	70		
TACTGTTGTG ACCTCACAAC ACTTGTGAAG GCTCACAACA CTCAGAGACC CATGGTGGTA 1320 GACATATGCA TTCGGGAAAT TGAAGAGAGA GGATTAAAAT CGGAAGGCCT TTACAGAGTC TCTGGGTTCA CTGAACACAT TGAAGAGTC AAAATGGCAT TTGACAGAGA TGGTGAAAAG GCCGATATAT CTGCCAATGT CTATCCAGAC ATAAACATCA TCACTGGAGC CCTTAAACTG TATTTCAGAG ACTTACCCAT CCCTGTCATC ACATATGATA CCTATCCAA ATTTATAGAT GCAGCAAAAA TCTCCAAATGC AGATGAGAGG CTGGAAGCCG TCCATGAAGT GCTGATGCTG CTGCCTCCTG CCCACTATGA AACCCTCCGG TACCTAAAGA TCCCCCTCAA AAAGGTTACT ATGAATGAAA AAGACAATTT CATGAATGCA GAAAATCTGG GGATCGTGTT TGGGCCCACT CTGATGAGGC CCCCTGAGGA CAGGCCCTG ACCACCCTGC ATGATATGCG GTACCAAAAG CTGATTGTGC AGATTTTAAT AGAAAACGAA GACGTTTAT TCTAATCCAT CAGGGAAATG AGCTGAATGG CCCAGCACCA TCAAGTTGAC ACAGCTAAGG ATAAAACATT TCTTACCACT 1920 TGATTTGTTT TCCAAGCAAG TGCTAGAATT TGCTGGACTG CAGAGGAATCG CTGAGTGGGG 1980			
75 GACATATGCA TTGGGAAAT TGAGCAAGA GGATTAAAAT GGGAGGCCT TTACAGAGTC 1380 TCTGGGTTCA CTGAACACAT TGAAGATGC AAAATGCAT TTGACAGAGC TGGTGAAAAG 1640 GCGATATAT CTGCCAATGC TCATCCACAC ATAAACATCA TCACTGGAGC CCTTAAACTG 1500 TATTTCAGAG ACTTACCCAT CCCTGTCATC ACATATGATA CCTATTCCAA ATTTATAGAT 1650 CTGCGTCCTG CCCATTGCA AACCCTCCGG TCCATAGAGT GCTGATGCTG 16680 ATGAATGAAA AAGACAATT CATGAATGCA GAAAATCTGG GGATCGTGT TGGGCCCACT 1740 CTGATGAGGC CCCCTGAGGA CAGCACCCTG ACCACCCTGC ATGATATGCG TCACAAAAG 1800 CTGATTGGC AGATTTTAAT AGAAAACGAA GACGTTTAT TCTAATCCAT CAGGGAAATG 1860 AGCTGAATGG CCCAGCACCA TCAAGATGAA GACGTTTATT TCTAATCCAT CAGGGAAATG 1860 AGCTGAATGG CCCAGCACCA TCAAGTTGAC ACAGCTAAGG ATAAAACATT TCTTACCACT 1920 TGATTTGTTT TCCAAGCAAG TGCTAGAATT TGCTGGACTG CAGAGGATCG CTGAGTGGGG 1980		TACTGTTGTG ACCTCACAAC ACTTGTGAAG GCTCACAACA CTCAGAGACC CATGGTGGTA	1320
TCTGGGTTCA CTGAACACAT TGAAGATGTC ANANTGGCAT TTGACAGAGA TGGTGAAAAG GCGGATATAT CTGCCAATGT CTATCCAGAC ATAAACATCA TCACTGGAGC CCTTAAACTG TATTTCAGAG ACTTACCCAT CCATGCACAC ATAAACATCA TCACTGGAGC CCTTAAACTG GCAGCAAAAA TCTCCCAATGC ACATGAGAGC CTGCAAGGC GCTGATGGTG CTGCCTCCTG CCCACTATGA AACCCTCCGG TACCACATATGA TCCACCTCAA AAAGGTTACT ATGAATGAAA AAGACAATTT CATGAATGCA GAAAATCTGG GGATCGTGTT TGGGCCCACT TAGACGAGC CCCCTGAGGA CAGCACCCTG ACCACCCTGC ATGATATGGG TACCAAAAG CTGATTGTGC AGATTTTAAT AGAAAACGAA GACGTTAAGT TCTTAATCCAAT CAGGGAAATG AGCTGAATGG CCCAGCACCA TCAAGTTACA CAGCTAAGG ATAAAACATT TCTTACCACT TGATTTGTTT TCCAAGCAAG TGCTAGAATT TGCTGGACTG CAGGGAATG CTGAGTGGGG 1980		GACATATGCA TTCGGGAAAT TGAAGCAAGA GGATTAAAAT CGGAAGGCCT TTACAGAGTC	1380
80 CCCGATATAT CTGCCAATGT CTATCCAGAC ATAAACATCA TCACTGGAGC CCTTAAACTG 1500 TATTTCAGAG ACTTACCCAT CCCTGTCATC ACATATGATA CCTATTCCAA ATTTATAGAT 1560 GCAGCAAAAA TCTCCAAATGC AGATGAGAGG CTGGAAGGCG TCCATGAAGT GCTGATGCTG 1620 CTGCCTCCTG CCCACTATGA AACCCTCCGG TACCTAATGA TCCACCTCAA AAAGGTTACT 1680 ATGAATGAA AAGACAATTT CATGAATGCA GAAAATCTGG GAATGATGTG GTGACCAAAAG CTGATGAGGG CCCCTGAGGA CAGGCACCTG ACCACCCTGC ATGATATGCG GTACCAAAAG 1800 CTGATTGTGC AGATTTTAAT AGAAAACGAA GACGTTTAAT TCTAATCCAT CAGGGAAATG 1860 AGCTGAATGG CCCAGCACCA TCAAGTTGAC ACAGCTAAGG ATAAAACATT TCTTACCACT 1920 TGATTTGTTT TCCAAGCAAG TGCTAGAATT TGCTGGACTG CAGAGGAATCG CTGAGTGGGG 1980	75		1440
80 TATTTCAGAG ACTTACCCAT CCCTGTCATC ACATATGATA CCTATTCCAA ATTTATAGAT GCAGCAAAAA TCTCCAATGC AGATGAGAGG CTGGAAGCCG TCCATGAAGT GCTGATGCTG CTGCTTCCTG CCCACTATGA AACCCTCGG TACCTAATGA TCCACCTCAA AAAGGTTACT 1680 ATGAATGAAA AAGACAATT CATGAATGCA GAAAATCTGG GGATCGTGT TGGGCCCACT CTGATGAGGC CCCCTGAGGA CAGCACCCTG ACCACCCTGC ATGATATGGG GTACCAAAAG CTGATTGGC AGATTTTAAT AGAAAACCAA GACGTTATA TCTAATCCAT CAGGGAAATG AGCTGAATGG CCCAGCACCA TCAAGTTGAC ACAGCTAAGG ATAAAACATT TCTTACCACT 1920 TGATTTGTTT TCCAAGCAAG TGCTAGAATT TGCTGGACTG CAGAGGATCG CTGAGTGGGG 1980		GCCGATATAT CTGCCAATGT CTATCCAGAC ATAAACATCA TCACTGGAGC CCTTAAACTG	
80 GCAGCARARA TCTCCRATGC ACATGAGAGG CTGGAGGCCG TCCATGARGT GCTGATGCTG 1620 80 ATGARTGARA AAGCCATCTG TACCTRATGA TCCACCTCAA AAAGGTTACT 1680 ATGARTGARA AAGCCARTT CATGARATGCA GARAATCTGG GGATCGTGTT TGGGCCCACT 1740 CTGATGAGGC CCCCTGAGGA CAGCACCCTG ACCACCCTGC ATGARTATGGG GTACCARAGG 1800 CTGATTGTGC AGATTTTAAT AGARAAACGAA GACGTTTAT TCTAATCCAT CAGGGAAATG 1860 AGGTGAATGG CCCAGCACCA TCAAGTTGAC ACAGCTRAGG ATAAAACATT TCTTACCACT 1920 TGATTTGTTT TCCAAGCAAG TGCTAGAATT TGCTGGACTG CAGAGGATCG CTGAGTGGGG 1980		TATTTCAGAG ACTTACCCAT CCCTGTCATC ACATATGATA CCTATTCCAA ATTTATAGAT	1560
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TGATTTGTTT TCCAAGCAAG TGCTAGAATT TGCTGGACTG CAGAGGATCG CTGAGTGGGG 1980			
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	TITUTANNO MANUCANA CITUTANNO GORCETONO CONCITUDAD OCTOR	
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	CHOIGICAND CICANCHARC CHITTCACID GCCICINGID AICCOCAGAN GACODI	

15.

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5	AAAATGACTG TAG	CCAACCAGGT	GCAGATCCCT	CGGGACAGAT	CCCAGTATAA	GCACATGGGC	840 843
	Nucleic Aci	154 DNA Seq d Accession lence: 261	#: NM_1445	86			
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	Seg In MA	: 156 DNA S	equence				
		cid Accessi		4833.1			
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75	1	11	21	31	41	51	
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						CAGTGGAGGA	660
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65	Coding sequ						
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•		id Accessio uence: 11		928.2			
	1	11	21	31	41	51	
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40						TTTGCTGGCT	60 120
						GCAACTCAGA ACTTGACTGC	180
	TGGAGAGGTG	GTCAAGTGTC	CCTCAAGGTC	AGTAATGATG	GCCTACACT	GATTGGTGCA	240
45	AATGCCTCCT	TCTCTATTGC	CTTGAACTTC	CCTGGAAGCC	AAAAGGTATT	GCCAGATGGG	300
45	CAGGTTATCT	GGGTCAACAA	TACCATCATO	AATGGGAGCC	: AGGTGTGGGG	AGGACAGCCA TTGCCCATCT	360 420
	GGCTCTTGGT	CTCAGAAGAG	AAGCTTTGTT	TATGTCTGGA	AGACCTGGGG	CCAATACTGG	480
	CAAGTTCTAG	GGGCCCAGT	GTCTGGGCTG	AGCATTGGGA	CAGGCAGGG	AATGCTGGGC	540
50	ACACACACCA	TGGAAGTGAG	TGTCTACCAT	CGCCGGGGAT	CCCGGAGCTA	GAGCGTGTCC	600 660
30	CAGTTGCGGG	CCTTGGATGC	AGGGAACAAG	CACTTCCTG	GAAATCAGC	TCTGACCTTT	720
	GCCCTCCAGC	TCCATGACCC	CAGTGGCTAT	CTGGCTGAAC	CTGACCTCTC	CTACACCTGG	780
						TCATACTTAC	840
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		י היירטבידרו	* ACCCACCAC			TCTCACCTCC	900 960
		CTGGCCAAGT	GCCTACTAC	GATGGGCACA GAAGTTGTGC	GGCCAACTGC GTACTACACC	AGAGGCCCCT TGGTCAGGCG	900 960 1020
	CCAACTGCAG	CTGGCCAAGT	GCCTACTAC	CATGGGCACI CAAGTTGTGC CTGCAGGTGC	GGCCAACTGC GTACTACACC CAACCACTG	AGAGGCCCCT TGGTCAGGCG AGTCATAAGC	960 1020 1080
	CCAACTGCAC	G CTGGCCAAGT G AGCCCTCTGG G TGCAGATGCG	GCCTACTACE AACCACATCE AACTGCAGAG	A GATGGGCACA A GAAGTTGTGG F GTGCAGGTGG B AGCACAGGTA	A GGCCAACTGC G GTACTACACC C CAACCACTGA A TGACACCTGA	AGAGGCCCCT TGGTCAGGCG AGTCATAAGC AGAGGTGCCA	960 1020 1080 1140
60	CCAACTGCAG ACTGCACCTG GTTTCAGAGG ACACCTGCAG	G CTGGCCAAGT G AGCCCTCTGC G TGCAGATGCC G TCATGGGTAC G AGGTATCAAC	GCCTACTACE AACCACATCE AACTGCAGAC CACACTGGCE TGTGGTGCT	A GATGGGCACA A GAAGTTGTGK T GTGCAGGTGK G AGCACAGGTA A GAGATGTCAA T TCTGGAACCA	A GGCCAACTGC G GTACTACACC C CAACCACTGI A TGACACCTGI A CTCCAGAGGG A CAGCTGCACI	AGAGGCCCCT TGGTCAGGCG AGTCATAAGC AGAGGTGCCA TACAGGTATG AGGTAACAACT	960 1020 1080
60	CCAACTGCAG ACTGCACCTG GTTTCAGAGG ACACCTGCAG ACAGAGTGGG	CTGGCCAAGT GCAGATGCG TGCAGATGCG TCATGGGTAG GGGTATCAACGTGGGACCAG	GCCTACTACE AACCACATCT AACTGCAGAC CACACTGGCE TGTGGTGCT AGCTAGAGAC	A GATGGGCACA A GAAGTTGTGC C GTGCAGGTGC A AGCACAGGTA A GAGATGTCAA C TCTGGAACCA C CTACCTATCC	A GGCCAACTGC G GTACTACACC C CAACCACTGI A TGACACCTGI A CTCCAGAGGG A CAGCTGCACI C CTGAGCCTGC	AGAGGCCCCT TGGTCAGGCG AGTCATAAGC AGAAGGTGCCA TACAGGTATG AGGTACAACT AGGTCCAGAT	960 1020 1080 1140 1200 1260 1320
60	CCAACTGCAG ACTGCACCTG GTTTCAGAGG ACACCTGCAG ACAGAGTGGG GCCAGCTCAJ	G CTGGCCAAGT G AGCCCTCTGG G TGCAGATGCG G TCATGGGTAG G AGGTATCAAT G TGGAGACCAG A TCATGTCTAG	GCCTACTACI AACCACATCT AACTGCAGAC CACACTGGCI TGTGGTGCT AGCTAGAGAC GGAAAGTAT	A GATGGGCACA A GAAGTTGTGC F GTGCAGGTGC A GAGATGTCAA F TCTGGAACCA C CTACCTATCC A ACAGGTTCCA C CTACCTATCC A ACAGGTTCCC A CAGGTTCCC	A GGCCAACTGC GTACTACACC CAACCACTGIA TGACACCTGIA CTCCAGAGGC A CAGCTGCACI CTGAGCCTGC TGGGCCCCC	AGAGGCCCCT TGGTCAGGCG AGTCATAAGC AGAAGGTGCCA TACAGGTATG AGGTACAACT AGGTCCAGAT GCTGGATGGT	960 1020 1080 1140 1200 1260 1320 1380
	CCAACTGCAG ACTGCACCTG GTTTCAGAGG ACACCTGCAG ACAGAGTGGG GCCAGCTCAJ ACAGCCACCT	G CTGGCCAAGT G AGCCCTCTGC G TGCAGATGCC G TCATGGGTAG G AGGTATCAAC G TGGAGACCA A TCATGTCTA T TAAGGCTGG	GCCTACTACE AACCACATCE AACTGCAGAC CACACTGGCE TGTGGTGCT AGCTAGAGAC GGAAAGTAT GAAGAGACAC	A GATGGGACI A GAAGTTGTGG G GTGCAGGTGG A GAGATGTCA A GAGATGTCA G TCTGGAACCI G CTACCTATC A CAGGTTCCC A GTCCCCTGG	A GGCCAACTGC GTACTACACC CAACCACTGA TGACACCTGA A CTGCAGAGGC C CTGGGCCCCCC G ATTGTGTTCC G GTGTGCTTCC G ATTGTGTTCC G GTGGCCCCCC G ATTGTGTTCC	AGAGGCCCT TGGTCAGGCG AGTCATAAGC AGAGGTGCA CTACAGGTATG AGGTAACACT AGGTCCAGAT GGTGGATGGT GGTATCGATAT	960 1020 1080 1140 1200 1260 1320
60 65	CCAACTGCAG ACTGCACCTG GTTTCAGAGC ACACCTGCAG ACAGAGTGGC GCCAGCTCAA ACAGGCCACCT GGTTCCTTTT GCTGTGCGG	G CTGGCCAAGT G AGCCCTCTGC G TGCAGATGC G TGCAGATGC G AGGTATCAAT G TGGAGACCAA A TCATGTCTAA T TAAGGCTGG T CCGTCACCCT C CCGGTGAGGG	GCCTACTACJ GCCTACTACJ AACCACATCC AACTGCAGAC TGTGGTGCT GCAAAGAGACA GGAAAGACAC GGAAAGTAT GGACATTGTG GGACATTGTG GGACATTGTG GGACATTGTG GGACATTGCATC	A GATGGCACI A GAAGTTGTGC A GGACAGGTI A GAGACAGGTI A GAGATGTCAI C TCTGGAACCI G CTACCTATCI A ACAGGTTCCC C CAGGGTATTI C GAGCTGACT C GAGCTGACT C G GAGCTGACT C G GAGCTGACT C G GAGCTGACT C G GAGCTGACT C G G G G G G G G G G G G G G G G G G G	A GGCCAACTGC GTACTACACC CTCAGAGGGA A CAGCTGCAC CTGAGCCTGC CTGAGCCTGC CTGAGCCTGC CTGAGCCTGC CTGAGCCTGC CTGAGCCCCC CTGAGCCCCCC CTGAGCCCCCC CTGAGCCCCCC CTGAGCCCCCC CTGAGCCCCCC CTGAGCCCCCC CTGAGCCCCCC CTGAGCCCCCC CTGAGCCCCCC	AGAGGCCCT TGGTCAGGG AGTCATAAGC AGAGGTGCCA AGGTACCAC AGGTACCACT AGGTCCAGAT GCTGGATGGT GTATCGATAT AGATCCTGCAG AAGGCGGCTG AAGGCGGCTG	960 1020 1080 1140 1200 1260 1320 1380 1440 1500
	CCAACTGCAG ACTGCACCTG GTTTCAGAGC ACACCTGCAG ACAGGGTGGG GCCAGCTCAA ACAGCCACCT GGTTCCTTTT GCTGTGCGGT	G CTGGCCAAGT G AGCCCTCTGG G TGCAGATGG G TGCAGAGGTAG G AGGTATCAA G TGGAGACCA A TCATGTCTAG T TAAGGCTGG C CCGTCACCG C CCGTCACGG G CCTGCATGG G CCTGCATGG G CCTGCATGG	GCCTACTACJ AACCACATCT AACTGCAGAC TGTGGTGCT AGCTAGAGACAC GGAAAGTAT GGAAGAGACA GGACATTGT AGATGCATT AGATCCATC	A GATGGCACA A GAAGTTGTGC A GAAGTTGTGC A GACACAGGT A GAGATGTCAA T CTGGAACCI T CACCTATCC A GTCCCCTGC C CAGGTATTC C CAGGTATTC G CAGGTATTC	A GGCCAACTGC G TTACTACACC G CAACCACTGG A TGACACCTGG C CTGAGCCTGG C TTGGCCCCC G ATTGTGTTC G AAAGTGCCG G TGTCCTGGCC C AGCCCCCTG	AGAGGCCCCT TGGTCAGGGG AGTCATAAGC AGAGGTGCCA TACAGGTATCA AGGTCCAGAT GCTGCAGGT GCTGCAGGT GTATCGATAT GGTGCATGGT GTATCGATAT AGGTCCAGAT AGGTCCAGAT AGGCGGGCTG CCAGCGGCTGC	960 1020 1080 1140 1200 1320 1380 1440 1500 1560 1620
	CCAACTGCAG ACTGCACCTG GTTTCAGAGG ACACCTGCAG ACAGGGTGGA GCCAGCTCAA ACAGCCACCT GCTTGCCTTTT GCCAAGGAAG TGCCAGCCT	G CTGGCCAAGT G AGCCTTCTG G AGCCTCTGG G TCATGGGTAG G AGGTATCAAT G TGGAGACCAA TCATGTCTAA TTAAGGCTGG CCGGTGAGGG CCTGCATGG G CTTGCATGG G TGCTACCCA	GCCTACTACJ ACCACATCC ACTGCAGAC CACACTGGCC TGTGGTGCT ACTAGGAGAC GGAAAGTAT GGACATTGT GGACATTGT GGACATTGT GGACATTGT GGACATTGT GGACATTGT GGACATCTCATC	A GATGGCACA A GAAGTTGTGG A GAAGTTGTGG A GAGCACAGGTI A GAGATGTCA T CTTGGAACCI T CTTGGAACCI A CAGGTTCC A GTCCCCCTGG C CAGGGTATTT G CCAGGGTGC C CAGGGTGC C C CAGGTGC C C CAGGTGC C C CAGGTGC C C C C C C C C C C C C C C C C C C C	A GGCCAACTEK G GTACTACACC G GTACCACTEG A TGACACCTEG A CTCCAGAGGG C CTGAGCCTG C TTGAGCCTG G ATTGTGTTC G AAGTGCCG G AGCCCCCTG C TGCACCAGA C TGCACCAGA C TGCACCAGA C TGCACCAGA	AGAGGCCCT TOGTCAGGG AGTCATAAGC AGAAGTTCCA AGGTACAACT AGGTACAACT AGGTCAGAT GGTCAGAT GGTCAGAT AGATCCTGCAG AGGCGGCTG CCAGCGGCTG TACTGAAGGT TACTGAAGGT ACTGAAGGT ACTGAAGGGT	960 1020 1080 1140 1200 1260 1320 1380 1440 1500
65	CCAACTGCAG ACTGCACTGCAG ACACCTGCAG ACAGCTGCAG ACAGCACCTCAA ACAGCCACCTCAG ACAGGAGCACCTCAGGTCCATTTT GCTTGCCGG CCCAAGGAAG GGCAGCTCGGGGGGGGGCTGGGGGGGGGG	CTGGCCAAGT CAGCCTCTGG AGCCTCTGG AGCCTCTGG TCATGGGTAG AGGTATCAAT ATCATGTCTAAT TAAGGCTGG CCGTCACCC CCGGTGAGG GTGCTCCCTGCATGG GTGCTCCCCTGCATGG GTGCTCACCCC ACATGCTCATGC ACATGCTCATGC ACATGCTCCCCCCCCCC	GCCTACTACE AACCGCACTACE AACCGCACTACE CACACCTGCC TGTGGTGCT AGCTAGAGA GGAAGTAT GGAGAGACAT GGAGAGACAT GGACATTGT GGATCCATC GGACTCCATC CCCACCCTC CCATTCT CCATTCT CCATTCT CCATTCT CCATTCT CCATTCT CCATTCT CCATTCT CCATTCT CCATTCT CCATTCT CCATTCT CCATTCT CCATTCT CATTCT CCATTCT CATTCT CCATTCT CATTCT CATTCT CATTCT CATTCT CATTCT CCATTCT CATTCT CATTCT CATTCT CATTCT CATTCT CATTCT CATTCT CATTCT CCATTCT CATTCT CATTCT CATTCT CATTCT CATTCT CATTCT CATTCT CATTCT CT CATTCT CT CATTCT CT CT CT CT CT CT CT CT CT CT CT CT	A GATGGCALI A GATGGGCALI G GTGCAGGTGTG A GAGACAGGT; A GAGATGTGA C TCTGGAACCI G CTACCTATCI A CAGGTTCCC C CAGGGTATT G GAGCTGATT G CAGGGTGC C CAGGGTGT T CTGGCTGATT C CTGGCTGATT	A GGCCAACTEG CAACCACTGG TGAACACCTGG A CTCCAGAGGG A CTCCAGAGGG C CTGAGCCTGC C CTGAGCCTGC C TGGGCCCCC G ATATGTGTTC G AAAGTGCCG G TGTCCTGCC C AGCCCCTG A TGCCCAGA A CCAACAGCC	AGAGGCCCCT TGGTCAGGGG AGTCATAAGC AGAGGTGCCA TACAGGTATCA AGGTCCAGAT GCTGCAGGT GCTGCAGGT GTATCGATAT GGTGCATGGT GTATCGATAT AGGTCCAGAT AGGTCCAGAT AGGCGGGCTG CCAGCGGCTGC	960 1020 1080 1140 1200 1320 1380 1440 1500 1560 1620 1680
	CCAACTGCAC ACTGCACTTGCACTGCAC ACAGGTGCAC ACAGGTGCAC ACAGGTCCAC ACAGGCACTCAC GGTTCCTTTT GCTGTGCCGC GGCTCGCGGC GGCTCGCGGG GGCACCCAGG GGCACCCAGG GGCACCTAGGGAC GGCACCTAGGGAC GGCACCCAGG GGCACCTAGGGAC GGCACCTAGGGAC GGCACCTAGG	E CTOSCCAAGO AGECTETOS TECAATGCO TECAATCCAATGCO TCCAATCCAATCCAATCCAATCCA	GCCTACTACE AACCACACTC AACTGCAGAA CCACACTGGC CCACACTGGCC CACACTGGCC CGAAAGTAC CGAAAGTAC CGAAAGTAC CGAAAGTAC CGAAAGTAC CGACATTGTC CGACATTGTC CCCCCC CCCCCC CCCCCCCCCC	A GATGGCALI A GAAGTTGTGG TGTGAGGTG A GAGATGTCA A GAGATGTCA CTACCTATC CTACCTATC CAGGTAC CAGGTATT CAGGTGCT CAGGGTATT CAGGTGCT CAGGGTATT CAGGTGCT CAGGGTGCT CAGGGTGCT CAGGGTGCT CAGGGCTGCT CAGGGCTCAT CAGGGCTCAT CAGGGCTCAT CAGGGCTCAT CAGGGCTCAT CAGGGCCTCAT CAGGCCTCAT CAGGCCTCAT CAGGCCTCAT CAGGCCTCAT CAGGCCTCAT CAGGCCTCAT CAGCTGCATC CAGGCCTCC	A GGCCACTIC S GTACTACAC C CAACCACTG A TGACACTG A CAGCACTG C CTGAGGCC C CTGAGCCTG G ATTGTTC G AAAGTGCCG C TGCCCCCTG C TGCACCAGA A CCAACAGC C TGCACCAGA C CAACAGCC C TGCACGAGTT C TGCATATATA	AGAGGCCCT TGGTCAGGGG AGTCATAAGC AGAAGATGCCA AGAGATACAACT AGGTCAGAT GGTACAGATAGT GGTACGATAGT AGATCCTGCAG AGGCGGGTG CCAGCGGTG ACTGAAGGT GGTATGAGGT GGTATGAGGT GCAGAGACTT GGTATGAGGT GCAGAGACTT	960 1020 1080 1140 1200 1260 1380 1440 1500 1620 1680 1740 1800 1860
65	CCAACTGCAC ACTGCACTTC GTTTCAGAGG ACACTGCAC ACAGATGGG GCAGGCTCAA ACAGGCACCT GCTTCCTTTT GCTCTGCCG CCCAAGGAAT GGCTCGCGG AGCACCCAG AGCACCCAG AGCACCCAG AGCACCCAG AGCACCAG ATGAAGCAA	E CTEGECAAG: AGCCETCTGG TEGAGATGCC TCATGGGTAI AGCACCAI TCATGGCTAI TCATGTCTAI TCATGTCTAI CCGGTGAGGG CCGGTGAGGG CTGCATCACCCAI CATACTGCCC TCATACTGCC TCATGCATGG CTGTATGGG ACTTCTCCG CTGGTGTTGA	GCCTACTACE AACTGCAGA CACACTGGC CACACTGGC CACACTGGC CACACTGGC CAGCAGAGACATAC GGAAAGTAT GGACATTGT GGACATTGT GGACATTGT CCCAGCTGC CCCAGCCTG CAATGTCAC CTGTCAAGA ACCCAGTT ACCCAGTT	A GATGGCACI A GAAGTTGTGC T GTGCAGGTGC A GCACAGGTI T TCTGGAACCI T TCTGGAACCI T TCTGGAACCI A GTCCCCTGC A GTCCCCTGC C CAGGGTATT T GAGGTGACT C CAGGGTGCT T CTGGACCTGCT C CAGGTGCT C CAGGTGCT C CAGGTGCT C CTTGCATCT G CCACATAGC	A GGCCACTGG G GTACTACAC C CAACCACTGA A TGACACTGG C CAGCAGGG A CAGCTGCAC C CTGAGCCTG C TGGGCCCCC G ATTGTGTTC G AAAGTGCCG C TGGCCCCCTG C TGCCCCCTG C TGCCCCCTG C TGCCCCCTG C TGCCCCTG C TGCACCAGA A CCAACAGCC G GCCAGTTC C TGATATATA A GCAGTCACT	AGAGGCCCT TGGTCAGGCG AGTCATAAGC AGAGGTCCCA AGGTCAGAT AGGTCAGAT GGTGATAGT GGTGATAGT GGTGATAGT GGTGATGT GTATCGTGAT AGGCGGCTG CCAGCGGCTG CGCAGAGTT GGCAGAGTT GGCAGAGTT GGCAGAGTT GGCAGAGCTT GGCAGAGCTT GGCAGAGCTT GGCAGAGCTT	960 1020 1140 1200 1260 1320 1380 1440 1500 1620 1680 1740 1800 1920
65	CCAACTGCAC ACTGCACTTC GTTTCAGAGG ACACTGCAC ACAGATGGG GCAGGCTCAA ACAGGCACCT GCTTCCTTTT GCTCTGCCG CCCAAGGAAT GGCTCGCGG AGCACCCAG AGCACCCAG AGCACCCAG AGCACCCAG AGCACCAG ATGAAGCAA	E CTEGECAAG: AGCCETCTGG TEGAGATGCC TCATGGGTAI AGCACCAI TCATGGCTAI TCATGTCTAI TCATGTCTAI CCGGTGAGGG CCGGTGAGGG CTGCATCACCCAI CATACTGCCC TCATACTGCC TCATGCATGG CTGTATGGG ACTTCTCCG CTGGTGTTGA	GCCTACTACE AACTGCAGA CACACTGGC CACACTGGC CACACTGGC CACACTGGC CAGCAGAGACATAC GGAAAGTAT GGACATTGT GGACATTGT GGACATTGT CCCAGCTGC CCCAGCCTG CAATGTCAC CTGTCAAGA ACCCAGTT ACCCAGTT	A GATGGCACI A GAAGTTGTGC T GTGCAGGTGC A GCACAGGTI T TCTGGAACCI T TCTGGAACCI T TCTGGAACCI A GTCCCCTGC A GTCCCCTGC C CAGGGTATT T GAGGTGACT C CAGGGTGCT T CTGGACCTGCT C CAGGTGCT C CAGGTGCT C CAGGTGCT C CTTGCATCT G CCACATAGC	A GGCCACTGG G GTACTACAC C CAACCACTGA A TGACACTGG C CAGCAGGG A CAGCTGCAC C CTGAGCCTG C TGGGCCCCC G ATTGTGTTC G AAAGTGCCG C TGGCCCCCTG C TGCCCCCTG C TGCCCCCTG C TGCCCCCTG C TGCCCCTG C TGCACCAGA A CCAACAGCC G GCCAGTTC C TGATATATA A GCAGTCACT	AGAGGCCCT TGGTCAGGGG AGTCATAAGC AGAAGATGCCA AGAGATACAACT AGGTCAGAT GGTACAGATAGT GGTACGATAGT AGATCCTGCAG AGGCGGGTG CCAGCGGTG ACTGAAGGT GGTATGAGGT GGTATGAGGT GCAGAGACTT GGTATGAGGT GCAGAGACTT	960 1020 1080 1140 1200 1260 1380 1440 1500 1620 1680 1740 1800 1860
65	CCAACTGCAC ACTGCACTGCACTGCACTGCACTGCACACACACACACACCTGCACACCTCACACACA	G CTGGCCAAG: G TGGCGAAG: G TGCAGGTAG G TGCAGGCAG A TCATGGCTAG T CAGGCTGG T CCGGCACCG C CCGGTGAGG G CTGCATCGC C TGATACTAC A CATACTGCC C TATACATGC C TGATACTAG G ACTTCTCCG T CTGCTTTCC T CTGCTTTT	GCCTACTACE AACTGCAGA CACACTGGC CACACTGGC CTGTGGTGCT GGAAAGTAT GGAAAGTAT GGAAATGAT GGAATTGAT GGACATTGAT GCCCAGCTG CCAGCCTG CAATGTGTC TGACATGAT ACCCAGTT GCCCAGTTGG TCCCATTGG	A GATGGCACI A GAAGTTGTGC T GTGCAGGTGC A GCACAGGTI T TCTGGAACCI T TCTGGAACCI T TCTGGAACCI A GTCCCCTGC A GTCCCCTGC C CAGGGTATT T GAGGTGACT C CAGGGTGCT T CTGGACCTGCT C CAGGTGCT C CAGGTGCT C CAGGTGCT C CTTGCATCT G CCACATAGC	A GGCCACTGG G GTACTACAC C CAACCACTGA A TGACACTGG C CAGCAGGG A CAGCTGCAC C CTGAGCCTG C TGGGCCCCC G ATTGTGTTC G AAAGTGCCG C TGGCCCCCTG C TGCCCCCTG C TGCCCCCTG C TGCCCCCTG C TGCCCCTG C TGCACCAGA A CCAACAGCC G GCCAGTTC C TGATATATA A GCAGTCACT	AGAGGCCCT TGGTCAGGCG AGTCATAAGC AGAGGTCCCA AGGTCAGAT AGGTCAGAT GGTGATAGT GGTGATAGT GGTGATAGT GGTGATGT GTATCGTGAT AGGCGGCTG CCAGCGGCTG CGCAGAGTT GGCAGAGTT GGCAGAGTT GGCAGAGTT GGCAGAGCTT GGCAGAGCTT GGCAGAGCTT GGCAGAGCTT	960 1020 1080 1140 1200 1320 1380 1440 1560 1620 1680 1740 1800 1800 1920
65	CCAACTGCAC ACTGCACCTGCACTGCACTGCACCTGCACCTCACCACCTGCACCACCTGGCACCACCGGCACCACCAGGCACCACCAGGCACCACCAGGCACCAC	G CTGGCCAAGG G TGCAGATGCC G TGCAGATGCC G TGCAGATGCC G TGCAGACCA A TCATGCTAL T TAAGGCTGG CCGGTCACCC CCGGTCACCC CCGGTCACCC CCGGTCACCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTTATCATGC CTTATCTCCT TCTGCTCTT : 164 DNA S	GCCTACTACE AACTGCAGA CAACTGCAGA CACACTGGC TGTGGTGCT CAGCTAGAGA GGAAAGTAT GGAAAGTAT GGAAAGTAT GGAATGCAT GGACATTGT GCCAGCCTG CCCAGCCTG CAATGTGT CAGCCAGCTG TCCATTGGT ACCCCAGTT TCCCATTGG	A GATGGCACA A GAAGTTGTGC T GTGCAGGTG G AGCACAGGT T TCTGGAACCA T TCTGGAACCA G TACCTATC T ACAGGTTATC C CAGGGTATT G CCAGGGTATT G CCAGGGTATT G CCAGGGTGC C CAGGGTGC C CAGCTGGTT A GCAGGGTGC C CAGCTGGTT A GCAGGGTGC C CAGCTGGTT T CTGGCTGAT A GCAGGCCTT C CCACATAGC T GAGAATAGC	A GGCCACTGG G GTACTACAC C CAACCACTGA A TGACACTGG C CAGCAGGG A CAGCTGCAC C CTGAGCCTG C TGGGCCCCC G ATTGTGTTC G AAAGTGCCG C TGGCCCCCTG C TGCCCCCTG C TGCCCCCTG C TGCCCCCTG C TGCCCCTG C TGCACCAGA A CCAACAGCC G GCCAGTTC C TGATATATA A GCAGTCACT	AGAGGCCCT TGGTCAGGCG AGTCATAAGC AGAGGTCCCA AGGTCAGAT AGGTCAGAT GGTGATAGT GGTGATAGT GGTGATAGT GGTGATGT GTATCGTGAT AGGCGGCTG CCAGCGGCTG CGCAGAGTT GGCAGAGTT GGCAGAGTT GGCAGAGTT GGCAGAGCTT GGCAGAGCTT GGCAGAGCTT GGCAGAGCTT	960 1020 1080 1140 1200 1320 1380 1440 1560 1620 1680 1740 1800 1800 1920
65	CCAACTGCAC ACTGCACTGC ACTGCACTGCAC ACAGCTGCAC ACAGCTCAA ACAGCCACCT GGTTCCTTT GCTGTGCGT CCCAAGGAAG TGCCAGGCAC GGCTCGGGG AGCACCCAG GGATCCTGGGGGAAGCCAGG TGCCAGGCAT ATGAAGCAAC CCCGCATC TGCTGCA Seq ID NO Nucleic A	G CTGGCCAAGG G TGCAGGTAGG G TGCAGGACCAG TCATGGCTAG G TGCAGGACCAG TCATGCCTAG T TAAGGCTGG T CCGTCACCC TCGGTGAGG G CCTGCATCAC C TTATCACCC C TGATCACCC TTATCACCC TATCACC TT	GCCTACTACE AACTGCAGA CAACTGGC CACACTGGC ACACTGGC CACACTGGC CACACTGGC CACACTGGC CACACTGGC CACACTGGC CACACTGGC CACACTGGC CACACTGGC CACACTGGC CACACTGGC CACACTGGC CACACTGGCCC CACACTGGCCCC CACACTGGCCCC CACACTGCCCCCCCC CACACTGCCCCCCCCCC	A GATGGCACA A GAAGTTGTGC T GTGCAGGTG G AGCACAGGT T TCTGGAACCA T TCTGGAACCA G TACCTATC T ACAGGTTATC C CAGGGTATT G CCAGGGTATT G CCAGGGTATT G CCAGGGTGC C CAGGGTGC C CAGCTGGTT A GCAGGGTGC C CAGCTGGTT A GCAGGGTGC C CAGCTGGTT T CTGGCTGAT A GCAGGCCTT C CCACATAGC T GAGAATAGC	A GGCCACTGG G GTACTACAC C CAACCACTGA A TGACACTGG C CAGCAGGG A CAGCTGCAC C CTGAGCCTG C TGGGCCCCC G ATTGTGTTC G AAAGTGCCG C TGGCCCCCTG C TGCCCCCTG C TGCCCCCTG C TGCCCCCTG C TGCCCCTG C TGCACCAGA A CCAACAGCC G GCCAGTTC C TGATATATA A GCAGTCACT	AGAGGCCCT TGGTCAGGCG AGTCATAAGC AGAGGTCCCA AGGTCAGAT AGGTCAGAT GGTGATAGT GGTGATAGT GGTGATAGT GGTGATGT GTATCGTGAT AGGCGGCTG CCAGCGGCTG CGCAGAGTT GGCAGAGTT GGCAGAGTT GGCAGAGTT GGCAGAGCTT GGCAGAGCTT GGCAGAGCTT GGCAGAGCTT	960 1020 1080 1140 1200 1320 1380 1440 1560 1620 1680 1740 1800 1800 1920
65	CCAACTGCAC ACTGCACTGC ACTGCACTGCAC ACAGCTGCAC ACAGCTCAA ACAGCCACCT GGTTCCTTT GCTGTGCGT CCCAAGGAAG TGCCAGGCAC GGCTCGGGG AGCACCCAG GGATCCTGGGGGAAGCCAGG TGCCAGGCAT ATGAAGCAAC CCCGCATC TGCTGCA Seq ID NO Nucleic A	G CTGGCCAAGG G TGCAGATGCC G TGCAGATGCC G TGCAGATGCC G TGCAGACCA A TCATGCTAL T TAAGGCTGG CCGGTCACCC CCGGTCACCC CCGGTCACCC CCGGTCACCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTGATACTGCC CTTATCATGC CTTATCTCCT TCTGCTCTT : 164 DNA S	GCCTACTACE AACTGCAGA CAACTGGC CACACTGGC ACACTGGC CACACTGGC CACACTGGC CACACTGGC CACACTGGC CACACTGGC CACACTGGC CACACTGGC CACACTGGC CACACTGGC CACACTGGC CACACTGGC CACACTGGCCC CACACTGGCCCC CACACTGGCCCC CACACTGCCCCCCCC CACACTGCCCCCCCCCC	A GATGGCACA A GAAGTTGTGC T GTGCAGGTG G AGCACAGGT T TCTGGAACCA T TCTGGAACCA G TACCTATC T ACAGGTTATC C CAGGGTATT G CCAGGGTATT G CCAGGGTATT G CCAGGGTGC C CAGGGTGC C CAGCTGGTT A GCAGGGTGC C CAGCTGGTT A GCAGGGTGC C CAGCTGGTT T CTGGCTGAT A GCAGGCCTT C CCACATAGC T GAGAATAGC	A GGCCACTGG G GTACTACAC C CAACCACTGA A TGACACTGG C CAGCAGGG A CAGCTGCAC C CTGAGCCTG C TGGGCCCCC G ATTGTGTTC G AAAGTGCCG C TGGCCCCCTG C TGCCCCCTG C TGCCCCCTG C TGCCCCCTG C TGCCCCTG C TGCACCAGA A CCAACAGCC G GCCAGTTC C TGATATATA A GCAGTCACT	AGAGGCCCT TGGTCAGGCG AGTCATAAGC AGAGGTCCCA AGGTCAGAT AGGTCAGAT GGTGATAGT GGTGATAGT GGTGATAGT GGTGATGT GTATCGTGAT AGGCGGCTG CCAGCGGCTG CGCAGAGTT GGCAGAGTT GGCAGAGTT GGCAGAGTT GGCAGAGCTT GGCAGAGCTT GGCAGAGCTT GGCAGAGCTT	960 1020 1080 1140 1200 1320 1380 1440 1560 1620 1680 1740 1800 1800 1920
65 70 75	CCAACTGCAC ACTGCACTGCACTGCACTGCACTGCACCTGCACCACCTGCACCACCTGCACCACCTGCACCACCACCACCACCACCACCACCACCACCACCACCAC	G CTGGCCAAGG G TGCAGATGCC G TGCAGATGCC G TGCAGACCAC G TGCAGACCAC G TGCAGCCCC C CCGGTGAGG G CCTGCACCC C CCGGTGAGG G CTTATCATGCC C TATACTGCC C TGATCTTCAC C TGGTGTTGA G ACTTCTCCG T TCTGCTCTT : 164 DNA S cid Accessi quence: 415 11	GCCTACTACE AACTGCAGA CAACTGGC AACTGCAGAA CAACTGGC CAACTGGC CAACTGGCC CAGATGTAC CAGATGT	A GATOGGCACI A GAAGTTGTGC T GTGCAGGTGC G AGCACAGGTI T TCTGGAACCI T TCTGGAACCI G CTACCTATO A GTCCCCCTGC C CAGGGTTGC C CAGGGTATT T GAGCTGACT T CTGGATCG T CAGGGTGC C CAGGGTGC C CAGGGTGC C CAGGGTGC C CAGGGTGC T CTTGCATCT G CCACATAGC T GAGAATAGC	A GGCCACTGG G GTACTACACC C CAACCACTGA A TGACACTGG C CTGAGCCGC C CTGAGCCGG G TGTGCTGCC G AATGTGTC G AAAGTGCCG C TGGCCCCC G AGCCCCCG G TGTCCTGCC C AGCCCCCTG C TGGACCACACA A CCAACAGCC G GGCAGGTTC C TGATATATA C GCAGTCACT C CCCTCCTCA	E AGAGGCCCT E TGGTCAGGCG A AGTCATAAGC A GAAGGTCCCA A GGTAACAACT A AGGTCCAGAT GGTAGTGGT GGTAGTGGT GGTAGTGGT GGTAGTGGT GGTAGTGGT GGTAGGAGGT GGCAGGGGTG GGCAGAGGT GGCAGGAGTT GGTGGAGAGT GGCAGGAGT GGCAGGAGT GGCAGGAGT GGCAGAGCT GGCAGGAGT GGCAGGAGT GGCAGGAGT GGCAGAGCT GGCAGGAGGT GGCAGGAGT GGCAGGAGGT GGCAGGAGT GGCAGGAGT GGCAGGAGT GGCAGGAGT GGCAGGAGT GGC	960 1020 1080 1140 1260 1320 1380 1440 1500 1620 1680 1740 1860 1920 1986
65	CCAACTGCAC ACTGCACTGCACTGCACTGCACTGCACTG	G CTGGCCAAGG G TGCAGATGCC G TGCAGATGCC G TGCAGATGCC G TGCAGACCAC G TGCAGACCAC A TCATGTCTAC T TAAGGCTAG C CCGTCACCCC C CCGGTGAGG G CCTGCATGG C CTGCATGG C TGATACTGCC C TGATACTGCC C TGATACTGCC C TGATACTGCC C TGATCATGC C TGATCTCCC C TGATCTCCC C TGATCTCCC C TCCCCTTT : 164 DNA S cid Accessi quence: 415 11 G TCAAGAGCT	GCCTACTACE AACTGCAGA CAACTGC AACTGCAGA CAACTGC	A GATOGGCACI A GAAGTTGTGC T GTGCAGGTG G AGCACAGGT G TCTGGAACCI G TACACTATC A GTCCACGTT G CACACTATC C CAGGGTGC C CAGGGTGC C CAGGGTGC C CAGGGTGC C CAGGGTGC C CAGGGTGC T CTGGATC G CACATAGC T GAGCTGAT A GCAGGCTT C CTGGATC C CAGGGTGC T GAGCTGAT A GCAGGCTGT C CTGCATC C CTGCATC T GAGCTGAT C CTGCATC T GAGCTGGT T GAGCTGGT T GAGCTGGT T GAGCTGGT T GAGCTGGT T GAGCTGGT T GAGCTGGT T GAGCATAGC T GAGAATAGC 1922.2 31	A GGCCACTGG G GTACTACACC C CAACCACTGG A TACACCTGG A CAGCTGCACC C TAGGCCTGC C TAGGCCTGC G TATTGTTC G AAACTGCCG C TAGCCCCCC G ATTGTGTTC G AAACTGCCG C TAGCCCCCTG C TAGCCCCCTG C TAGCCCCCTG C TAGCCCCTG C TAGCCCCCTG C TAGCCCCCTG C TAGCCCCCTG C C CCCCCCTG C C CCCCCCCCC A 41	E AGAGGCCCT E TGGTCAGGCG A AGTCATAAGC A GAAGGTECCA A GAGGTCAGAT A AGGTCAGAT T GCTGGATAGT C GTATCGATAT C GATCATGAT C GATCATGAT C CCAGCGGCT C CCAGCGGCT C CCAGCGGCT C GCTGATCGT G GCTGGTGGT C GCTGGTGGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTTA G GCTGGATGTT G GCTGGTTTA G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGT G GCTGGATGT G GCTGGATGT G GCTGGATGT G GCTGGATGT G GCTGGATGT G GCTGGATGT G GCTGGATGT G GCTGGATGT G GCTGGATGT G G GCTGATGT G G G G G G G G G G G G G G G G G G	960 1020 1080 1140 1260 1320 1380 1500 1500 1620 1680 1740 1800 1920 1986
65 70 75	CCAACTGCAC ACTGCACTGCACTGCACTGCACTGCACCACGCATGCAC ACAGCACGCCCCGGGTCCATGCACCAGCAAC GGCTCGGGTCGGG	G CTGGCCAAGG G TGCAGGACCA G TGCAGGACCA G TGCAGGACCA G TGCAGGACCA A TCATGTCTA T TAAGGCTGG C TGCTCACCC C CCGGTGAGG G TGCTACCCA C CTGATCACCC C TGGTGAGG G TGCTACCCA C ATACTGCC C TGATCATCC C TGGTGTTGA G ACTTCTCCG T TCTGCTCTT : 164 DNA S cid Accessi quence: 415 11	GCCTACTACE AACTGCAGA CAACTGCC AACTGCAGA CACACTGCC CACACTCC CACACTC	A GATGGCALI A GAAGTTGTGC T GTGCAGGTG G AGCACAGGT A TCTGGAACCI G TACCTATC A GTCCCCTG C CAGGGTATT T GAGCTGAT C CAGGGTATT T GAGCTGAT C CAGGGTAT T CTGGATGC C CAGCTGGT T GAGCTGAT T GAGCTGAT T GAGCTGAT T GAGCTGAT T GAGCTGAT T GAGCATAGC T GAGAGGGTT T GAGCATAGC T GAGAATAGC 1922.2 31 i G GAGAGGGGT T CAATTAGAC T CAATTAGAC T CAATTAGAC T CAATTAGAC T CAATTAGAC T CAATTAGAC T CAATTAGAC T GAGAGGGGTT T CAATTAGAC T CAATTAGAC T GAGAGGGGTT T CAATTAGAC T CAATTAGAC T CAATTAGAC T CAATTAGAC T CAATTAGAC T CAATTAGAC T CAATTAGAC T CAATTAGAC T CAATTAGAC T CAATTAGAC T CAATTAGAC T CAATTAGAC T CAATTAGAC T CAATTAGAC T CAATTAGAC T CAATTAGAC T CAATTAGAC T CAATTAGAC T CAATTAGAC T C T C T C T C T C T C T C T C T C T	A GGCCACTGG S GTACTACACC C CAACCACTGA A TACACCTGA A CACCAGGGC C CTGAGCCCGC G ATTGTTC G AAAGTGCCG C TGGACCAGA C TGCACCAGA C TGACCAGA C TGACCAGA C TGACCAGA C TGCACCAGA A CCAACAGCC C TGCACCAGA C CCACCAGA C CCACCAGA C CAACAGCC C TGCACCAGA A CCAACAGCC C TGATATATA C CCCTCCTCA 41 IT I AGAAATACC A AAGCCTGAC A AAGCCTGAC A AAGCCTGAC A AAGCCTGAC A AAGCCTGAC C CAACACTCAC A AAGCCTGAC A AAGCCTGAC A AAGCCTGAC C AAGCCTGAC A AACCCTGAC A AACCCTGAC A AACCCTGAC A AACCCTGAC A AACCCTGAC A A	E AGAGGCCCT T TGGTCAGGCG A GATCATAAGC A GAAGGTGCCA A GAGGTCCAGAT T GCTGGATGT T GCTGGATGT T GTATCGATAT A GATCCTGCAG C CAGCGGCTG C CAGCGGCTG C CAGCGGCTG T ACTGAAGGT T GCTGATCGT G GTGATCGT G GTGATCGT G GCTGATCGT G GCTGATCGT G GTGCAGTGGT C GCTGATCGT G GTGCGCT G GTGCGTCAG T TGGCAGCGG 51 L A GCATAATAAG T TAACGGGGGA T TAACGGGGGA	960 1020 1080 1140 1260 1320 1380 1440 1500 1620 1680 1740 1860 1920 1986
65 70 75	CCAACTGCAC ACTGCACTGCACTGCACTGCACTGCACTG	G CTGGCCAAGG G TGCAGATGCC G TGCAGATGCC G TGCAGATGCC G TGCAGACCAC G TGCAGCCCC T CCGGTCACCC T CCGGTCACCC T CCGGTCACCC T CCGGTCACCC T CCGGTCACCC T CCGGTCACCC T CTGCTCATCG C TGCTACTCCC TTATCTGCC TTATCTGCC T TCTGCTCTT : 164 DNA S cid Accessi quence: 415 11 G TCAAGAGCT T GGGTCTCT G GAGGCCTCT G GAGGCCTCT G AGGCCTCT G AGGCCTCT G AAGCGCTAC A GTTCTTTTCA	GCCTACTACE AACTGCAGA CAACTGC AACTGCAGA CACACTGC TGTGGTGCT CAGAGAGACA GGGAAGTAT GGAGAGACA GGGATGCAT GGACATTGT GCCCAGCCTG CCCAGCCTG CCCAGCCTG CCCAGCCTG CCCAGCCTG CCCAGCCTG CAATGTCT CTGGTCAAGA CGCCCAGTT CACCCAGTT CACCCAGTT CACCCAGTT CCCCATTGG CCCAGCGG CTAATTACC CTGTCATTAAC CCCATTAAC CCCACTTAAC CCCCACTTAAC CCCACTTAAC CCCACTTAAC CCCACTTAAC CCCACTTAAC CCCACTTAAC CC	A GATGGGCAE A GAAGTTGTGC T GTGCAGGTG G AGCACAGGT G TCTGGAACCL G CTACCTATC A GTCCACGTTC C CAGGGTGC C CAGGGTGC C CAGGGTGC C CAGGGTGC C CAGGGTGC C CAGGGTGC T CTGGATC G CACATAGC T GAGCTAGAC T GAGCTGAT A GCAGGGTGT C CTGGATC T GAGCTGAT A GCAGGGTGT T CTGGATC T GAGCTGGT T TTGGATC T GAGATAGC T GAGAATAGC 1922.2 31 6 6 6 6 6 6 6 6 6 6 6 7 7 7 7 7 7 7 7	A GGCCACTGG G GTACTACACC C CAACCACTGG A TACACCTGG A CAGCACTGG C CTGAGCCCGC G ATTGTGTTC G AAACTGCCG C TGGCCCCCC G ATTGTGTTC G AAACTGCCG C TGCACCAGG C TGCACCAGG C TGCACCAGG C TGCACCAGG C TGCACCAGG C TGCACCAGG C CACCCCTC C CCCCCTCA 41 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	E AGAGGCCCT E TGGTCAGGCG A AGTCATAAGC A GAAGGTECCA A GAGGTCAGAT A AGGTCAGAT T GCTGGATAGT C GTATCGATAT C GATCATGAT C GATCATGAT C CCAGCGGCT C CCAGCGGCT C CCAGCGGCT C GCTGATCGT G GCTGGTGGT C GCTGGTGGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTGT G GCTGGTTTA G GCTGGATGTT G GCTGGTTTA G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGTT G GCTGGATGT G GCTGGATGT G GCTGGATGT G GCTGGATGT G GCTGGATGT G GCTGGATGT G GCTGGATGT G GCTGGATGT G GCTGGATGT G GCTGGATGT G G GCTGATGT G G G G G G G G G G G G G G G G G G	960 1020 1080 1140 1200 1320 1320 1500 1620 1680 1740 1800 1980 1986

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	AAGAAAATA AAAAAT.					360 420
	ACGACAGAGA CAAGGA CCCCTTTGGT GGGGGT	AAGT AAGAGAGAGA	TTCCCCCCC	ABBTOTTOT I	GCATGAGC	480
	GGTCAGTTCC CCCGAG	TOTAL CATGARGETS	GACAGCCTAG	TGAACAAGGA (TGCTGCCCA	540
5	CGCCTGGGTG CAGAGT	CGGC CAATGTCTGT	GGCTCTCAGC	AAGGCCGGGG (CAGTGCACA	600
_	GAGGTGCGAG CCGACA	CAAG GCCCTGGAGT	GGTCCCTACA	TCCTACGAAA (CAGGATGAC	660
	CGTGAGCTGT GGCCAA	GAAA ATTCTTCCAC	CGGACCTGCA	AGTGCACAGG /	LAACTTTGCC	720
	GGCTATAATT GTGGAG	ACTG CAAGTTTGGC	TGGACCGGTC	CCAACTGCGA (GCGGAAGAAA	780
10	CCACCAGTGA TTCGGC	AGAA CATCCATTCC	TTGAGTCCTC	AGGAAAGAGA (CAGTTCTTG	840
10	GGCGCCTTAG ATCTCG	CGAA GAAGAGAGTA	CACCCCGACT	ACGTGATCAC (CACACAACAC	900
	TEGETEGGCC TECTTE	GGCC CAATGGAACC	CAGCCGCAGT	TIGCCAACIG (CAGIGITIAT	960
	GATTTTTTG TGTGGC	TCCA TIAITATICI	CCACCTCCAT	TTCTTACCTC	CACCACCAC	1020 1080
	CATTTGTTGT GTCTGG					1140
15	CCCTACTGGA ACTITO	CCAC TGGGAGGAAC	GAGTGTGATG	TGTGTACAGA	CCAGCTGTTT	1200
1.5	GGGGCAGCGA GACCAG	ACGA TCCGACTCTG	ATTAGTCGGA	ACTCAAGATT	CTCCAGCTGG	1260
	GARACTGTCT GTGATA	GCTT GGATGACTAC	AACCACCTGG	TCACCTTGTG	CAATGGAACC	1320
	TATGAAGGTT TGCTGA	GAAG AAATCAAATG	GGAAGAAACA	GCATGAAATT	GCCAACCTTA	1380
20	AAAGACATAC GAGATT					1440
20	TCTACCTTCA GTTTC	IGGAA TGCTTTGGAA	GGGTTTGATA	AAGCAGATGG	GACTCTGGAT	1500
	TCTCAAGTGA TGAGCC	TTCA TAATITGGTT	CATTCCTTCC	TGAACGGGAC	AAACGCTTTG	1560
	CCACATTCAG CCGCC	LATGA TCCCATTTT	GIGGITCITC	ATTCCTTTAC	CONCERCO	1620 1680
	TTTGATGAGT GGATG/ CCTATTGGTC ACAATO	CARAG ATTTARTCCT	CTTCCTTTCT	TOTAL	CACTANTONA	1740
25	GAACTCTTTT TAACCT	COAL CIACANCAL	TACACCTATG	CATCGATCT	GCCAGTTTCA	1800
23	GTTGAAGAAA CTCCAC	CONCRETE GOOGLESTOO	CTCTTAGTAG	TCATGGGAAC	ACTGGTGGCT	1860
	TIGGITGGIC TITII	TGCT GTTGGCTTT	CTTCAATATA	GAAGACTTCG	AAAAGGATAT	1920
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	CATGCCTTAC CTAAG	AGAAG AGGCTGGCC	AGCCACAGTT	CTGACGCTGA	CAATAAAGGA	2040
30	ACTANTOCTO ACTGT	ICCTT CTTGAGTTG	AGATETTTGA	CATAGGTTCT	TCTATAGTGA	2100
	TGATGATCTC ATTCA	GAAGA TGCTTAGCT	TAGTTTCCGC	TTTGCTTGCT	TGTTTAACAA	2160
	ACCCAACTAA AGTGC					2220
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55	Seg ID NO: 165 D	Na Camience				
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45	CGCGGTCGTC CTTGG					240 300
43	CTGTGACGCT GCCTT CCAACACGGG GATCC					360
	TGATCTCTCC CCATG	CONT COTOCTO	C TEGEGRATECT	TORGETTEGGG	GOGGAOGGCA	420
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50	ACGCCGTGTT TGTTA	AGAAT GCCTCTGAA	A TTGAAGTGCC	TTTTGTTACA	AGGAACAAAG	600
	ATGTGTTCCA GTGTG	AGGTC CGGAATGTG	A ACTITICAGGA	TCCAGCCTCT	GCCTGTGATT	660
	CCATCAATGC ATGGC	TTAAA AATGAAACC	A GGGATATGAT	TGACAATCTG	CTGTCCCCAG	720
	ATCTTATTGA TGGTG	TGCTC ACCAGACTO	G TCCTCGTCAA	CGCAGTGTAT	TTCAAGGGTC	780
55	TGTGGAAATC ACGGT	TCCAA CCCGAGAAC	A CAAAGAAACG	CACTITUGIG	GCAGCCGACG	840 900
33	GGAAATCCTA TCAAC GTGCCCCCAA TGATT					960
	GCATGCTGAT TGCAG					1020
	TCAGCACCAA GACCA					1080
	TCCTGCCCAA GTTC	CAGCT GTAGCACAA	A CAGATTTGA	GGAGCCGCTG	AAAGTTCTTG	1140
60	GCATTACTGA CATG	TTTGAT TCATCAAAG	G CAAATTTTGG	CAAAAATAACA	AGGTCAGAAA	1200
	ACCTCCATGT TTCTC	CATATO TTGCAAAAA	G CAAAAATTG/	A AGTCAGTGAA	GATGGAACCA	1260
	AAGCTTCAGC AGCA	ACAACT GCAATTCTC	A TTGCAAGAT	ATCCCCTCCC	TGGTTTATAG	1320
	TAGACAGACC TTTT	TGTTT TTCATCCG/	C ATAATCCTAC	AGGTGCTGTG	TTATTCATGG	1380
65	GGCAGATAAA CAAA	CCTGA AGAGTATAC	A AAAGAAACC	A TGCAAAGCAA	CGACTACTT	1440
U.J	GCTACGAAGA AAGA CGCTTCTTTT TCAA	ACTION TOUTGOATO	. TTCATAGTTO	L IGIIAAATAT	TITIGIACAT	1500 1560
	AGGTATTGGA GGGA	NACIAG IICIIAGG	O CAGACICGA	C TOTACTGACO	DATGAATAGA	1620
	AAGGCTTCCA GATG					1680
	CCTGTTGAGT ATTT	GCTGTT TGTCCAGT	C AGGAATTTT	T GTTTTGTTT	GTCTATATGT	1740
70	GCGGCTTTTC AGAA					1800
	TTACTTTTTA TGAA	AAAAAA ATTATTTG	CC TTTTAAATT	C TTTTCCCCC	TCCCCCTCCA	1860
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75	TAAAAAACTC CTGT	CTTGCT AGACAAGG	TT GCTGTTGTG	C AGTGTGCCTC	TCACTACTGG	2040
75	TCTGTACTCC TTGG	ATTIGC ATTITIGT.	AT TTTGTACAA	a gtaaaaataj	ACTUITATGA	2100
	GTAGT					2105
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	TGCTCCCTGG	AGCAGCCAGG	CCAGGGGGGG	AGCACCAGCG	CCTTCGAGCA	GCTGCAGAGG	240
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_	AACGCCCCTC	TCCGGAGATG	TCGAACTCTC	TCAGGTTCAC	CCAGACCAAA	GAATTTTAAG	360
5	AAGATTCATT	TTATCAAGAA	CATGCGGCAA	CACGATACCA	GGAATGGCAG	AATAGTCCTT	420
	ATCAGTGGCA	GAAGATCCTT	CTGTAGTATA	TITTCAGTGC	TGCCGTATCG	CGACAGTACC	480
	CAAGTCGGGG	ACTTGAAGTT	GGACGGAGGA	AGACAATCAA	CTGGTGCAGT	GAGTTTGAAA	540
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	CAATTTCTGT	TACCCACAAA	TGCCTTTGGA	GCCCGGAGAA	ATACCATAGA	CTCCACCTCC	660
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	ACCCAGGGGA	GCCTCGACAC	AGGTAGTGAC	CTGGGAGACT	TTATGGACTA	TGACCCAAAT	780
	CTCTTGGATG	ACCCCCAGTG	GCCTTGTGGC	AAACACAAAC	GCGTTCTGAT	CTTCCCTTCC	B40
	TACATGACAA	CAGTGATTGA	CTACGTGAAG	CCCTCGGATC	TCAAGAAGGA	CATGAACGAG	900
	ACCTTCAAGG	AGAAGTTTCC	TCACATTAAG	CTGACACTCA	GCAAAATTAG	GAGTCTGAAA	960
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			GCTCGCCCTC				1080
			GCTGTTAGCA				1140
			CAAACTGGAA				1200
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~0			GCTTGGTGGA				1380
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			TCTTGGGTGT				1500
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			GAAGTTGGGG				1740
			TTTTGTATCA				1800
			GTGTCTGAGA				1860
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			ACTGACATTG				2040
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			TCTGCCACCC				2160
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		163 DNN E					2587
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45 50	Seq ID NO: Nucleic Ac Coding sec 1 GGCACGAGGG CTCTCTCCAC	id Accessic quence: 188. 11 TCCGGCCTCT	n #: BC0088 .2695 21 GGACTAGGAA GAGGGGCTCT	31 CCGACAGCCC	C CCCTCCCCGC G GATAGTTCCC	GTCCCTCCCT GAGGGTCATC	60 120
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50	Seq ID No: Nucleic Ac Coding sec I GCCACGAGG CTCTCTCCAC CCCCAGGAT CAACCAGCT GATCGTGGA GTCCTCCAGGG TGGTGCCAT GGATACAA GGATACAA GGATACAA CGATCAGT AGTAAATT AAGCAGAGA CCAATCAGA	id Accessic puence: 188. 11	IN B: BC0088 .2695 21 GGACTAGGAR G GAGGGCTCT G TTTCGCCTT G CCGGGCTGT T TTCCCCTGG T TTATCAACGC A AGATCCTGT A AGCCCAAGGT C CGGCATGT C CGGCATGT C CGGCATGT C CGGCATGT C CGGCATGT C CGGCATGT C CGGCATGT C CGGCATGT C CGGCATGT C CGCATGT C CGCATGT C CGCATGAT C CAGCATCGG C ACAGCATCGG C ACAGCATCGG C ACAGCATCGG C ACAGCATCGG C ACAGCATCGG C ACAGCATCGG C ATATTGACTT F TCACAGCAGG	31	I COCCTOCCCOS G GATAGTTCCC A TAATTTCCGA G ATGCGCCCGS G CCCAACCACA C ATCTCCGGCC G GAGACTGGT T TCCATCAGCC G GAGAGGAACG G AGGAGGGAACG G AGGAACG G AGGAGGGAACG G AGGAGGAACG G AGGAGGAACG G AGGAGGAACG G AGGAGGAACG G AGGAGGAACG G AGGAGGAACC G AGGAGGAACG G AGGAGGAACG G AGGAGGAACG G AGGAGGAACG G AGGAGGAACC G AGGAGGAACG G AGGAGGAACG G AGGAGGAACG G AGGAGGAACG G AGGAGGAACG G AGGAGGAACG G AGGAGGAACG G AGGAGGAACG G AGGAGGAACG G AGGAGGAACG G AGGAGGAACG G AGGAGGAACG G AGGAGGAACG G AGGAGGAACG G AGGAACG G AGGAGGAACG G AGGAACG G AGGAGGAACG G AGGAGGAACG G AGGAGGAACG G AGGAGGAACG G AGGAACG G AGGAGGAACG G AGGA	GETCCTCCT GAGGGTCATC GGCAAGCTGC GCCCGGGGCA AGGGCCACAA AGGTGCGCT CCATAGGTCC AGAAAATTGA AATTACTCAA AGGATCTGAG GCATCTGAG AGCAGAGGA CCTCAGCACC AGAGGAAACA CGTGCTTTTGA	60 120 180 240 300 360 420 480 540 660 720 780 840 900
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50 55 60 65	Seq ID No: Nucleic Ac Coding Sec I GCACCAGGG CTCTCTCCAC CCCCAGGAT CAACCAGCT GATCGTGGAC GGATACAAC GGATACAAC GGATACAAC GGATACAAC GGATACAAC GGATACAAC GGACCCT AGCCAGAGG GGCATCA GGCACAAC GGCATGT AGCACAAG CCGACCTT ACCCACAGC CATGAACCC CATGACCC CATGACCC CATGACCC CCTACACAG	puence: 188. 11	IN B: BC0088 .2695 21 GGACTAGGAA G GAGGGCTCT G GTTTGGCCTT T TCCCCCTGGT T TCCCCCTGGT T TCCCCTGGT T TCCCCTGGT T TCCCCTGGT T TCCCCTGGT T TCCCCTGGT T TCCCCAGGGAGGGGG A AGCCCAAGGT T AACCCTAGCC G AAAGCCAGGAGGG T ATATTGACT T TCACAGCAG A TTTATACTAG T GGTTTAGCAG T CCAACCAT C CAGCCGTTC C AGCTGTCGG T CCAACCAT C CAGCCGTTC C AGCTGTCGG T ATACAGAC T CCAACCCAG T ATACAGACC T ATACAGCAC T ATACAGCAC T ATACAGCAC T GTGTGCAGA	31	C CCCTCCCCCC G GATAGTTCCC G GATAGTTCCC G CCCAACCACA C ATATTCCGGC G CCCAACCACA G ATCCGGCC G GAGACTGGCT G ACCTGGCC G GAGACTGGCT T CAACTAGC G GAGAGGAAC T TTACACTAA G GAACTGGAG G GAATGGAGG G GAATGGAGG G GAATGGAGG G GAATGGAGG G GAGTGAGC G GACCAGAGC C CCCCAGAC A AGATGGAGG G GCCCAGAGC C CAGCCCAGAC C CAGCCCAGAC T CCGTCCGGGGG T CCATCTGCT C CGCTGGGGGGGT T CCATCTGCT T CGGAAAAAGT T TCAATTCGT	GTCCTTCCT GAGGGTCATC GAGGGTCATC GCCAAGCTCC GCCAGGGCA AGGGCCGCGT CCCATACGTCC AGAAAATTCA AATTACTCAA GCATCCTGAG CCTCAGCACC AGAAGCTCAC AGAGCTCAC AGGAACTCAC CCACAGCACT CTATTCCACA CAGCACTCC CCACACC CCACAGCACTGC CCACTGCACC CCATACGCACC CATAACACTGT CTCCAACCC CATAACTCTGC CATAACTCTGC CTTCGTGGAT	60 120 180 240 300 420 480 540 600 660 720 780 900 960 1020 1080 1140 1260 1380 1380
50 55 60 65	Seq ID No: Nucleic Ac Coding sec I GGCACGAGGG CTCTCTCCAC CGCCCCAGAGT GAACTAGCCC CAACCAGCT GATGAGCCC GATGAGCG TGGTGCCAT AGGACTACACAG GGAGATACAA AGGAGAAT AAGTAATT AAGGAGAAA CCAATCAGA GGAGACCG GGCAATCA AGCAGCAG GGCCAATCA CCACCAGGC GCCAATCA ACCCACAG GCCAATCA ACCCACAG CCACCAGAGC CCACCAGAGC CCACCAGAGC CCACCAGAGC CCACCAGAGC CCACCAGAGC CAGGCCAGC CATGAACCC CCTACACAG GCCCATACCC CCTACACAG GCCCAATCA	id Accessic puence: 188. 11	IN B: BC0088 .2695 21	31 CCGACAGCCC CACCTGGATA CACCTGTGATA A CACCTGTGTGATA CACCTGTGTGATA CACCTGTGTGTGCC CACCTGTGTGCC CACCTGTGTGTGCC CCTGTGTGTGCC CACCTGTGCC CACCTGTGTGTCC CACCTGTGTGCC CACCTGTGTC CACCTGTGTCC CACCTGTGTCC CACCTGTGTCC CACCTGTGTCC CACCTGTGTCC CACCTGTGTCC CACCTGTGTCC CACCTGTGTCC CACCTGTGTCC CACCTGTGTCC CACCTGTGTCC CACCTGTGTCC CACCTGTGTCC CACCTGTGTCC CACCTGTGTCC CACCTGTTCC CACCTGTGTCC CACCTGTGTCC CACCTGTGTCC CACCTGTGTCC CACCTGTGTCC CACCTGTGTCC CACCTGTTCC CACCTGTTCC CACCTGTTCC CACCTGTTCC CACCTGTTCC CACCTGTTCC CACCTGTTCC CAC	C CCCTCCCCCC G GATAGTTCCCA A TAATTTCCAA A TAATTTCCAA C CCCTCGGCC G CCCAACCAAC C CCCTCGGCC G GAGACTGGCT G GAGATGGCT T TCATCAGCC G GAGAACGAAC T TCATCAGCC G GAGCAGGAAC T TTACCACTAI G GACCAGAGGAAC T TTACCACTAI G GACCAGAGGAAC C GCCCAGAGGAAC C CCGCCCAFA C CGCTTACTGC C CAGCCCAFA C CGCTTACTGC T CCGTCGGGG T TCAATTCCTT T GGAAAAAGT T GGAAAAAGT G GAGAAAAAGT T GAAAAAAGT G GAGAAAAAGT C GAGAGAAAAGT C GAGAGAAAAGT C GAGAGAAAAGT C GAGAGAAAAGT C GAGAGAAAAGT C GAGAGAGACT C GAGAGAAAAGT C GAGAGAGACT C GAGAGAAAAGT C GAGAGAGACT C GAGAAAAAGT C GAGAGAGACT C GAGAGAGACT C GAGAGAGACT C GAGAGAGACT C GAGAAAAAGT C GAGAGAGACT C GAGAGAGACT C GAGAGAGACT C GAGAGAGACT C GAGAGAGACT C GAGAGAGACT C GAGAGAGACT C GAGAGAGACT C GAGAGAGACT C GAGAGAGACT C GAGAGAGCT C C C C C C C C C C C C C C C C C C C	GTCCCTCCT GAGGGTCATC GAGGGTCATC GCCAAGCTGC GCCAGGGCA AGGGCCGCGT CCCATACGTCC AGAAAATTGA AATTACTCAA GCATCCTGAG AGGCAGAGGA AGGCAGAGGA AGGCAGCAC AGAGGAAACA GTCCTTTTGA GCATCCTCAC AGCAGCTCAC AGCAGCTCAC CAAGCACTCCC CAAGCACTCCCAC CCATCCCCAC CCCCCCCCCC	60 120 180 240 300 360 420 540 650 720 780 840 900 1020 1080 1140 1200 1330 1430 1500
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50 55 60 65 70	Seq ID No: Nucleic Ac Coding sec I GGCACGAGGG CTCTCTCCAC CCCCAGGATT GAACTACCAC CACCAGGATG GTCCAGCATT AGTATACCAC GGATGAGGG GGCATAGAGG GGAATACAA CCAATCAGG GGAATACAA CCAATCAGG GGAATCAGG GGCAATAGA GGGCAATCA GGAGCCTT ACCTGTCT ACCTGAGG CAGGCATG CAGGCATG CAGGCATG CAGGCATG CAGGCATG CAGGCATG CAGGCATG CAGGCATG CAGGCATG CAGGCATG CAGGCATG CAGGCATG CAGGCATG CAGCAATCA CAGGCATG CAGCAATCA CAGGCATG CAGCAATCA CAGGCATG CAGCAATCA CCCTTGCCCC CAACACAG CTCTGGCCC CCCTGGCCT CCCGGCTC CCCTGGCCT CCCGGCTC CCGCTGGCTC CCGCTGGCTC CCGCTGGCTC CCCTGGCCTC CCCTGGCCTC CCGCTGCTC CCGCTGGCTC CCCTGGCTC CCCTGGCTC CCCTGCTC CCCTGGCTC CCTGCTC CCCTGGCTC CCCTCCCT	id Accessic puence: 188. 11	IN B: BC0088 .2695 21	31 CCGACAGCTCC CACCTGGATA CCACCGGATA CACCTGGATA CACCTCAA CACCTGGATA CACCTCAA CA	C CCCTCCCCCC G GATAGTTCCCA A TAATTTCCAA A TAATTTCCAA G ATGGGCCGG G CCCAACCAAC G CACCACCAC G GAGACTGGCC G GAGACTGGCC T TCCATCAGC T TCCATCAGC T TCCATCAGC T TCCATCAGC G GAGAAGGAAC T TTACCACTA G GACCAGAGGAAC T TTACCACTA G GCCCAGAGGAA A CCGCTTCCT C CAGCCCAC T CCGTCGGGG IT TCAATTCCT T CCGTCGGGG IT TCAATTCCT T CAATTCCT T CAA	GTCCCTCCT GAGGGTCATC GAGGGTCATC GCGAAGCTGC GCCACACACACACACACACACACACACACACACACAC	60 120 180 240 300 360 420 540 660 720 780 840 900 1020 1080 1140 1320 1380 1440 1560 1660
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50 55 60 65 70	Seq ID No: Nucleic Ac Coding sec I GGCACGAGG GCCCCCACGATT GATTGTCACG CCCCAGGATT GATTGTGGAG GTCCCACGG GTGGTGCCATT AAGCGAGATACACC CCAACAAT GAATACACC GCCAGAAT GAGCACGAAT GAGCACGAAT CAATCACC GCCACATT ACCTACACG GCCAAACA GCCACATT ACCTACACG CCTCAATCC CTCAAATCC CTCAAATCC CTCAAATCC CCTCAATCC CCCACAATCA CACCTTCC CCACAATCA CACCTTCC CCCACAATCA CCCCTCAATCC CCCACAATCA CCCCCCCC	puence: 188. 11	IN B: BC0088 .2695 21 GGACTAGGAA G GAGGGCTCT G GTTTGCCCTT TTTTACAACGG C AGGATTACACAC C AGGATTCC A AGATCCTGT A AGCCCAAGGT T TCCGCTTGG C CGGGCATGT T TCACACGG C AGGATCCC A AGATCCTGT C AGCGTTGC C AGGATCCT C CAGCCATGT T TCAACCGTGC C TCAACCGTGC T TAACACAC T TCAACCATC C CAGCACCTTC C CAGCACCTTC C CAGCACCGTTC C CAACCCGGA A AGGACCGGA A AGGACCGGA A AGGACCGGA A AGGACCGGA C GTGTGCAGA C GTGTGCAGA C GTGTGCAGA C GTGTGCAGA C GTGTGCAGA C GTGTGCAGA C GTGTGCAGA C GTGTGCAGA C GTGTGCAGA C GTGTGCAGA C GTGTGCAGA C GTGTGCAGA C TCAACCTTAA C GTGTGCAGA C G GTGTGCAGA C G G G G G G G G G G G G G G G G G G G	31 CGGACAGCOC CACCTGGAT GCCAGGATGCAC GAGGACGCTCC GAGGACGCCT GAGGACGCAC GAGGACGCAC GAGGACGCAC GAGGACGCAC GAGGACGCAC GAGGACGCAC ACAGCGGGAC ACAGCGGGAC ACAGCACCAC GAGAGAACAC CACTGGAA ACAGCTGGA ACAGCTGGA ACAGCTGGA ACAGCTGGA ACAGCTGGA ACAGCTGGA ACAGCTGGA ACAGCTGGA ACAGCTGGA ACAGCTGGA ACAGCTGGA CACTTTGTGGC CTGATCCCAG ACAGCAGCTC CTGACCAC CTGATCCCAC CCGAAAACAC CCGCAAACAC CCGCAAACAC CCCGAAACAC CCCGAAACAC CCCGAAAACAC CCCGAAAACAC CCCGAAAACAC CCCGAAAACAC CCCGAAAACAC CCCGAAAACAC CCCGAAAACAC CCCAAAACAC CCCAAAACAC CCGAAAACAC CCGAAAACAC CCCAAAACAC CCCAAAACAC CCCAAAACAC CTGTTTCGAC CCAAAAACAC CCCAAAACAC CTGTTTCGAC CCAAAAACAC CTGTTTCGAC CTGTTTCGAC CTGTTTCGAC CTGTTTTCGAC CTGTTTTTCGAC CTGTTTTTCGAC CTGTTTTCGAC CTGTTTCGAC CTGTTTCGAC CTGTTTCGAC CTGTTTTCGAC CTGTTTCCTAC CTGTTTTCGAC CTGTTTTCGAC CTGTTTTCGAC CTGTTTTCGAC CTGTTTTCGAC CTGTTTTCGAC CTGTTTTCGAC CTGTTTTCTTCTTCTTCTTCTCTCT CTGTTTTTCTCTTCTCT CTGTTTTTCTCT CTGTTTTTCT CTGTTTTTCT CTGTTTTTCT CTGTTTTTTCT CTGTTTTTTCT CTGTTTTTTTT	G CCCTCCCCCC G GATAGTTCCC G GATAGTTCCC G GATAGTTCCC G GAGACTGGC G CCCAACCACA T TCCATCGGC G GAGACTGGC T CCCTCGGC G GAGACTGGC T TCCATCAGC G GAGACTGGC T TCCATCAGC G GAGACTGGC T TACCACTA T TCCATCAGC G GAGCGGAAC G GACCGAGAGC A AGATCGAG C CAGCCCAA C CAGCCCAC T CCCTCCTC T CCCTCGCGC T CCCTCCGC T CCATCGCC T CAGCAGAGAC T TCAATTCGC T CAGCAGAGAC T TCAATTCGC T AGAAGAAA T TCCCCAAAG T TCCCCCAAAG T TCCCCCAAAG T GCACCCAAA T GCCCCAAAG T GCACCCCAA T GCCCCAAAG T GCCCCAAAG T GCACCCCAA T GCCCCAAAG T GCACCCCAA T GCCCCAAAG T GCACCCCAA T GCCCCAAAG T GCACCCCAA T GCCCCAAAG T GCACCCCAA T GCCCCAAAG T GCACCCCAA T GCCCCAAAG T GCACCCCCA T G GAAAAATCTT C CAGCCCTC T CAGTCCCTC T CAGCCCTC T CCCCCAAAG T G GAAAAATCT T CCCCCAAAG T GCCCCCAAAG T G GAAAAATCT T CCCCCAAAG T G GAAAAATCT T CCCCCCAAAG T G GAAAAATCT T CCCCCCAAG T G GAAAAATCT T CCCCCCAA T G GAAAATCT T CCCCCCAA T G GAAAATCT T CCCCCCAA T G GAAAATCT T CCCCCCAA T G G GAAAATCT T CCCCCCAA T G G GAAAATCT T CCCCCCAA T G G GAAAATCT T CCCCCCAA T G G GAAAATCT T CCCCCCAA T G G GAAAATCT T CCCCCCAA T C CCCCCAAAG T G G GAAAATCT T CCCCCCAA T C CCCCCAAAG T C CCCCCAAAG T C CCCCCAAAG T C CCCCCAAAG T C CCCCCAAAG T C CCCCCAAAG T C CCCCCAAAG T C CCCCCAAAG T C CCCCCAAAG T C CCCCCAAAG T C CCCCCAAAG T C CCCCCAAAG T C CCCCCAAAG T C CCCCCAAAC T C CCCCCAAAC T C CCCCCAAAC T C CCCCCAAAC T C CCCCCAAAC T C CCCCCAAAC T C CCCCCAAAC T C CCCCCAAAC T C CCCCCAAAC T C CCCCCAAAC T C CCCCCAAAC T C C C C C C C C C C C C C C C C C C	GTCCCTCCT GAGGGTCATC GAGGGTCATC GCGAAGCTCC GCCAGGGCA AGGGCCGCGT TCCGCCACAA AATTACTCAA CGCATCCTGAG AGCAGGAAGCA AGCAGGAAGCA AGCAGGAAGCA AGCAAGCTCAC AGAAGCTCAC AGAGCATCAC CCTCCAACCC CATACTCCACA CCTCCAACCC CTTGGTGGAT CCATCCACACC CTTGGTGGAT CCATCCACACC CATACTCCACACC TACTCCACACC CATACTCCACC ATACTCCACC ATACTCCACC ATACTCCACC CATACTCACC CATACTCACC CATACTCACC CATACTCACC CATACTCACC CA	60 120 180 240 300 480 540 660 720 780 960 1020 1080 1140 1200 1260 1320 1440 1500 1620 1680 1740 1800 1800
50 55 60 65 70	Seq 1D No: Nucleic Ac Coding sec 1	rid Accessic puence: 188. 11	IN B: BC0088 .2695 21 GAGCGGCTG GGAGGGCTCT GTTTCGCCTT GTTTCACCTG AGCCAAGGAA AGATCCTGTC AAGCCAAGGA GAAGAGAGGG TATATCAACGA AGATCCTGTC AAGCCAAGGAG TATATCACTT CAACCCAAGGAG TATATCACT CAACCCAGCAG ATTATACTA TACAGCAG TATACACACA AGATCCTGC CAACCCAGGAG TATACACACA AGACCGTTC CGGTTGCAGA AAGACCGAA AAGACCGAA AAGACCCAAG TATACACCAG TATACACCAG TATACAGCAG TATACAGCAG TATACAGCAG TATACAGCAG TATACAGCAC TATACAGCAG	31 CCGACAGCTCC CACCTGAT/ CACCTGAT/ CACCTGAT/ CACCTGAT/ CACCTGAT/ CACCTGAT/ CACCTGAT/ CACCTGAT/ CACCTGAT/ CACCTGAT/ CACCTGAT/ CACCTGAT/ CACCTGAT/ CACCTGAT/ CACCCATA CACCATA CACCCATA CACCCATA CACCCATA CACCCATA CACCCATA CACCCATA CACCATA CACCCATA CCCTCCCCCC G GATAGTTCCC A TAATTTCCCA G TATCCCGCC G CCCAACCACA C CCCCTCGGCC G CCCAACCACA C CCCCCCCC G GAGACTGGCC G GAGACTGGCC T TCCATCAGCC G AGCGAGGAA T TTCATCAGCC G GAGACGAAC G GACCCACA C CCCCCCACA C CCCCCCACA C CCCCCCACA C CCCCCCACA C CCCCCCACA C CCCCCCCC	GTCCCTCCT GAGGGTCATC GAGGGTCATC GCCAAGCTGC GCCAGGGCA AGGGCCGCT CCCCCACAA AATTACTCAA GCATCCTGAG AGGAGAAACTGA CCTCAGGACCA AGGAGCAACAA CGCAGCACAA CGCAGCACAA CGCAGCACAA CCACAGCACCA CCATACCGCC AGAAACTTGA CCAAGCACCAC CCAACCACCAC CCAACCACCAC CCATACCGCAC CCATCCCAACCC CATAATCTGTC CATGGGATC CCTCGAACCC CATCCCCAGC CCTCGAACCC CATCCCCAGC CCTCGAACCC CATCCCCAGC CCTCGAACCC CTCGAACCC CTCGAACT CTCCCAACC CTCCAACC	60 120 180 240 360 420 540 660 720 1020 1020 1140 1200 1320 1380 1440 1500 1560 1620 1680 1740 1860 1980	
50 55 60 65 70	Seq ID No: Nucleic Ac Coding sec I GGCACGAGG GCCCCCCAGGAT GAACTACCC CCAGCAT GAACTACCC CCAGCAT AGTACACC GCCCAGA GCCCCAGA GCCCCAGA GCCCCAGA GCCCACAG GCCCACA GCCCACA GCCCACAG GCCCACAG GCCCACAG GCCCACAG GCCCACACA CCCCCACACA GCCCCCCCC	id Accessic puence: 188. 11	IN B: BC0088 .2695 21 Committee	31 CGGACAGCCC CACCTGGAT CACCTGGAT GCCAGGAT CACCTGGAT CACCTGGAT CACCTGGAT CACCTGGAT CACCTGGAT CAGCCGCAT CACCTGGAT CACCTGTGAT CACCTGAT CACCGCAT CACCTGGAT CACCGCAT CACCGCAT CACCGCAT CACCGCAT CACCGCAT CACCGCAT CACCGCAT CACCGCAT CACCGCAT CACCGCAT CACCGCAT CACCGCAT CACCGCAT CACCTGGAT CACCTGGAT CACCTGGAT CACCGCAT CACCTGGAT CACCTGAT CACCTG	C CCCTCCCCCC G GATAGTTCCCA A TAATTTCCGA G ATAGTTCCCA G CCCAACCACA G CCCAACCACA G CCCAACCACA G CACCACCAC G GAGACTGGCC G GAGACTGGCC T TCCATCAGC G GAGACTGGCC T TCCATCAGC G GAGAACGAC T TTACCACTA G GACACTGAGC A AGATGGAGA A AGATGGAGG A AGATGGAGG C CAGCCCACA A CCGCTTCC T CCGTCGGGG T TCAATTCGT C CAGCCCACA A CCGCTTCC T CCGTCGGGG T TCAATTCGT C AGAAAAGT T TCCAACGAC T TCAATTCGT C AGAAAAGT T TCCACGGGG T TCAATTCGT C AGAAGAGA T ACTTTCCC T AGCCCCAAAG G TTTCCAAC T AGCCCCAAAG C CACCCTCC C CACCCCCAAC C CACCCTCC C CACCCCCCAAC C CACCCTCC C CACCCCTCC C CACCCCTCC C CACCCCTCC C C CCCCCTCC C C CCCCCTCC C C CCCCCCAACG C C CACCCTCC C C CCCCCTCC C C C C C C C C C C	GTCCCTCCT GAGGGTCATC GAGGGTCATC GAGGGTCATC GCCACACACACACACACACACACACACACACACACACA	60 120 180 240 300 360 420 540 660 720 780 900 1020 1080 1140 1200 1340 1340 1500 1560 1620 1680 1740 1860 1920 1980
50 55 60 65 70	Seq 1D No. Nucleic Ac Coding sec 1 GGCACGAGGG CTCTTCTCCAC CGCCCCACAC CCCCAGGATT GAACTACCC CAACCAGGT GGTCCCAT AGGTACACAC GGACGAGGG GGAATACAC CCAACAGGT CGAGGAGG CGAATCAC CGAGCAGG GGCAATCA GCCACAAG CCACCAAG CCGCAAAC CCTACCAAG CCTCACAG CCTCACAG CCTCACAG CCTCACAG CCTCACAG CCTCACAC CCTGGCCC CCCAGCT CCAAATCC CCACCAGGC CCCTGGCCC CCCAACTC CCCAACTC CCCAACTC CCCAACTC CCCAACTC CCCACCAGGC CCCTGGCCC CCCACCTC CCCAACTC CCCAACTC CCCAACTC CCCAACTC CCCAACTC CCCCAACTC CCCAACTC CCCAACTC CCCAACTC CCCAACTC CCCAACTC CCCAACTC CCCAACTT TATACCAAC CCCAACTT TATACCAAC CCCAACTT TATACCAAC CCCAACTT TATACCAAC CCCAACTT TATACCAAC CCCAACTT TATACCAAC CCCAACTT TATACAAC CCCAACTT TATACCAAC CCCAACT TTT TATACCAAC CCCAACT TTT TATACCAAC CCCAACT TTT TATACCAAC CCCAACT TTT TATACCAAC CCCAACT TTT TATACCAAC CCCAACT TTT TATACCAAC CCCAACT TTT TATACCAAC CCCAACT TTT TATACCAAC CCCAACT TTT TATACCAAC CCCAACT TTT TT	puence: 188. 11	IN B: BC0088 .2695 21 GACTAGGAA G GAGGGCTCT G GTTTGCCCTT TTATCACCG A CASTCCTGGA A CACCCTGGC A CASTCCTGGC A CASTCCTGC C ACGGCATGT C CCGCCCAGGT T TATCACCG C ACGGCATGT C CACCCTAGG A TATTACACCG A TATTACACCG A TATTACACCG C AGCTGTCCG A CACCCTTC C AGCTGTCCGC A CACCCTTC C C AGCTGTCCGC A TATACACCAC T CAACCCAGG T TATACACCAC T CAACCCAGG T ATACACCAC G ATACCTTC C GTGTGCAGA A GAGGCGGAA C GATCACTTC C GTGTGCAGA C GATCACTTC C GTGTGCAGA C GATCACTTC C GTGTGCAGA C GATCACTTC C GTGTGCAGA C GATCACTTC C GTGTGCAGA C GATCACTTC C GTGTGCAGA C GATCACTTC C GTGTGCAGA C GATCACTTC C GTGTGCAGA C GATCACTTC C GTGTGCAGA C GATCACTTC C GTGTGCAGA C GATCACTTC C GTGTGCAGA C GATCACTTC C GTGTGCAGA C GATCACTTC C GTGTGCAGA C GTGGGAGAC C ATAGCACT C CAATCATTACCCC C ATATAGCCC C ATAGGTCC A ATAAGCC A ATAAGCC A ATAAGCCC A ATAAGCCC A ATAAGCCC A ATAAGCCC A ATAAGCCC A ATAAGCC A ATAAGCCC A ATAAGCCC A ATAAGCCC A ATAAGCCC A ATAAGCCC A ATAAGCC A A	31 CCGACAGCTCC CACCTGGAT CCACCGGAT GCCCAGGAT GCCCAGGAT GCCCAGGAT GCCAGGAT GCCAGGAT GACACGCC GACACGCC GACACGCC GACACGCC CACCTGGAT ACGCAGCAC ACGCACCAC ACACCCC ACCCGGAT ACACCCC ACCCGGAT ACACCCC CACCTGGA ACACCTCA ACACCTCA ACACCTCA ACACCTCA ACACCTCA ACACCTCA ACACCTCA ACACCTCA ACACCTCA ACACCTCA ACACCACA ATAACTGGAC CTGATCACCAT ACCCGCATC CTGATCACCAT ACCCGCATC CTGATCACCAT ACCCGCATC CTGAAAACAT ACCGCCATC CTGTTTCGAC CTGTTCTCAC CTGTTTCGAC CTGTTTCGAC CTGTTTCGAC CTGTTTCGAC CTGTTTCGAC CTGTTTCGAC CTGTTTCGAC CTGTTTCGAC CTGTTTCGAC CTGTTTCGAC CTGTTTCGAC CTGTTTCGAC CTGTTTCGAC CTGTTTCGAC CTGTTTCTTCAC CTGTTTCTTCAC CTGTTTCGAC CTGTTTCTTCAC CTGTTTCTTCAC CTGTTTCTTCAC CTGTTTCTTCAC CTGTTTCTTCAC CTGTTTTCTTCAC CTGTTTTCTTCAC CTGTTTTCTTCAC CTGTTTTCTTCAC CTGTTTTCAC CTGTTTTTCAC CTGTTTTTCAC CTGTTTTTCAC CTGTTTTTTCAC CTGTTTTTTCAC CTGTTTTTTTCAC CTGTTTTTTTTTT	G CCCTCCCCGC G GATAGTTCCC G GATAGTTCCC G GATAGTTCCC G CCCAACCACA G ATACTCCGGC G CCCAACCACA G CCCAACCAC G GAGACTGGGC G CCCAACCAC G GAGACTGGGC G GAGACTGGGC G GAGACTGGGC G GAGAGGAA T TACCACTA G GACTGGAG G GAGAGGAGA C TACCACTA C GAGCCACA C CAGCCCAC C CAGCCCAC T CCCTCCC C CAGCCCAC T CGAAAAACT T GGAAAAACT T GGAAAAACT T CAATTCGT T CAATTCGT T CAATTCGT T CAACCCAAAG G GCCCAAAG G GAAAATCT C CAGCCCAAAG C CACCCTTCC C CAGCCCAAG C CACCCCTCC C CAGCCCCAAG C CACCCCTCC C CAGCCCCAAG C CACCCCTCC C CAGCCCCCAAG C CACCCCTCC C CAGCCCCCCAAG C CACCCCTCC C CAGCCCTCC C CAGCCCTCC C CAGCCCTCC C CAGCCCTTCC C CAGCCCTTCC C CAGCCCTTCC C CAGCCCTTCC C CAGCCCTTCC C CAGCCCTTCC C CAGCCCCTTCC C C C C C C C C C C C C C C C	GTCCCTCCT GAGGGTCATC GAGGGTCATC GCCAAGCTGC GCCAGGGCA AGGGCCGCT CCCCCACAA AATTACTCAA GCATCCTGAG AGGAGAAACTGA CCTCAGGACCA AGGAGCAACAA CGCAGCACAA CGCAGCACAA CGCAGCACAA CCACAGCACCA CCATACCGCC AGAAACTTGA CCAAGCACCAC CCAACCACCAC CCAACCACCAC CCATACCGCAC CCATCCCAACCC CATAATCTGTC CATGGGATC CCTCGAACCC CATCCCCAGC CCTCGAACCC CATCCCCAGC CCTCGAACCC CATCCCCAGC CCTCGAACCC CTCGAACCC CTCGAACT CTCCCAACC CTCCAACC	60 120 180 240 360 420 540 660 720 1020 1020 1140 1200 1320 1380 1440 1500 1560 1620 1680 1740 1860 1980

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	TCCCAGCTCC CATACCCACC CTGGACATGC TCAGCAGACA TCTGCAGTTA ACGGGCGTCC CCTGCCCCAC ACGGTAAGCA CCATGCCCCA CACCTCGGGT ATGAACCGCC TGACCCAAGT	2340 2400
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,	CTCCTCCTC ACCACCTCCA ATGCCTATGG CAGAATGGGC CTTCTCCACC AGGAGAAGCT	2520
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10	ACTURGUEGO TERCACTERA ARCTACTICA GATTGTCTGA CAGCAGGAAC TGAGAGAAGC	2760
10	AGTECAAAGA TGTETTEAC CAACTECETT TIAGTTTTET TGGTTAAAAA AAAAAAAAA	2820
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15	Seq ID NO: 168 DNA Sequence Nucleic Acid Accession #: NM_005761.1	
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	CANTOCCOT CONTROLLES CONSCIONS CONTROLLES CO	180
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	CCCAGCCCCA TGGAGGTCTC CCGGAGGAAG GCGCCGCCGC GCCCCCCGCG CCCCGCAGCG CCACTGCCCC TGCTGGCCTA TCTGCTGGCA CTGGCGGCTC CCGGCCGGG CGCGGACGAG	360
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	TETOTOCOCA COCCOACTE OCTEGACIAC CTEGACTACA GCCTGGAGCA CAGCCTCTCG	480
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	CONTROPER CONTROTECT CACCEGCTEG ACCTTCGACC GGGGCGCCTG CGAGGTGCGG	660
30	CCCCTGGGCA ACCTGAGCCG CAACTCCCTG CGCAACGGCA CCGAGGTGGT GTCGTGCCAC	720
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4.0	CAGGAGCGGC GCTCCCCCAC CACCACGGCG CTCTGCCTCT TCAGAATGAG TGAGATCCAG	1260
40	GCGCGCGCCA AGAGGGTCAG CTGGGACTTC AAGACGGCCG AGAGCCACTG CAAAGAAGGG	1320 1380
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	CAGTTACTTA AGGTTATTCT TGGTGAGAAT TTGACTTCAA ATTGTCCAGA GGTTATCTAT	1500
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	CTACANACCT CCACTTTTCA ACGAGATTCT GTACATTCAG AGAACTTAGA AAACTGGCTG	1740
	GATATTTCGT CTGGAGCAAA AAAGTGCCCT AAAATTCAGA TAATTCGAAG CAGTAAAGAA	1800
50	AAGACTACAG TGACTATGGT GGGAAGCTTC TCTCCAAGAC ACTCAAAGTG CATGGTGAAG AATGTGGACT CTAGCAGGGA GCTCTGCCAG AATAAAAGTC AGCCCAACCG GACCTGCACC	1860 1920
30	TGTAGCATCC CAACCAGAGC AACCTACAAA GATGTTTCAG TTGTCAACGT GATGTTCTCC	1980
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			GAAGATAGCA				4200
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			TTATTACAAA				4740
			AACTCAGGAA				4800
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1.5			GCTGGAAGAA				4920
							4980
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			1		COMOL NOTICE	CATTOTTOTT	60
			ACCAGCTGAT				
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00			ATCTTCCTAT				180
30	CTGGCTCTCA	CCTTCTGGCA	TTTACTGTCT	ATGTTTGGAT	TCTTCATCGT	GTCCTATGGC	240
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4.5	1	11 	21 	1	1	1	
45	1 ATGGAGCCAA	11 GCCACAGCCA	21 ACCCACAATG	GACATGAAGC	 ACATGCAAGA	GCGTCCAGCT	60
45	1 ATGGAGCCAA	11 GCCACAGCCA	21 ACCCACAATG	GACATGAAGC	 ACATGCAAGA	GCGTCCAGCT	60 120
45	1 ATGGAGCCAA GCCTCGCCTT	11 GCCACAGCCA TAAAATGCCA	21 ACCCACAATG GGACGGCCGC	GACATGAAGC GGCTCCGCTC	ACATGCAAGA AGAGCCCCCT	GCGTCCAGCT CTCGGCTGCT	120
45	1 ATGGAGCCAA GCCTCGCCTT GGCCCGGGCT	11 GCCACAGCCA TAAAATGCCA CGCCCGCGCC	21 ACCCACAATG GGACGGCCGC GCTGGGGGCT	GACATGAAGC GGCTCCGCTC CTGACTCCTG	ACATGCAAGA AGAGCCCCCT CCGAGCCGGG	GCGTCCAGCT CTCGGCTGCT CCTGGGCAGC	120 180
45	1 ATGGAGCCAA GCCTCGCCTT GGCCCGGGCT GCCCCCGGGG	11 GCCACAGCCA TAAAATGCCA CGCCCGCGCCCG	21 ACCCACAATG GGACGGCCGC GCTGGGGGCT CCGCGCCCCC	GACATGAAGC GGCTCCGCTC CTGACTCCTG GTCACCGGGA	ACATGCAAGA AGAGCCCCCT CCGAGCCGGG AACGCCGTAG	GCGTCCAGCT CTCGGCTGCT CCTGGGCAGC CCGGCGATCC	120 180 240
	1 ATGGAGCCAA GCCTCGCCTT GGCCCGGGCT GCCCCCGGGG GCGGTCGCCC	11 GCCACAGCCA TAAAATGCCA CGCCGCGGCC CCCCGCGAGC TGGGCTCGGC	21 ACCCACAATG GGACGGCCGG GCTGGGGGCCCCG GCCGGCCCCAG	GACATGAAGC GGCTCCGCTC CTGACTCCTG GTCACCGGGA	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC	GCGTCCAGCT CTCGGCTGCT CCTGGGCAGC CCGGCGATCC GGGACGGCC	120 180 240 300
45 50	ATGGAGCCAA GCCTCGCCTT GGCCCGGGCT GCCCCCGCG GCGGTCGCCC	11 GCCACAGCCA TAAAATGCCA CGCCCGCGCCC CCCCGCGCGCCC TGGGCTCGGCC	21 ACCCACAATG GGACGGCCGG GCTGGGGGCCCG GCCGGCCCCG GCCGGCCCAG CTCTGACCTG	GACATGAAGC GGCTCOGCTC CTGACTCCTG GTCACCGGGA CCAGGACCCC	ACATGCAAGA AGAGCCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT	GCGTCCAGCT CTCGGCTGCT CCTGGGCAGC CCGGCGATCC GGGACGGGCC AGCTACTGGG	120 180 240 300 360
	ATGGAGCCAA GCCTCGCCTT GGCCCCGCCCG GCGTCGCCCC TCGCCAGCCC ACACCACCCC	11	21	GACATGAAGC GGCTCOGCTC CTGACTCCTG GTCACCGGGA CCAGGACCCC TTGTCCAAGG	ACATGCAAGA AGAGCCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCCACC	GCGTCCAGCT CTCGGCTGCT CCTGGGCAGC CCGGCGATCC GGGACGGCC AGCTACTGGG TCTCACCACT	120 180 240 300 360 420
	ATGGAGCCAA GCCTCGCCTT GCCCCCGCG GCGGTCGCCC TCGCCAGCC ACACCACCCC CACCCCGAGC	11 GCCACAGCCA TAAAATGCCA CGCCCGCGCC CCCCGCGAGC TAGAAATAC TAGAAAATC GTGAAGACTC TGGTGGGCAC	21 ACCCACAATG AGGACGCCGC GCTGGGGCCCG CCCGGCCCCGG CTCTGACCTGC CTACCATTGCA	GACATGAAGC GGCTCCGCTC CTGACTCCTG GTCACCGGGA CCAGGACCCCC TTGTCCAAGG	ACATGCAAGA AGAGCCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCCACC CCTTCTGGCA	GCGTCCAGCT CTCGGCAGC CCTGGGCAGC CCGGCGATCC GGGACGGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT	120 180 240 300 360 420 480
	ATGGAGCCAA GCCTCGCCTT GCCCCCGCG GCGTCGCCC TCGCCAGCCC ACACCACCCC ACACCACCCC ACTTTTGGAG	11	21	GACATGAAGC GGCTCCGCTC GTCACCCGGA CCAGGACCCC TTGTCCAAGG AGGTTCTAC TTTCTCAAGG	ACATGCAAGA AGAGCCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCCACC CCTTCTGGCAG CATTTGGCAG	GCGTCCAGCT CTCGGCTGCT CCTGGGCAGC CCGGCGATCC GGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTTC	120 180 240 300 360 420 480 540
50	ATGGAGCCAA GCCTCGCCTT GGCCCGGGCT GCCCCCGGC ACACCACCCT CACCCCGAGC ATGTTTGGAT CACTTGGATC	11	21 ACCCACAATG GGACGGCCGC GCTGGGGCCCCC GCCGGCCCAG CTCTGACCTC TACCATTGCA CTCTATGCA CAACCTTACA	GACATGAAGC GGCTCCGCTC GTCACTCCTG GTCACCGGGA CCAGGACCCC TTGTCCAAGG AGGTTCTACC CTGGCTCTCA	ACATGCAAGA AGAGCCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCCACC CCTTCTGGCAG TTGACAAGTA	GCGTCCACCT CCTGGGCAGC CCGGGGATCC GCGACGGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTTC CACTGGCCAG	120 180 240 300 360 420 480
	ATGGAGCCAA GCCTCGCCTT GGCCCGGGCT GCCCCCGGC ACACCACCCT CACCCCGAGC ATGTTTGGAT CACTTGGATC	11	21 ACCCACAATG GGACGGCCGC GCTGGGGCCCCC GCCGGCCCAG CTCTGACCTC TACCATTGCA CTCTATGCA CAACCTTACA	GACATGAAGC GGCTCCGCTC GTCACTCCTG GTCACCGGGA CCAGGACCCC TTGTCCAAGG AGGTTCTACC CTGGCTCTCA	ACATGCAAGA AGAGCCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCCACC CCTTCTGGCAG TTGACAAGTA	GCGTCCAGCT CTCGGCTGCT CCTGGGCAGC CCGGCGATCC GGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTTC	120 180 240 300 360 420 480 540
50	ATGGAGCCAA GCCTCGCCTT GCCCCCGCG GCGGTCGCCC ACACCACCCT CACCCCGAGC ATGTTTGGAT CACCTCGAGC CTCCTCGAGG	11 GCCACAGCCA TAAAATGCCA CGCCGCGCGC CGCCGCAGG TAGAAATAA TAGAAAATAA TAGAAAATAA TAGAAAATAA TAGAAAATAA TAGTAGAAGCTC TAGTAGAACCC TTGTTCATCGT TCTTCATCGT	21 A ACCACAATG A GGACGCCCC C GCTGGGGCT C CCCGCCCCAG A CTCTGACTC C TACCATTGCAC C CAGCCAGGAA C CAACCTTAGCA	GACATGAAGC GGCTCCGCTC CTGACTCCTG GTCACCGGGA CCAGGACCCC TTGTCCAAGG AGGTTCTACC CTGGCTCTAC CTTCACAGG TTTCTCACAG TTTCTCACAG TTTCTCACAG TTTCTCACAG TTTCTCACAG TTTCTCACAG TTTCTCACAG TTTCACAGCT	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAC CCTTCTGGCA CATTTGCAAG TTGACAAGTA TCCACTGGAG	GCGTCCAGCT CTCGGCAGC CCGGCGATCC GGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTTC CACTGCCAG CCACGGCCAG CCAGGGACTG	120 180 240 300 360 420 480 540
50	1 ATGGAGCCAA GCCTGCCTT GGCCGGGCT GCCCCGGGC TCGCCAGCCC ACACCACCCT CACCCCGAGC ATGTTTGGAT CACTTGGAT CTCTCGAGC TGCATTTGGT	11	21 ACCCACAATG AGGACGCCCCC GCTGGGGGCCCCC CCCGCCCCCCC CTCCATGCCT TACCATTGCA CTCTATGCC CAACCTTACA CTCAAAGTAT CTGTAAAGTAT	GACATGAAGC GGCTCCGGCA CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCAAGG CTAGCCAAGG AGGTTCTACC CTGGCTCTCA CTTCCACAGG CCTTCACAGG CCTTCACAGG CCTTCACAGG CGGGTGGAAA	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCCACC CCTTCTGGCA CATTTGCAG TTGACAAGTAA TCCACTGGAG ATGGTACCAG	GCGTCCACCT CCTGGCAGC CCTGGCAGC CCGGCGATC AGCTACTGG TCTCACCACT TTTACTGTCT GACTCTTTC CACTGGCCAG CCAGGGACTG TCAGGACTG	120 180 240 300 360 420 480 540 600 660
50	ATGGAGCCAA GCCTCGCCTT GCCCCGGGC GCGCTCGCCCCGGG ACACCACCCT CACCCCGAGC ATGTTTGGAT CTCCTCGAGC GCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGACACACCCT	11 GCCACAGCCA TAAAATGCCA CACCCGGAGC CCCCGGAGC CTGGGCTGGG	21 ACCCACAATO A GGACGGCCCC C GGCGCCCCC C GCGGCCCCAC C TACCATTGACTC C TACCATTGCACTC C TACCATTGCACAC C CAACCTTATGC C C CAACCTTATGC C C C C C C C C C C C C C C C C C C C	GACATGAAGC GGCTCGGTC CTGACTCCTG GTCACCGGGA CCCG TTGTCCAAGG AGGTTCTACC CTGGCTCTA CTGGCTCTAC CTGGCTCTACGCT GTACTGACGGA CCTTCACGGT GTACTGACGA CCGGAGAATGC	ACATGCAAGA AGAGCCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCCACC CATTTGGCAG TTGACAAGTA TCCACTGGAG ATGGTACCAG AGGAGCCCAC	GCGTCCACCT CCTGGGCAGC CCGGGGATCC GGGACGGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTTC CACTGGCAG CCAGGGACTG TCAACCCGA	120 180 240 300 360 420 480 540 600 660 720 780
50	1 ATGGAGCCAA GCCTGGCCTG GCCCCGGGG GCGTGCCCCGGG GCGTGCCCCCGAG ACACCACCCCCGAGC ATGTTTGGAT CACTTGGATC CTCCTCGAGG GCCGAGGGG GTCTATGTCC	11	21 ACCCACAATG A GGACGCCCC GCTGGGGGCCC GCTGGCCCAG A CTCTGACCTC CAGCCCAGGAA GTCTATGCC CAGCCATGCA CTCTATGC CAGCCATGCA CTCTATGC CAGCCATGCA A CTCTAAAGTAT CTGTGAAGCA A CTCAAAGTAT CTGTGAAGCA A AGGGCTGCCTGC A AGGGCTGACCAA	GACATGAAGC GGCTCGGCTC CTGACTCCGG GTCACCGGGA GCAGGACCCC TTGTCCAAGG AGGTTCTACC CTGGCTCTAC CTTGCACGC GTGACTACCC GGGTGGAAA GGGGGGGAAA CGCGGAGATGC TTGCCCTGC	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCACC TTGGCAG TTGACAAGTA TCCACTGGGAA ATGGTACCAG ATGTACCAG AGGAGCCCAC TCGTCTTCCT	GCGTCCAGCT CCTGGCTGCT CCTGGGCAGC CCGGGGATCC GGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTTC CACTGGCAG CCAGGGCCAG CCAGGGCCAG CCAGGGACTG TCAAACCCGA GCCCGAGCCC CTGCCTTC	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	I I ATGGAGCCAA GCCTCGGCT GGCCCCGGGG GGGTCGCCC ACACCACCCT ACACCACCCT ACACTGGAT CACTTGGAT CTCCTCGAGG GGCGAGGAC GTTATTGCT CTTATGTC	11	21 ACCCACAATO A GAAGGCCCCC GCGGGCCCAC CCGGGCCCAC TACCATTGCA TACCATTGCA TACCATTGCA CTCTATGCC CAACCTTACC CAACCTTACC CAACCTTACC CAACCTTACC CAACCTTACC CAACCTTACC CAACCTTACC CATCGCTGC CAACCTTACC CTCTGAAGCCTGC CATCGCTGC CATCGCTGC	GACATGAAGC GGCTCGGCTC CTGACTCCTG CTGACCCGGA CCAGGACCCC TTGTCCAAGG AGGTTCTACC CTGCTCTCACGCT CTTCTCACGCT CTTCTCACGCT CGTACTCACGCT CGTACTCACGCT CGTACTCACGCT CGTACTCACGCT CGTACTCACGCT CGTACTCACGCT GGCTGCAATGCCTGCT GTCATCACCCT	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCACC TTGGCAG TTGACAAGTA TCCACTGGGAA ATGGTACCAG ATGTACCAG AGGAGCCCAC TCGTCTTCCT	GCGTCCACCT CCTGGGCAGC CCGGGGATCC GGGACGGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTTC CACTGGCAG CCAGGGACTG TCAACCCGA	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50	I I ATGGAGCCAA GCCTCGGCT GGCCCCGGGG GGGTCGCCC ACACCACCCT ACACCACCCT ACACTGGAT CACTTGGAT CTCCTCGAGG GGCGAGGAC GTCTATGTC CTTGTGGTG	11	21 ACCCACAATG A GGACGCCCC GCTGGGGGCCC GCTGGCCCAG A CTCTGACCTC CAGCCCAGGAA GTCTATGCC CAGCCATGCA CTCTATGC CAGCCATGCA CTCTATGC CAGCCATGCA A CTCTAAAGTAT CTGTGAAGCA A CTCAAAGTAT CTGTGAAGCA A AGGGCTGCCTGC A AGGGCTGACCAA	GACATGAAGC GGCTCGGCTC CTGACTCCTG CTGACCCGGA CCAGGACCCC TTGTCCAAGG AGGTTCTACC CTGCTCTCACGCT CTTCTCACGCT CTTCTCACGCT CGTACTCACGCT CGTACTCACGCT CGTACTCACGCT CGTACTCACGCT CGTACTCACGCT CGTACTCACGCT GGCTGCAATGCCTGCT GTCATCACCCT	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCACC TTGGCAG TTGACAAGTA TCCACTGGGAA ATGGTACCAG ATGTACCAG AGGAGCCCAC TCGTCTTCCT	GCGTCCAGCT CCTGGCTGCT CCTGGGCAGC CCGGGGATCC GGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTTC CACTGGCAG CCAGGGCCAG CCAGGGCCAG CCAGGGACTG TCAAACCCGA GCCCGAGCCC CTGCCTTC	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	ATGGAGCCAA GCCTGGCCTG GCCCCGGGG GCGGTGGCCC TCGCCAGCCC ACACCACCCCAAC ACACTGGATC CACTTGGATC CACTTGGATC CTCCTGAGG GCGCGAGGAG GTCTATGTCC CTTGTGTGGAT ACACTCACCC	11	21	GACATGAAGC GGCTCGGCTC CTGACTCCTG CTGACCCGGA CCAGGACCCC TTGTCCAAGG AGGTTCTACC CTGCTCTCACGCT CTTCTCACGCT CTTCTCACGCT CGTACTCACGCT CGTACTCACGCT CGTACTCACGCT CGTACTCACGCT CGTACTCACGCT CGTACTCACGCT GGCTGCAATGCCTGCT GTCATCACCCT	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCACC TTGGCAG TTGACAAGTA TCCACTGGGAA ATGGTACCAG ATGTACCAG AGGAGCCCAC TCGTCTTCCT	GCGTCCAGCT CCTGGCTGCT CCTGGGCAGC CCGGGGATCC GGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTTC CACTGGCAG CCAGGGCCAG CCAGGGCCAG CCAGGGACTG TCAAACCCGA GCCCGAGCCC CTGCCTTC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55	I I ATGGAGCCAA GCCTCGCCTTGGCAGCCCCGGGGGTGGCCCCACCCTACACCCCTACACCCCTACACCCCTACACCCCTACACCCCGAGCCCTTCGCAGAGACCCCCTTGCATTGGATCCTCCTCGAGGCTCATTTTGGTGATCATTTGGTATCCTTCTTGTGATCCTTTTTCGTTGATCCTTTTCGTGGCGGAGAACTCTTCTCTTGTGATCCTTTTCGTTGATCACACCCCTACTTCCTTGTGATCCTTGATCCTTGATCCTTGATCACACCCCTTTCTCTTGTGATCACACCCCTTTCTCTTGTGATCACACCCCTTTCTTCTTGATGATCACACCCTTTCTTCTTGATGATCACACCCTTTCTTCTTGATGATCACACCCTTTCTTCTTGATGATCACACCCTTTCTTCTTGATGATCACACCCTTTCTTCTTGATGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTTCT	11	21 ACCCACAATO A GCACCACAATO A GCACCACCAC C GCTGGGGGCCT C CCGGGCCCCC C GCGGCCCAC C TACCATTGCA C TACCATTGCA C CAACCTTACA C CCAAAGTAT C CTGTGAAGCC C CACCTGAGC C CACCTGAGC C CACCTGAGC C CACCTGAGC C CACCTGAGC C CACCTGAGC C CACCTGAGC C CACCTGAGC C CACCTGAGC C CACCTGAGC C CACCTGAGC C CACCTGAGC C CACCTGAGC C C C C C C C C C C C C C C C C C C C	GACATGAAGC GGCTCGGCTC CTGACTCCTG CTGACCCGGA CCAGGACCCC TTGTCCAAGG AGGTTCTACC CTGCTCTCACGCT CTTCCCACGC CTTCCCGCAC CCTGCCTCACGC CTTCCCGCT CTTCCCGCT CTTCCCGCT CTTCCCGCT CTTCCCGCT CTTCCCGCT CTTCCCGCT CTTCCCGCT CTTCCCGCT CTTCCCCTGCT CTTCCCCTGCT CTTCCCCTGCT CTTCCCCTGCT CTTCCCCTGCT CTTCCCCTGCT CTTCCCCTGCT CTCCCTGCT CTCCCTGCT CTCCCTGCT CTCCCTGCT CTCCCTGCT CTCCTCTCT CTCCTCTCT CTCCTCTCT CTCCTCTCT CTCCTC	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCTTAG GGGAGGCAC CATCTGCTAT TGCCCCACC CCTTCTGGCA CATTTGGCAG TTGACAAGTA TCCACTGGAA ATGGTACCAG AGAGCCCAA TGGTACCAG ACCCTTACAC	GCGTCCAGCT CCTGGCTGCT CCTGGGCAGC CCGGGGATCC GGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTTC CACTGGCAG CCAGGGCCAG CCAGGGCCAG CCAGGGACTG TCAAACCCGA GCCCGAGCCC CTGCCTTC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55	I I ATGGAGCCAA GCCTCGCCTTGGCAGCCCCGGGGGTGGCCCCACCCTACACCCCTACACCCCTACACCCCTACACCCCTACACCCCGAGCCCTTCGCAGAGACCCCCTTGCATTGGATCCTCCTCGAGGCTCATTTTGGTGATCATTTGGTATCCTTCTTGTGATCCTTTTTCGTTGATCCTTTTCGTGGCGGAGAACTCTTCTCTTGTGATCCTTTTCGTTGATCACACCCCTACTTCCTTGTGATCCTTGATCCTTGATCCTTGATCACACCCCTTTCTCTTGTGATCACACCCCTTTCTCTTGTGATCACACCCCTTTCTTCTTGATGATCACACCCTTTCTTCTTGATGATCACACCCTTTCTTCTTGATGATCACACCCTTTCTTCTTGATGATCACACCCTTTCTTCTTGATGATCACACCCTTTCTTCTTGATGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTGATGATCACACCTTTCTTCTTTCT	11	21	GACATGAAGC GGCTCGGCTC CTGACTCCTG CTGACCCGGA CCAGGACCCC TTGTCCAAGG AGGTTCTACC CTGCTCTCACGCT CTTCCCACGC CTTCCCGCAC CCTGCCTCACGC CTTCCCGCT CTTCCCGCT CTTCCCGCT CTTCCCGCT CTTCCCGCT CTTCCCGCT CTTCCCGCT CTTCCCGCT CTTCCCGCT CTTCCCCTGCT CTTCCCCTGCT CTTCCCCTGCT CTTCCCCTGCT CTTCCCCTGCT CTTCCCCTGCT CTTCCCCTGCT CTCCCTGCT CTCCCTGCT CTCCCTGCT CTCCCTGCT CTCCCTGCT CTCCTCTCT CTCCTCTCT CTCCTCTCT CTCCTCTCT CTCCTC	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCTTAG GGGAGGCAC CATCTGCTAT TGCCCCACC CCTTCTGGCA CATTTGGCAG TTGACAAGTA TCCACTGGAA ATGGTACCAG AGAGCCCAA TGGTACCAG ACCCTTACAC	GCGTCCAGCT CCTGGCTGCT CCTGGGCAGC CCGGGGATCC GGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTTC CACTGGCAG CCAGGGCCAG CCAGGGCCAG CCAGGGACTG TCAAACCCGA GCCCGAGCCC CTGCCTTC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55 60	I HATGGAGCCAA GCCTCGCCTTGGCCCCCGGGGGGGGGGGG	11	21 ACCCACAATO A GCACCACAATO A GCACCACCAC C GCGGGCCCCC C GCGGCCCCAC C TACCATTGCC C TACCATTGCC C CAACCTTACGC C CAACCTTACGC A CTCTAAGTAT C CTGTGAAGC C CAACCTTACA G CTCTAAGTAT C CTGTGAAGC G CAGTCCTTAC C CAGCCTTGCA C CACCTTGCA C CACCTTGCA C CACCTTGCA C CACCTTGCA C CAGCCTTGCA C CAGCCTTGCA C CAGCCTTGCA C CCTGGAC C C CGCCTTGCA C C CGCCTTGCA C C C C C C C C C C C C C C C C C C C	GACATGAAGC GGCTCGGCTC CTGACTCCTG CTGACTCCTG CCAGGACCCC TTGTCCAAGG AGGTTCTACC CTTGCCTCACGCT CTTACCACG TTTCTCACAGG CCTTCACGCT CTTACTGACCA GGGGTGGAAA CGCGTGGAAG CGCCTGCTGCCC TTGGCCTGC TTGGCCTGC CTTCACGCT CTACTGACCA GGGTGGAAA	ACATGCAAGA AGAGCCCCTC CCGAGCCGGG AACGCCTTAG GGGAGCGCAC CATCTGCTAT TGCCCCACC CTTTTGGCAG TTGACAAGTA TCCACTGGGAA ATGGTACCAG ATGTTACCAG AGGGAGCCCAC TGGTCTTCCT ACCCTTACAG	GCGTCCAGCT CCTGGGCAGC CCTGGGCAGC CCGGGGATCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTC GACTCTTTC CACTGGCCAG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGCCAC CCTGCCCAGCCC CTGCCTTTC CGCCATCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55	I HATGGAGCCAA GCCTCGCCTTGGCCCCCGGGGGGGGGGGG	11 GCCACAGCCA TAAAATGCCA TAAAATGCCA CGCCCGGAGC CCCCGGAGC TGGAAAATAA TGTGAGACTC TGGTGGGCA TTGTACATCT TGTTACAACTC TCCTCACATCT GACCAGCCCC GACCATCACCT GACCAGCGCCC TCGGAGAGACA TGATCACCCC TCGGAGAGCCCC TCGGAGAGACA TGATCACCCC TCGGAGAGGCCC TGGGAGAGGCCC TGGGAGAGAGCACCCC TGGGAGAGAGCCCC TGGGAGAGGCCCC TGGGAGAGGCCCC TGGGAGAGAGCCCC TGGGAGAGGCCCC TGGGAGAGGCCCC TGGGAGAGAGCCCCC TGGGAGAGGCCCCC TGGGAGAGCCCCC TGGGAGAGGCCCCC TGGGAGAGCCCCC TGGGAGAGCCCCC TGGGAGAGCCCCC TGGGAGAGCCCCC TGGGAGAGCCCCCC TGGGAGAGCCCCCC TGGGAGAGCCCCCC TGGGAGAGCCCCCC TGGGAGAGCCCCCC TGGGAGAGCCCCCC TGGGAGAGCCCCCC TGGAGAGCCCCCC TGGGAGAGCCCCCC TGGAGAGCCCCCC TGGGAGAGCCCCCC TGGGAGAGCCCCCC TGGGAGAGCCCCCC TGGGAGAGCCCCCC TGGGAGAGCCCCCCC TGGGAGAGCCCCCCC TGGGAGAGCCCCCCC TGGGAGAGCCCCCC TGGGAGAGCCCCCCC TGGGAGAGCCCCCCC TGGGAGAGCCCCCCC TGGGAGAGCCCCCC TGGGAGGAGCCCCCCC TGGGAGAGCCCCCCC TGGGAGAGCCCCCCC TGGGAGAGCCCCCCC TGGGAGAGCCCCCCC TGGGAGAGCCCCCCCC TGGGAGAGCCCCCCC TGGGAGAGCCCCCCC TGGGAGAGCCCCCCC TGGGAGAGCCCCCCC TGGGAGAGCCCCCCC TGGAGAGCCCCCCC TGGAGAGCCCCCCC TGGAGAGCCCCCCC TGGAGAGCCCCCCC TGGAGAGCCCCCCCC TGGAGAGCCCCCCC TGGAGAGCCCCCCC TGGAGAGCCCCCCCC TGGAGAGCCCCCCCC TGGAGAGCCCCCCC TGGAGAGCCCCCCC TGGAGAGCCCCCCCC TGGAGAGCCCCCCC TGGAGAGCCCCCCCC TGGAGAGCCCCCCCC TGGAGAGCCCCCCC TGGAGAGCCCCCCCC TGGAGAGCCCCCCCC TGGAGAGCCCCCCCC TGGAGAGCCCCCCC TGGAGAGCCCCCCC TGGAGAGCCCCCCCC TGGAGAGCCCCCCC TGGAGAGCCCCCCC TGGAGAGCCCCCCC TGGAGAGCCCCCCC TGGAGAGCCCCCCC TGGAGAGCCCCCCC TGGAGAGCCCCCCCC TGGAGAGCCCCCCC TGGAGAGCCCCCCCC TGGAGAGCCCCCCCC TGGAGAGCCCCCCCC TGGAGAGCCCCCCCC TGGAGAGCCCCCCCC TGGAGAGCCCCCCC TGGAGAGCCCCCCCC TGGAGAGCCCCCCCCC TGGAGAGCCCCCCCCCC	21 ACCCACAATO A GCACCACAATO A GCACCACCAC C GCGGGCCCCC C GCGGCCCCAC C TACCATTGCC C TACCATTGCC C CAACCTTACGC C CAACCTTACGC A CTCTAAGTAT C CTGTGAAGC C CAACCTTACA G CTCTGAAGC G CAGTCCTTAC G CAGTCCTTACC G CAGTCCTTACC C CAACCTTACA C CCAACTTACA C CCAACTTACAC C CAACCTTACAC C CAACCTTACAC C CAACCTTACAC C CACCTTGCAA C CCACTTGCCAAC C CACCTTGCAC C C C C C C C C C C C C C C C C C C	GACATGAAGC GGCTCGGCTC CTGACTCCTG CTGACCCGGA CCAGGACCCC TTGTCCAAGG AGGTTCTACC CTGCTCTCACGCT CTTCCCACGC CTTCCCGCAC CCTGCCTCACGC CTTCCCGCT CTTCCCGCT CTTCCCGCT CTTCCCGCT CTTCCCGCT CTTCCCGCT CTTCCCGCT CTTCCCGCT CTTCCCGCT CTTCCCCTGCT CTTCCCCTGCT CTTCCCCTGCT CTTCCCCTGCT CTTCCCCTGCT CTTCCCCTGCT CTTCCCCTGCT CTCCCTGCT CTCCCTGCT CTCCCTGCT CTCCCTGCT CTCCCTGCT CTCCTCTCT CTCCTCTCT CTCCTCTCT CTCCTCTCT CTCCTC	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCTTAG GGGAGGCAC CATCTGCTAT TGCCCCACC CCTTCTGGCA CATTTGGCAG TTGACAAGTA TCCACTGGAA ATGGTACCAG AGAGCCCAA TGGTACCAG ACCCTTACAC	GCGTCCAGCT CCTGGCTGCT CCTGGGCAGC CCGGGGATCC GGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTTC CACTGGCAG CCAGGGCCAG CCAGGGCCAG CCAGGGACTG TCAAACCCGA GCCCGAGCCC CTGCCTTC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55 60	ATGGAGCCAA GCCTGGCCTG GCCCCGGGG GCGGTGGCCC CACCCGAGC ATGTTTGGAT CACTTGGAT CTCTCGAGC GCGGAGGAG GTCTATGTCC CTTGTCGTG ACACTCACCC Seq ID NO Nucleic Ac Coding sec	11	21 ACCCACAATG A GGACGGCCCC C GCGGCCCCAC C CGCGCCCCAC C CAGCCCAGAA C CTCTAGACTC C CAGCCATGAA C CTCTAGACTC C CAACCTTACA A CTCTAAAGTAT C CTGTAAAGTAT C CTGTAAAGTAT C CTGTAAAGTAT A GCACCTGCAA A GCACCTGCAA A GCACCTGCAA C CAGCCTACAA C CAGCCTACAA C CAGCCTTACAA C CACCTTACAAA C C CACCTTACAAA C C C C C C C C C C C C C C C C C	GACATGAAGC GGCTCGGCTC CTGACTCCGG CTGACTCCGG CTGACTCCGG CTGACTCCACG CTGGCTCTACGC CTGGCTCTACGC CTTGCCACG CTTGCCACG CTTGCCACG CTTGCCACG CTTGCCACG CTTCTACCCT CTTACCGCT CTTACTGCCA CGGGTGGAAA CGGGTGGAAA CGCGTGACACG CTGGCTGCACG CTGCTGCACG CTGCTGACCA CGGGTGGAAA CGCGTGAAA CGCGAGATGC CTGCTGCACG CTCACCTGC CTCACGCTGC CTCACGCTGC CTCACGCTGC CTCACGCTGC CTCACGCTGC CTCACGCTGC CTCACGCTGC CTGACGCTGC CTGACCTGC CTGACGCTGC CTGACGCTGC CTGACGCTGC CTGACGCTGC CTGACGCTGC CTGACCTGC CTGCC CTGACCTGC CTTCACCTGC CTGACCTGC CTG	ACATGCAAGA AGAGCCCCTC CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCACC CCTTCTGGCA CATTTGCAAGT TTCACTGGGA ATGGTACAGT ATGTACTACAG ATGGTACAGT AGGAGCCAAC TCGTCTTCCT ACCCTTACAG	GCGTCCAGCT CCTGGGCAGC CCTGGGCAGC CCGGGGATCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTC CACTGGCAG CCAGGGACTG TCAAACCCGA GCCGAGCCC CCGGCTCTTC CGCCATCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55 60	ATGGAGCCAA GCCTGGCCTG GCCCCGGGG GCGGTGGCCC CACCCGAGC ATGTTTGGAT CACTTGGAT CTCTCGAGC GCGGAGGAG GTCTATGTCC CTTGTCGTG ACACTCACCC Seq ID NO Nucleic Ac Coding sec	11	21 ACCCACAATG A GGACGGCCCC C GCGGCCCCAC C CGCGCCCCAC C CAGCCCAGAA C CTCTAGACTC C CAGCCATGAA C CTCTAGACTC C CAACCTTACA A CTCTAAAGTAT C CTGTAAAGTAT C CTGTAAAGTAT C CTGTAAAGTAT A GCACCTGCAA A GCACCTGCAA A GCACCTGCAA C CAGCCTACAA C CAGCCTACAA C CAGCCTTACAA C CACCTTACAAA C C CACCTTACAAA C C C C C C C C C C C C C C C C C	GACATGAAGC GGCTCGGCTC CTGACTCCGG CTGACTCCGG CTGACTCCGG CTGACTCCACG CTGGCTCTACGC CTGGCTCTACGC CTTGCCACG CTTGCCACG CTTGCCACG CTTGCCACG CTTGCCACG CTTCTACCCT CTTACCGCT CTTACTGCCA CGGGTGGAAA CGGGTGGAAA CGCGTGACACG CTGGCTGCACG CTGCTGCACG CTGCTGACCA CGGGTGGAAA CGCGTGAAA CGCGAGATGC CTGCTGCACG CTCACCTGC CTCACGCTGC CTCACGCTGC CTCACGCTGC CTCACGCTGC CTCACGCTGC CTCACGCTGC CTCACGCTGC CTGACGCTGC CTGACCTGC CTGACGCTGC CTGACGCTGC CTGACGCTGC CTGACGCTGC CTGACGCTGC CTGACCTGC CTGCC CTGACCTGC CTTCACCTGC CTGACCTGC CTG	ACATGCAAGA AGAGCCCCTC CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCACC CCTTCTGGCA CATTTGCAAGT TTCACTGGGA ATGGTACAGT ATGTACTACAG ATGGTACAGT AGGAGCCAAC TCGTCTTCCT ACCCTTACAG	GCGTCCAGCT CCTGGGCAGC CCTGGGCAGC CCGGGGATCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTC CACTGGCAG CCAGGGACTG TCAAACCCGA GCCGAGCCC CCTGCCTCTTC CGCCATCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55 60	I HATGGGCAAGG ATGGAGCCAAGGCCTGGCCTGGCAGCCCCAGCGAGCCCACCCCAGCGCAGCCCTACCCCAGAGCCCTGCCAGCCCACCCCAGCCCTGCCACCCCAGCCCTGCCACCCCAGCCCACCCCAGCCCCACCCCAGCCCCAGCCCCACCCCAGCACCCCAGCACCCCAGCACCCCACCCCACCCCAGCCCCACCCCACCCCACCCCACCCCACCCCACCCCCACCCC	III	21 ACCCACAATO A GCACACAATO A GCACACAATO C GCAGGGGGCT C CCGCGGCCCAC C CCGGGCCCAC C TACCATTGCA C TACCATTGCA C TACCATTGCA C CAACCTTACA C CTCTGAAGCT C CAGCCTGGA C CAACCTTGCA C CAGCCTGGA C CAACCTTGCA C CAGCCTGGA C CAACCTTGCA C CAGCCTGGA C CACCTGGAC C CAACCTGGAC C CAACCTGGAC C CAACCTGGAC C CAACCTGGAC C C C C C C C C C C C C C C C C C C C	GACATGAAGC GGCTCGGCTC CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCAGG AGGTTCTACC CTTGTCACAGC TTGTCACAGG CTTACTCACGCT GTACTACCG TTGTCACCG TTGTCACCG TTGTCACCG GCTGACTACCG TTGTCACCG GCTGACTACCG TTGCCTGCT GTACTACCG TTGCCTGCT GACTGA SH predictec	ACATCCAAGA AGAGCCCCTCCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCACC CATTTGGCAG TTGACAAGTA TCACCTGGAA ATGTACAGA ATGTACAG TCGTCTTCCT ACCCTTACAG	GCGTTCCAGCT CCTGGGCAGC CCTGGGCAGC CCGGGGAGCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTC GACTCTTTC CCACGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCGAGCCC CTGCCTCTTC CGCCATCCCC	120 180 240 300 360 420 480 540 660 720 780 840 900 936
50 55 60	I HATGGGAAGAAAAATGGGAAGAAAAATGGGAAGAAGACCAAAGAAAAAAGGGAAAGAAGACCAAAGAC	11 GCCACAGCCA TAAAATGCCA TAAAATGCCA CGCCCGGAGG CCCCGGAGG TGGAAAATA TGTGAGGCT TGGTAGGCA TTCTTCACTGC TTCTTACAACC TCCCAGTTCC GAGCAGCCCC GACGTAGACAA TGATCAACC TCGGAGAGGCCCC GACGTAGACAA TGATCAACC TGGGAGGAGCCC TAATTCATGTC TAATTAAACC TAATTAAACC TAAATTAAACC TAATTAAACC TAAATTAAACC TAAATTAAACC TAAATTAAACC TAAATTAAACC TAAATTAAACC TAAATTAAACC TAAATTAAACC	21 ACCCACAATO A GCACCACAATO A GCACCACAATO C GCAGGGCCCCC C GCCGGCCCCAC C TACCATTGCC C TACCATTGCC C CACCCTACC C CACCCTACC C CACCCTACC C CACCCTACC C CACCCTACC C CACCCTGAC C CACCCTGAC C CACCCTGAC C CACCCTGAC C CACCCTGAC C CACCCTGAC C CACCCTGAC C CTGACCCAC C CTGAAGCAC C CTAAAACACC C TAAAACACC C TAAACACC C TAAAACACC C TAAAACACC C TAAAACACC C TAAAACACC C TAACACC C TAAAACACC C TAAAACACC C TAAAACACC C TAAAACACC C TAAACC C TAAAACACC C TAAAACACC C TAAAACACC C TAAAACACC C TAAAACACC C TAACACC TAACACC C TAACA	GACATGAAGC GACATGAAGC GACATCAGG GACATCAGG GACACCC CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCAGC CTTGCCAAGC CTTGCCAAGC CTTCACGCT CTGACTGACC CTGACTGACC CTGACTGACC CTGACTGA CCGCAAATGC CTGCACACCC CTGACATGC CTGACATGC CTGCACACCC CTGCACACCC CTGCACACCC CTGCACACCCC CTGCACACCCC CTGCACACCCC CTGCACACCCC CTGCACACCCC CTGCACACCCC CTGCACACCCC CTGCACACCCC CTCCACACCCC CTCCACCCC TCCACCC CTCCACCCC CTCCACC CTCCACCC CTCCC	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TOCCCCCACC CATTTGCAA TCCACTGGAA TCCACTGGAC ATGGACAAGTA TCCACTGGAC AGGAGCCCAC TGGTCTTCCG	GCGTCCAGCT CTGGGCAGC CCGGGCATCC GGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGCT GACTCTTTCC CACTGGCAGC CCACGGACCG CCACGGACCC CCTGCCTCTC CGCCATCCCC 51 CCACAGCCCC CCCCACCCC CCCCACCCC CCCCCCCC	120 180 240 300 360 420 480 540 660 720 780 900 936
50 55 60 65	I HATGGGAAGA AAAAGGACAA	11 GCCACAGCCA TAAAATGCCA GCCACGGAGC CCCCGGAGC CCCCGGAGC TGGGAGAGAGAATA TGTGAGAAATA TGTGAGAGCTC TGGTGGCAC TTCTTCATCGT CTGCAGATCA TCCTCACATC GGACAGCCCC ACGTACACAC TGGTACACAC TGGTACACAC TGGTACACAC GGACAGCGCC ACGTACACAC TGGTACACAC TGGGAGGGGC 1 171 DNA Sc cid Accessic quence: 1-20 11 GATTTCATGT CTAATTCATGT CTAATTAAAC C CTACAGAATT	21 ACCCACAATO A GGACGGCCCC C GGCGCCCCC C GCGGCCCCAC C TACCATTGCACTC C TACCATTGCACTC C CAACCTTACGC C CAACCTTACGA A CTCTAAGGTAA C CTCAAAGTAA C CTGAAGTAA C CTGAAGTAA A GCACCTTGCAA A GCACCTTGCA A GGCCTGCAC C TACAAGTAA C TAAAAACACC C GGAGAAAAT	GACATGAAGC GGCTCGGCTC CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGCACCCC CTGTCTCACG CTGCTCTCACG CTGCTCTCACG CTGCTCTCACGCT CTTACTCACCA CGGGTGGAAA CGGGTGGAAA CGGGTGAAA CGGGTGAAA CGGGAATGC CTGCACACCA CGGTGAAA CGCGAAATGC CTGCACACCACAC	ACATGCAAGA AGAGCCCCCC CCGAGCCGGG AACGCCCTACG GGGAGCGCAC CATCTGCTAT TGCCCCCACC CCTTCTGGCA TTGACAAGTA TCCACTGGAG ATGTTACCAC TGGAGCCCA TCGTCTTCCT ACCCTTACAC 41 1 5 CAACACAAGTA AAGAAACTAC AAGAAACTAC AAGAAACTAC AAGAAACTAC ACTCTCTCT ACCCTCTCT ACCCTTACAC 41 1 1 CCAACACAAGTA AAGAAACTAC AAGAAACTAC AAGAAACTAC AACACATCTG	GCGTCCAGCT CTGGGCAGC CCGGGCATCC GGGACGGCCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTTC CACTGGCCAG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGCCC CTGCCTCTTC CGCCATCCCC	120 180 240 300 360 420 480 540 660 720 840 900 936
50 55 60	I HATGGGCAAGAAAATGGGATAAAAAAAAAAAAAAAAAAAA	II GCCACAGCCA TAAAATGCCA CACCAGGACA CACCAGGACA CACCAGGACA CACCAGGACA CACCAGGACA CACCAGGACA CACCAGGACA CACCAGATCA CACCAGTTCA CACCAGACAT CACCAGAAT CACCACAGAAT CACCACAGAAT CACCACAGAT CACCACAGAT CACCACAGAT CACCACAGAT CACCACAGAT CACCACAGAT CACCACAGAT CACCACAGAT CACCACAGAT CACCACAGAT CACCACAGAT CACCACAGAT CACCACAGAT CACCACAGAT CACCACACAGAT CACCACAGAT CACCACACAGAT CACCACACAGAT CACCACACACAC CACCACACACAC CACCACACACAC CACCAC	21 A ACCCACAATO A GGACGCCCCC GCCGGCCCCAC CCGCGCCCAC CCGCGCCCAC CCGCCCCCCC CCGGCCCCAC CCGCCCCAC CCGCCCCAC CCGCCCCAC CCGCCCCAC CCCCCCCC	GACATGAAGC GACATGAAGC GACATCAGG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG TTGTCCAAGG AGGTTCTACC TTGTCACAG CTGACTCACGCT TTGTACTCACGCT TTGTCACCG TTGTCACCG TTGTCACCG TTGTCACCG GACTGACCG TTGGCTGCT GTACTCACCCT GTACTCACCCT GTACTCACCCT GTCATCACCCC TTGGCCTGCT GTCATCACCCC TTGCACACCCC TTGCACACCCC TTTTGCAATCC TTTGCAATCC AATTTACAAGCA	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCTTAG GGGAGCGCA CATTGCTAT TGCCCCACC CTTTTGGCAG TTGACAGTA TCACTGGAA ATGGTACAG ATGGTACAG ACCTTACAG CTTCTTCT CCCTTCCCC CTTTTGCAG TCACTTACAG AACAAACAAG AACAAACAAAG AAAAACAAA	GCGTCCAGCT CCTGGGCAGC CCGGGGATCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTC CACTGGCCAG CCACTGGCCAG CCACTGGCCAG CCACTGGCCAG CCACTGGCCAG CCACTGGCCAG CCACTGGCCAG CCACTGGCCAG CCACTGGCCAG CCACTGCCAG CCACTGGCCAG CCACTGCCCAG CCACTGCCAG CCACTGCCAG CCACTGCCAG CCATCCCC 51 CCACATGGCAG CCAAAATTGAC CATCAGAGTG CCAAAGGGCTA CCACCCTATC	120 180 240 300 360 420 480 540 660 720 780 840 900 936
50 55 60 65	I HATGGGCAAG GCCTCGCCTT GGCCCCGGG GCGCCCCGGG GCGTCGCCC CCCCCGAG ATGTTTGGAT CCCTCCGAG GTGATTTGGAT GCCTCTCGAG GTGATTTGGAT GCCTTGTGAT ACATCCACC Seq ID NO Nucleic AC Coding set I ATGGGCAAG AAATGGGAT AAAGACAA ATATCCAGA AATACAGACAA ATATCCAGA	11 GCCACAGCCA TAAAATGCCA TAAAATGCCA TAAAATGCCA CCCCCGGAGC CCGCGGAGC TGGGTCGGG TGGAAAATAA GTGAAGACTC TGCTACAACC TCCCAGTTCC TGCTACAACC TCCTCACTCC GAGCAGCCCC ACGTAGACAA TGATCATCCC GGGAGGAGCCCC CGCACAGCCAACC CGCACAGCACACC CGCACAGCACC CGCACAGCACC CGCACAGCACC CGCACAGCACC CGCACAGCACC CGCACAGCACC CGCACAGCACC CGCACAGCACC CCCACAGCACC CCCCCACACC CCCCCACC CCCCCACACC CCCCCACACC CCCCCACACC CCCCCCACC CCCCCACACC CCCCCCACC CCCCCCACC CCCCCCACC CCCCCCACC CCCCCACACC CCCCCCACC CCCCCCACC CCCCCCACC CCCCCCACC CCCCCCCCC CCCCCCCCC CCCCCCCC CCCCCCCC	21 ACCCACAATO A GAACGCCCC C GCGGCCCCC C GCGGCCCCC C GCGGCCCCA C TACCATTGCT C TACCATTGCT C CAACCTTACE C CACCTTACE C CAACCTTACE C CAACCAACAA C TAAAACACCT T AAAACACCT T AAAACACCT C G GGGAAAAT A ACCCAAACA C GAACAACA C GAACAACAA C GAACAACAA C GAACAACAA C GAACAACAA C GAACAACAA C GAACAACAA C GAACAACAA C GAACAACAA C GAACAACAA C GAACAACAA C GAACAACAA C GAACAACAA C GAACAACAA C GAACAACAA C GAACAACAA C GAACAACAA C GAACAACAACA C GAACAACAACAACAA C GAACAACAACAA C GAACAACAACAACAACAACAACAACAACAACAACAACAAC	GACATGAAGC GACATGAAGC GACATCAGG GACATCAGG GACACCC CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCTCA CTGGCTCTCA CGGGACCC CTGCACACCC CTGACTCACC CGGACATGC CGGACATGC CGGACATGC CTGACATGC CTGCACACCC CTGCACACCC CTGCACACCC CTGCACACCC CTGCACACCC CTGCACACCC CTGCACACCC CTGCACACCC CTGCACACCC CTTGCACACCC CTTGCACACCC CTTCCAAAAC CTTTCCAAAAC CTTTCCAAAAC CTTTCCAAAAC CTTTCCAAAAC CTTCCAAAAC CTTTCCAAAAC CTTTCCAAAC CTTTCCAAAC CTTTCCAAAC CTTTCCAAAC CTTTCCAAAC CTTTCCAAAC CTTTCCAACC CTTTCCAACC CTTTCCAACC CTTTCCAAAC CTTTCCAACC CTTTTCCAACC CTTTTCCAACC CTTTCCAACC CTTTTCCAACC CTTTTCCAACC CTTTTCTCAACC CTTTTCCAACC CTTTT	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCGAGC GGGGAGCGCC CATCTGCTAT TOCCCCCACC CATTTGCAG TTGACAAGTA TCCACTGGAG ATGGTACAAGTA TCCACTGGAG ATGGTACAAGTA TCCACTGGAG AGAGCCCAC TGGTCTTACAC	GCGTCCAGCT CTGGGCAGC CCGGGCATCC GGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGCT GACTCTTTCC CACTGGCAG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTC CCACTGCAGCCC CTGCCTCTTC CGCCATCCCC	120 180 240 300 360 420 480 540 660 720 840 936
50 55 60 65	I HATGGGAGCAN ATATCCAGA ATATCCAGA ATGGGAACATATCAGATA ATACAGACATA GACCACACACACACACACACACACACACACACACACAC	11 GCCACAGCCA TAAAATGCCA CACCAGGAGC CACCAGGAGC CACCAGGAGC CACCAGGAGC TAGGAAATAA TAGAAATAA C CACAGGAGGAGGAGAGAGAGAA TAGAATAAAC CATACAGAATAAAC CATACAGAATAAAC CATACAGAATAAAC CATACAGAATAAAC CATACAGAATAAAC CATACAGAATAAAC CATACAGAATAAAAAAAAAA	21 ACCCACATO A GGACGGCCCC C GGCGCCCCC C GCGGCCCCC C GCGGCCCCA C TACCATTGCA C TACCATTGCA C CAACCTTACGC C CAACCTTACGC A CTCTAGAGC C CAACCTTACA A CTCTAGAGC C CAACCTTGCA C CTAAAGTAT C CTGTGAAGC C CAACCTTGCA C CTAAAGTAT C CTGTGAAGC C TAAAAACACC T AAAAACACC C TAAAACACC C ATCATCACT C GAGGAAAAT A ACCCAAACA C ATCATCACT C ATCATCACT C ATCATCACT C ATCATCACT C ACCACAACA C ATCATCACT C AACCACAC C ATCATCACT C ACCACAACA C ATCATCACT C ACCACACAC C ATCATCACT C ACCACACAC C ATCATCACT C C C C C C C C C C C C C C C C C C C	GACATGAAGC GGCTCGGTC CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGCTCTCACG CTTGCCAAGG CCTTCTACCC CTTGCCACGC CTTGCCTCCC CTTGCCACGC CTTGCCACGC CTTGCCACGC CTTGCCACGC CTTGCCTGC CTTCACCAC CTTGCCTGC CTTGCACACCA AATTACAAGC TTTTCCAAACG ATTTCCAAAGG CTTCCAAAACG CTTCCAAACC CTTCCAAAACG CTTCCAAAACG CTTCCAAAACG CTTCCAAAACG CTTCCAAAACG CTTCCAAAACG CTTCCAAAACG CTTCCAAAACG CTTCCAAAACG CTTCCAAAACG CTTCCAAACC CTTCCAAAACC CT	ACATGCAAGA AGAGCCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TCCACCTGACT TTGACAACTA TCCACTGGAA TTGACAACTA TCCACTGGAA TTGACAACTA TCCACTGGAA TTGACAACTA TCCACTGGAA TTGACAACTA TCCACTGGAA TAGTTACCAC AGAGCACAAAG AAGAAACTAA AAGAAACTAA AAGAAACTAA AAGAAACTAI AACACAATG AAAAACAAAG AAAAACAAAG AAGAACTTGG AAAAAACAAAG AAAAACAAAG AAAAAACAAAG AAAAAACAAAG AAAAAACAAAG AAAAACAAAG AAAAACAAAG AAAAACAAAG AAAAACAAAG AAAAACAAAG AAAAAACAAAG AAAAAACAAAG AAAAAACAAAG AAAAAACAAAG AAAAAACAAAG AAAAAACAAAG AAAAAAAA	GCGTCCAGCT CTGGGCAGC CCGGGGATCC GGGACGGCCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTTC CACTGGCCAG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTC CGCATCCCC 51 1 CCAAAATTGAC CAAAACCGAC CGAAACCGACC CTGCGCTAGCC CACTGGGGCAGCC CACTGGGGCC CACTGCCCC CACTGCCCC CCAAAATTGAC CAAAACCAAC CCAAAACCAAC CCAAAACCAAC CCAAAACCAAC CCAAAACCAAC	120 180 240 300 360 420 480 540 660 720 840 903 660 120 180 240 300 360
50 55 60 65	I HATGGGAGCAN ATATCCAGA ATATCCAGA ATGGGAACATATCAGATA ATACAGACATA GACCACACACACACACACACACACACACACACACACAC	11 GCCACAGCCA TAAAATGCCA CACCAGGAGC CACCAGGAGC CACCAGGAGC CACCAGGAGC TAGGAAATAA TAGAAATAA C CACAGGAGGAGGAGAGAGAGAA TAGAATAAAC CATACAGAATAAAC CATACAGAATAAAC CATACAGAATAAAC CATACAGAATAAAC CATACAGAATAAAC CATACAGAATAAAC CATACAGAATAAAAAAAAAA	21 ACCCACATO A GGACGGCCCC C GGCGCCCCC C GCGGCCCCC C GCGGCCCCA C TACCATTGCA C TACCATTGCA C CAACCTTACGC C CAACCTTACGC A CTCTAGAGC C CAACCTTACA A CTCTAGAGC C CAACCTTGCA C CTAAAGTAT C CTGTGAAGC C CAACCTTGCA C CTAAAGTAT C CTGTGAAGC C TAAAAACACC T AAAAACACC C TAAAACACC C ATCATCACT C GAGGAAAAT A ACCCAAACA C ATCATCACT C ATCATCACT C ATCATCACT C ATCATCACT C ACCACAACA C ATCATCACT C AACCACAC C ATCATCACT C ACCACAACA C ATCATCACT C ACCACACAC C ATCATCACT C ACCACACAC C ATCATCACT C C C C C C C C C C C C C C C C C C C	GACATGAAGC GGCTCGGTC CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGCTCTCACG CTTGCCAAGG CCTTCTACCC CTTGCCACGC CTTGCCTCCC CTTGCCACGC CTTGCCACGC CTTGCCACGC CTTGCCACGC CTTGCCTGC CTTCACCAC CTTGCCTGC CTTGCACACCA AATTACAAGC TTTTCCAAACG ATTTCCAAAGG CTTCCAAAACG CTTCCAAACC CTTCCAAAACG CTTCCAAAACG CTTCCAAAACG CTTCCAAAACG CTTCCAAAACG CTTCCAAAACG CTTCCAAAACG CTTCCAAAACG CTTCCAAAACG CTTCCAAAACG CTTCCAAACC CTTCCAAAACC CT	ACATGCAAGA AGAGCCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TCCACCTGACT TTGACAACTA TCCACTGGAA TTGACAACTA TCCACTGGAA TTGACAACTA TCCACTGGAA TTGACAACTA TCCACTGGAA TTGACAACTA TCCACTGGAA TAGTTACCAC AGAGCACAAAG AAGAAACTAA AAGAAACTAA AAGAAACTAA AAGAAACTAI AACACAATG AAAAACAAAG AAAAACAAAG AAGAACTTGG AAAAAACAAAG AAAAACAAAG AAAAAACAAAG AAAAAACAAAG AAAAAACAAAG AAAAACAAAG AAAAACAAAG AAAAACAAAG AAAAACAAAG AAAAACAAAG AAAAAACAAAG AAAAAACAAAG AAAAAACAAAG AAAAAACAAAG AAAAAACAAAG AAAAAACAAAG AAAAAAAA	GCGTCCAGCT CTGGGCAGC CCGGGCATCC GGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGCT GACTCTTTCC CACTGGCAG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTC CCACTGCAGCCC CTGCCTCTTC CGCCATCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 936
5055606570	I I ATGGGCCAA GCACACACA AACAAGTGGAACACAA GCACACACACACACACACACACACACACAC	II GCCACAGCCA TAAAATGCCA CACCAGGAGC CACCAGGAGC CACCAGGAGC TAGAAAATACCA TAGTGAGAACT TAGTGAGAACT TAGTGAGAACT TAGTGAGACC TAGCAATCC TAGCAATCC TAGCAATCC TAGCAATCC TAGCAATCC TAGCAATCC TAGCAATCC TAGCAATCC TAGCAATCC TAGCAATCC TAGCAATCC TAGCAATCC TAGCAATCAACC TAGCAATCAACC TAGCAATCAACC TAGCAATCAACC TAGCAATCAACC TAGCAACCAACC TAGCAACCAACC TAGCAACCAACC TAGCAACCAACC TACCAACCAACC TACCAACCAACC TATCAAATCAACC TATCAACAACC TATCAACAACC TATCAACAACC TATCAACAACC TATCAACAACC TATCAACAACC TATCAACACC TATCAACACC TATCAACACC TATCAACACC TATCAACACC TATCAACC TATCAACACC TAGCAACC TACCACACC TAGCAACC 21 ACCCACAATO A GGACGCCCCC GCCGGCCCCCC CCCGGCCCCAC CCCGGCCCCAC CCCGCCCCAC CCCGGCCCCAC CCCGCCCCAC CCCGCCCCAC CCCCGCCCCAC CCCCGCCCAC CCCCCCCC	GACATGAAGC GGCTCGGTC CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCAGG AGGTTCTACC CTTGTCACGT CTTACTCACGT CTTACTCACGT CTTACTCACGT CTTACTCACGT CTTACTCACGT CTTACTCACGT CTGACTACCA AGGGTGGAAA CGCTGACTGAC CTGCACACGA TTTGCACA AAAAGCAATGC CTGCACACGAA TTTTCCAATGC AATTTACAAGG CTTCTCAAAAAG CGCCATCAAAA	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCTTAG GGGAGCGCA CATTGCTAT TTGCCCCACC TTGGCAG TTGACAGTA TTGACAGTA TTGACAGTA TTGACAGTA TTGACAGTA TTGACAGTA TTGACAGTA TTGACAGTA TTGACAGTA TTGACAGTA TTGACAGTA TTGACAGTA TTGACAGTA AGAGCACTAC AGAGAACTAC AGAGAACTAC AGAGAACTAC AGAGAACTAC AAAAAACAAG AAAAACAAG AAAACAAG AAAACCAAG AAAACCAAG AAAACCAAG AAAACCAAGC AAAAACCAAGC AAAACCAAGC AAAACCAAGC AAAACCAAGC AAAACCAAGC AAAACCAAGC AAACCAAGC AAAACCAAGC AAAACCAAGC AAAACCAAGC AAAAACCAAGC AAAAACCAAGC AAAAACCAAGC AAAAACCAAGC AAAAACAAAC	GCGTCCAGCT CTGGGCAGC CCGGGGATCC GGGACGGCCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTTC CACTGGCCAG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTC CGCATCCCC 51 1 CCAAAATTGAC CAAAACCGAC CGAAACCGACC CTGCGCTAGCC CACTGGGGCAGCC CACTGGGGCC CACTGCCCC CACTGCCCC CCAAAATTGAC CAAAACCAAC CCAAAACCAAC CCAAAACCAAC CCAAAACCAAC CCAAAACCAAC	120 180 240 300 360 420 480 540 660 720 840 903 660 120 180 240 300 360	
50 55 60 65	I HATGGGCCAA GCCTCGCCTT GGCCCCCGGGGGGGGGACCCCCT CACCCCGAGGATCTCCTCGAGCCTTCCTCGAGCCTTCTCTCAGATCCTCTCTCAGATCCTCTCTCAGATCCTTCTCTCAGATCATTTGGATCATTTCGTACACACAC	11 GCCACAGCCA TAAAATGCCA TAAAATGCCA TAAAATGCCA CCCCCGGAGC CCGCGGAGC TGGGAGAATAA GTGAAGACTA TCTTCACCAGTCC TCGCACTACCAGTCC TCGCACTACCAGTCC TCGCACTACCAGTCC TCGCACTACCAGTCC TCGCACTACCAGTCC TCGCACTACCAGTCC TCGCACTACCAGTCC TCGCACTACCAGTCC TCGCACTACCAGTCC TCGCACACTACCAGTCC TAATAAACCC TAACACAGATTACCACTACCAGCCCAGCAGCATTACACATCC CCGAAGGATTACACTCC CCGAAGGATTACACTCC CCGAAGGATTACACTCC CCGAAGGATTACACTCC CCGAAGGATTACACTCC CCGAAGGATTACACTCC CCGAAGGATTACACTCC CCGAAGGATTACCACTCC CACCACCCCACCCC TAACTCCACACCC CCGAAGGATTACCCCC CCGAAGGATTACCCCC CACCACCCCCC CACCACCCCCCCCCCCC	21 ACCCACAATO A GAACGCCCC C GCGGCCCCC C GCGGCCCCA C CACCTTACC C TACCATTGC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTACC C TAAACACC C TAAACACC C TAAACACC C TAAACACC C ACCTACAC C ACTACACT C ACTACACT C ACTACACT C ACTACACT C ACTACACAC C ACTACACAC C ACTACACAC C ACTACACAC C ACTACACT C ACTACACAC C ACTACAC GACATGAAGC GACATGAAGC GACATCAGG GACATCAGG GACACCC CTGACCCG CTGACCCG CTGACCCG CTGACCCG CTGACCCG CTGACCCG CTGCACCC CTGCCTCAC CTGCCTCAC CTGCCTCAC CTGCCTCAC CTGCCTCAC CTGCCTCAC CTGCCACAC CTGCACACA CACCACACA CTTCCAAAA CTTCCAAAAC CTTCCAAAAC CTTCCAAAAC CTTCCAAAAC CTTCCAAAAC CTTCCAAAAC CTTCCAAAAC CTTCCAAAAC CTCCAAAAC CTCCAAAAC CTCCCAAACACAC CTTCCAAAAC CTCCCAAACACAC CTTCCCAAAAC CTCCCAAAAC TCCCAAAAC CTCCCAAAAC CTCCCAAAAC CTCCCAAAC CTCCAAAC CTCCCAAAC ATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCGAGC GGGGAGCGCC CATCTGCTAT TCCCCCCACC CATTTGCAA TCCACTGGAA TCCACTGGAC TGACAAGTA TCCACTGGAC TGACAAGTA TCCACTGAC TGACAAGTA TCCACTGAC TGACAAGTA TCCACTGAC TAGACAAAGC TAGACAAAGC AAGAAACTAA	GCGTCCAGCT CTGGGCAGC CCGGGCATCC GGGACGGCC AGCTACTGG TCTCACCACT TTTACTGTCT GACTCTTTC CACTGGCAG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACCC CTGCCTCTTC CGCCATCCCC 51 CAAAATTGAC CATCAGAGTG CGAAACCCAAC CAAAACCACA CAAAACCACA CAAAACCACA CAAAACACAA CAAACACAA CAAACACACA CAAACCACAA CAAACACAA CAAACACCAC	120 180 240 300 360 420 480 540 600 660 720 780 840 936		
5055606570	I I ATGGGCCAA GCCTCGCTT GCCTCGCGAGCC ACACCACCCT TCCCCAAGCC ATGTTTGGAT CTCTCCAGG GCGAGGAGAA ACATCACCT I I I ATGGGCAAGAAAAATGGAAAAATGGAAAAATGGAAAAAATGGAAAAAA	11 GACCACAGCCA TANANTGCCA TANANTGCCA GCCCCGGAGG CCCCCGGAGG CCCCCGGAGG CTGGAGACTG CTGGCAA TGTGAAGACTG CTGTCACAACG CACAGTTC TGTCACAACG ACGAGAGACACG CACAGAGATA ATATAAAC CTACAGATTC CTACAGATTC I I GATTCACATC CTACAGATT CTACAATG CTACAGAAT ATCATCACAC CTACAGAAT ATCACAATG CTACAGAAT ATCTACAATG CTACAGAAT ATCTACAATG CAACAGCCAA AAAAATGCT CATCCACAC GACAGACGACA GACAGCCCAA	21 A ACCCACAATO A GAACGCCCC GCGGGCCAG CCGGGCCAG CTACCATTACA CTCTAACTA CTCTAACTA CTCTAACTA CTCTAACTA CTCTAACTA CTCTAACTA CTCTAACTA CTCTAACTA CTCTAACTA CTCTAACTA CTCTAACTA CTCTAACTA CTCTAACTA CTCTACAACTA CTCTACAACTA CTCTACAACTA CTCTACAACTA CTCTACAACTA CTCTACAACTA CTCTACAACTA CTCTACAACTA CTCAAACAA CTCAAACAA CTCAAACAA CTCAACAACA CTCATCACTC CATCATCACTC CATCATCACTC CATCATCACTA CTCACACTCAT CACACTCAT CTCACACTCAT CACACTCAT CTCACTCA	GACATGAAGC GACATGAAGC GGCTCGGTC CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGCTCTCACGCT CTGCTCTCACGCT CTGCTCTCACGCT CTGCTCTCACGCT CTGCTCACGCT CTGCACCAC CTGCACTCCACGCT CTGCACCACCACCACCACCACCACCACCACCACCACCACCAC	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCCTAC GGGAGCGGC CATCTGCTAT TGCCCCCACC CCTTCTGGCA TTGACAAGTA TCCACTGGAA TTGACAACTA TCCACTGGAA TTGACAACTA ACCCTTACAC 41 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GCGTCCAGCT CTGGGCAGC CCGGCGATCC GGGACGGCCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTTC GACTCTTTTC CACTGGCAG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCACTGCCTCTTC CGCCATCCCC 51 1 2 CAAAATTGAC CATCAGAGTG CGAAACCGAA CGAAACCACA CAAACCACA CAAACCACA CAAACCACA CAAACCACA CAAACCACA CAAACACACA CAAACACACA CAAACCACA CACGCCACC CACGCCACC CACGCCACC CACGCCACC CACGCCACC CACGCCACAC CACACCCACA CACGCCACAC CACACCCACAC CACACAC CACACCCACAC CACACAC CACACCCACAC CACACCCACAC CACACCCACAC CACACCCAC CACACCCAC CACACAC CACACCCAC CACACCCAC CACACCCAC CACACCCAC CACACCCAC CACACCCAC CACACCCAC CACACCCAC CACACCCAC CACACCCAC CACACCCAC CACACCCAC CACACAC CACACCCAC CACACCCAC CACACCCAC CACACCCAC CACACCCAC CACACCCAC CACACCCAC CACACCCAC CACACCAC	120 180 240 300 360 420 480 540 660 720 840 903 660 120 180 240 300 420 480 420 480 540
5055606570	I HATGGAGCCAA GCCCCCGAGC GCGGCCCCCCACCCCACC	II GCCACAGCCA TAAAATGCCA CACCAGGAG CCCCGGAGG CCCCGGAGG CTGGAAAATACCCA TAGAAAATACC TAGCAGACCA TAGCAACCCA TACTACAACC TACTACAACC TACTACAACC TACTACAACC TACTACAACC TACTACAACC TACTACAACC TACTACAACC TACTACAACC TACTACAACC TACTACAACC TACTACAACC TACAGAATA TACTACAACC TACTCACACC TACTTCACACC TACTTCACACC TACTTCACACC TACTTCACACC TACTTCACACC TACTTCACACC TACTTCACACC TACTTTTAA	21 ACCCACAATO A GAACGCCCC C GCGGCCCCCC C GCGGCCCCCC C GCGGCCCCC C GCGGCCCCC C GCGGCCCCC C GCGGCCCCA C CAACTATGCA C CAACCTTACA A CTCTAAGCT C CAACCTTACA A CTCAAAGTAT A AGGGCTGAC C CAACCTGGAC C C TAAAACACC C TAAAACACC T AAAGAGCTT G GGAGAAAT A ACCCAAACA T GAACAGCA C ATTACAACC C ATTAGAACA C ATCACAACA T GAACAGCA C ATCACACCAT T CAGTTAGGAAA A C ACCACCAT T AACCAACCA T CAGTTAGAAT A ACCGAGAAA T CACACCCAT T CGCACTGGT C AGTTAGAAT A CCCAACCTCAT T GCCACTGGT T GCCACTGGT	GACATGAAGC GACATGAAGC GACATGAAGC CTGACTCCTG CTGACCCGG TTGTCCAAGG AGGTTCTACC TTGTCACAGG TTGTCACAGG TTGTCACAGG TTGTCACAGG TTGTCACAGG TTGTCACAGG TTGTCACAGG TTGTCACAGG TTGTCACAGG TTGTCACAGG TTGCACAGGATTG GACTGA AAAAGCAATGC TTTCCAAAGG TTTTCAAAGG TTTTCAAAGG ATTTTCAAAGG GCCATCAGA GGCCATCAGG GGCAATCAGG TTTTCCAAATC TTTCCAAATC TTTCCAAAGG GGCCATCAGG TTTTCCAATC TTTCCAAAGG GGCCATCAGG TTTTCCAAAGT TTTCCAATC TTTCCAAAGT TTTCCAAAGT TTTCCAATC TTTCCAAACT TTTCCAAACT TTTCCAAACT TTTCCAAACT TTTCCAAACT TTTCCAACT TTCCAACT TTTCCAACT TTTCAACT TTTCCAACT	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCTTAG GGGAGCGCA CATTGCTAT TGCCCCACC CATTGGCAG TTGACAGTA TCACTGGCAG ATGGTACCAG ATGGTACCAG CATTGCAG AAGAACTAC AAGAACTAC AAAAAACAAA AAAAACAAA AAAAACAAA AAAAACAAA AAAAACAAA AAAAACAAA AAAAACAAA AAAAACAAA AAAAACAAA AAAAACAAA	GCGTCCAGCT CTGGGCAGC CCGGGGATCC AGCTACTGGG AGCTACTGGG TCTACCACT TTTACTGTCT GACTCTTTC CACTGCCAG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAAAATTGAC CATCAGGTAG AGAGGGCTA CACACACA CAAAACCACA CAAAACCACA CAAAAACACAA CAAAAACACAA CCTTATTAGT	120 180 240 300 360 420 480 660 660 720 780 840 936 60 120 180 360 360 420 480 540 660
5055606570	I HATGGAGCCAA GCCTCGCCTT GGCCCCCGGG GGGTCGCCC CACCCCAGGG ATGTTTGGAT CACTTGGATC CTCTCCAGG GTGATTTGGT GGCGGAGGAA CACACACCACCT ACACCACACC	11 GCCACAGCCA TAAAATGCCA TAAAATGCCA TAGAAATAA GCCCCGGGAC TGGGGCGGAC TGGGAAATAA GTGAAGACTA TCTTCACCAGTCC TCCACTCCAGTCC TCGTACACCC TCCACTCCAGTCC TCGTACACCC TCCACTCCAGTCC TCGTACACCCC TCCACTCCCAGTCC TCGTACACCCC TCCACTCCCAGTCC TCGTACACACCCC TCCACACCCCCC TAATAAACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	21 ACCCACAATO A GAACGCCCC C GCGGCCCCC C GCGGCCCCC C GCGGCCCCA C CACCTTACC C TACCATTGC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCTTACC C CACCAAGTAA A CACCAACAA A CACCAACAA A ACTGAGAA C AACTACACT A AACTGAGAA C AACTACACT C ACACTCAT C ACCACTCAT C ACCACTCAT C ACCACTCAT C ACCACTCAT C ACCACTCAT C CACACCACA C CACACCACA C ACACACACA C ACACACAC	GACATGAAGC GACATGAAGC GACATCACGCA CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCTAC CTGCCTCTCACCT CTGACTCTACCC CTGACTCTACCC CTGACTCTACCC CTGACTGACCC CTGACACCAC CTGACACCAC CTGACACCAC CTGACACCAC CTTCCAACAC CTTCCAACAC CTTCCAACAC CTTCCAACACCAC CTTCCAACACCACCACCACCACCACCACCACCACCACCAC	ACATGCAAGA AGAGCCCCT CGAGCCGGG AACGCCGAGCGGG GGGAGCGCC CATCTGCTAT TCCCCCCACC CATTTGGCA TTGACAAGTA TCCACTGGAT TCCACTGCAT TCCACTGCAT TCCACTGCAC TTGACAAGTA TCCACTGCAC TGACAAGTA TCACTGCAC TGACAAAGT AACAAAAGCAAG AAAAAACAAAG AAAAACAAAG AAAACAAAG AAACAAAG AAAACAAAG AAACAAAG AAAACAAAG AAACAAAG AAAACAAAG AAG AAAACAAAACAAAC	GCGTCCAGCT CTGGGCAGC CCGGGCATCC GGGACGGCC AGCTACTGG TCTCACCACT TTTACTGTCT GACTCTTTCC CACTGGCCAG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTC CCACTACTACCCC 51 CCACAAACTCCAC CGAAACTCACC CAAAACTCACA CAAAACCACAA CAAAACCACAA CAAAACAACAA	120 180 240 300 360 420 480 540 660 720 780 840 900 936 60 120 180 240 360 420 480 540 660
5055606570	I I ATGGAGCCAA GCCTCGCGT GGAGCCTCGCGAGCC ACACCACCCT ACACCACCCT ACACCACCCT ACACCACCACCACCACCACCACCACCACCACCACCACCA	11 GCCACAGCCA TAAAATGCCA TAAAATGCCA TAAAATGCCA COCCGGAGG CCCCGGAGG CCCCGGAGG TGGAGAACTC TGGTGGCAG TGTTATCATG TGTTATCATG TGTACAACTC TGGTACAACTC TGATTAAACTC TATTAAACTC TATTCAACTA TATTCAACTC TATCAACTC TATCTACACC TATCTACACC TATCTACACC TATCTACACC TATCTACACC TTCCTTTAA TCTCATTTAACTC TTCCTTTAACTC TCCTTTAACTC TTCCTTTAACT TTCCTTTAACTC TTCCTT	21 A ACCCACAATO A GAAGGGCCCC GCGGGCCCAG CGGGGCCAG CTACCATTACA CTCTAAGCT CTACCATTACA CTCTAAAGTAT CTCTAAAGTAT CTCTAAAGTAT CTTACAAGTAT CTTAAAACACA CTAAAACAAA A ACCCAAACA CTAAAACAAA A ACCCAAACA CATCATCACT C AGTTAGAAC C ATCATCACT C AGTTAGAACA A ACCCAAACA A CACCATCAT C AGTTAGAAT A ACCCAAACA A T CAACATCAT T GACCATCAT C AGTTAGAAT A CACCATCAT T GCACTCAT C AGTTAGAAT A CACCATCAT T GCACTCAT C AGTTAGAAT A CACCATCAT T GCACTCAT T GCACTCAT C AGTTAGAAT A CACCATCAT T GCACTCAT A CACAACAAA T GTTGACCT T GTTGACCT	GACATGAAGC GGCTCGGTC GGACTCCGG GGCTCGGTC GGACTCCGG GCACACCGG CTGACTCCAG CCAGGACCCC TTGTCCAAGG ACGTTCTACCC GTACTCACGC GGAGTGAAA GGGGTGAAA GGGGTGAAA GGGTGAAA GACCTGCAGCA GACCTGCAGCAGACCC TTGCCTGC GTCATCAACC TTGCACCAGCAA ATTTACAAAC GGCCATCAACA GGCCATCAATG GGCCATCAATG GGCATCAATG GATCAATG GGCATCAATG G	ACATGCAAGA AGAGCCCCA AGAGCCCGAG ACACCCCACC CATTGCTAT TGCCCCCACC CATTGCTAT TGCCCCACC CATTGCGAG ATGGTACAGA ATGGTACAGAG AGAGCCCAAC TCGTCTTCCT ACCCTTACAG 41 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GCGTCCAGCT CTGGGCAGC CCGGCGATC CGGGCAGC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTTC GACTCTTTTC CCACTGGCAG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGAGGCC CTGCCTCTTC CGCCATCCCC 51 1 2 CAAAATTGAC CAAAATTGAC CAAAACGGAAC CAAAACGAA ACAACACA AAACACAA AGATATTCGC CACTGATCCCC CACTGGTCAAT CCATATATAGT CTCAAGAGAG TCCTGCCTTTT CTCAAGAGAAG TTCTGCCTTTT CTCAAGAAGAAC TTCTGCCTTTT CTCAAGAAGAAC TTCTGCCTTTT CTCAAGAAGAAC TTCTGCCTTTT CTCAAGAAGAAC TTCTGCCTTTT CTCAAGAAGAAC TTCTGCCTTTT CTCAAGAAGAAC TTCTGCCTTTT CTCAAGAAGAAC TTCTGCCTTTT CTCACTCTCTTT CTCACTCTCTTT CTCACTCTCTTT CTCACTCTCTTT CTCACTCTCTT CTCACTCTCTT CTCACTCTCTT CTCACTCTCTT CTCACTCTCTT CTCACTCTCT CTCACTCTCTT CTCACTCTT CTCACTCTCT CTCACTCTCT CTCACTCTCT CTCACTCTCT CTCACTCTCT CTCACTCTCT CTCACTCTCT CTCACTCTCT CTCACTCTCT CTCACTCTCT CTCACTCTCT CTCACTCTCT CTCACTCT CACTCT CTCA	120 180 240 300 360 420 480 540 660 720 840 903 660 120 180 240 300 420 480 660 660 720
505560657075	I HATGGAGCCAA GCCTCGCCTTGGCAGCACCCACCCACCCACCCACCCACCC	11 GCCACAGCCA TAAAATGCCA TAAAATGCCA CACCCGGAGC CGGGAGC CGGGCCGGAGC TGGAAAATAA GTGAAGACTC TGCTACAACC TCCTACAACC TCCTACACCACC GAGCAGCCCC GAGCAGCCCC GAGCAGCCCC GAGCAGCCCC GAGCAGCCCC GAGCAGCCCCC GAGCAGCCCCCC GAGCAGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	21 ACCCACAATO A GAACGACCCC C GCGGGCCCCC C GCGGGCCCCC C GCGGCCCCC C CACCTTGAC C CACCTTGAC C CACCTTGAC C CACCTTGAC C CACCTGAC C GCGCCCC C CACCTGAC C CACCTGAC C CACCTGAC C TAAAACACC C TAAAACACC C TAAAACACC C ATCACCTGAC C ACCACCAT A ACCCAAACA T GAACAGAAA T GAACACAA T GCCACTGGT A CTGAGCAA T GCCACTGGT A CTGAGCAC T GCCACTGGT A CACAACAA T GCCACTGGT A CACAACAA T GCCACTGGT A CACAACAA T GCCACTGGT T GCCACTGGT T GCCACTGGT T TTCCTTGTGT T TTCCTTGTG	GACATGAAGC GACATGAAGC GACATGAAGC GACATCAGG CTGACCCG CTGACCCG CTGACCCGG CTGACCCG CTGTCTCAC CTGCTCTCA CTGCTCTCA CTGCTCTCA CTGCTCTCACT CTGACTCAC CTGCACACCC CTGCACACCC CTGCACACCC CTTCACACC CTGCACACCA CTGCACACCA CTGCACACCA CTGCACACCA CTTCCAAAAC CTGCACACCA CTTTCCAAAAC CGCCATCAGA CGCACACCAC CTTTCCAAAAC CGCACACCAC CTTTTCCAAAC CGCATCAGAC CGTATTACATC CGTATTACACT CGTATTACAC CGTATTACACT CGTATTACT CGTATTACT CGTATTACT CGTATT CGTATTACT CGTATT CGT	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCGAG GGGAGCGCAC CCTTCTGGCA CCTTTTGGCA TCGACCAGG ATGCAAGT TCCACTGGAT TCCACTGGAC AAGAAACTAC AAGAAACTAC AAGAAACTAC AAGAAACTAC AAGAAACTAC GATCATTGGA AAGAAACTAC AAGAAACTAC GATCATCGG AAGAACTAC GATCATCGG AAGAAACTAC GATCATCGG AAGAACTAC GATCATCGG AAGAAACTAC GATCATCGG AAGAACTAC GATCATCGG AAGAAACTAC GATCACCG AAGAAACTAC GATCACCG AAGAAACTAC GATCACCG AAGAAACTAC GATCACCG AAGAAACTAC GATCACCG AAGAAACTAC GATCACCG AAGAAACTAC GATCACCG AAGAAACTAC GATCACCAC AAGAAACTAC GATCACCAC AAGAAACTAC GATCACCAC AAGAAACTAC GATCACCAC AAGAAACTAC GATCACCAC AAGAAACTAC GATCACCAC AAGAAACTAC AAGAACTAC AAGAACTAC AAGAAACTAC AAGAAACTAC AAGAAACTAC AAGAAACTAC AAGAACTAC AAGAAACTAC AAGAACTAC AAGAACTACAC AAGAACCAAAC AAGAAACTAC AAGAACTACAC AAGAACCAAC AAGAAACTAC AAGAACAAAC AAGAACTAC AAGAACAAAC AAGAACTAC AAGAACAAAC AAGAACAAAC AAGAACAAAC AAGAACAAAC AAGAACAAAC AAGAACAAAC AAGAACAAAC AAGAACAAAC AAGAACAAAC AAGAACAAAC AAGAACAAAC AAGAACAAAC AAGAACAAAC AAGAACAAAC AAGAACAAAC AAGAACAAAC AAGAACAAAC AAGAACAAAC AAGAAACAAAC	GCGTCCAGCT CTGGGCAGC CCGGGCATCC GGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGCT GACTCTTTC CACTGGCAGC CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGAGCCC CTGCCTCTTC CGCCATCCCC 51 CAAAATTGAC CAAAACCACA CAAAACCACA CAAAAACCACA CAAAAACCACA CACGGTCATC CACTGGTCATT CTGCACCTTTG CTGCACTTTG CTGCACCTTTG CTGCAGCAGAGGG CACTGGTCAAT CCTTATTAGT CTGCACCTTTG CTGCCCTTTG CTGCCCTTTG CTGCCCTTTG CTGCCCTTTG CTGCCCTTTG CTCCCCTTTG CTCCCTTTG CTCCCCTTTG CTCCCCTTTG CTCCCCTTTG CTCCCTTTG CTCCTTTG CTCCCTTTG CTCCTCCTTTG CTCCTTTG CTCCTTTG CTCCTTTG CTCCTTTG CTCCTTTG CTCCTTTTTC CTCCTTTTTTTT	120 180 240 300 360 420 480 540 660 720 780 840 936 540 360 240 360 480 540 480 540 660 720
5055606570	I HATGGAGCCAA GCCTCGCCTT GCCCCCGAGGGGGGGGGAGGAGGAGGAGGAGGAAGAAGGGAAGAA	11 GCCACAGCCA TAAAATGCCA TAAAATGCCA TAGAAATAA GTGAGGCA TGGGTGGGC TGGGAGAATAA TGTCACACTC TGCTACAACTC TGCTACACTC TGCTACACTC TGGTACACCC ACCATTACACTC GGGAGGAGC 171 DNA S CID ACCACTC TACAACTC TACAACTC TACAACTC TACAACTC TACAACTC CAACAGCCAA CAACACCAACTA CAACAACTA GAACAGCCAA GAACAGCCAA GAACAGCCAA GAACAGCCAA GAACACCAACTA GAACAACTA CAACAACTA CAAC	21 ACCCACAATO A GGACGCCCC C GCGGGCCCCC C GCGGGCCCAC C TACCATTGCA C CAACCTTACC C TACCATTGCA C CAACCTTACA C CAACCTTACA C CAACCTTACA C CAACCTTACA C CAACCTTACA C CAACCTTACA C CAACCTTACA C CAACGCAA C CAACCCTGCA C CAGCCCCGCA C CAGCCCCGCA C CAGCCCTGCA C CAGCCCTGCA C CAGCCCTGCA C CACCCAACCA C ATCATCACT C AGTTAGAAT T GAACAGCA T GAACAGAAA T GACACCTCAT T GCCACCCCT A CACACCAACAA T GTTGACCCT T TTCCTTGTC T TTCCTTCT T TTCCTTCT T TTCCTTCTTC T TTCCTTCTTC T TTCCTTCT T TTCCTTCT T TTCCTTCT T TTCCTTCTTC T TTCCTTCTTC T TTCCTTCT T TTCCTTCT T TTCCTTCTTC T TTCCTTCT T TTCCTTCTTC T TTCCTTCT T TTCCTTCT T TTCCTTCT T TTCCTTCT T TTCCTTCT T TTCCTTCT T TTCTTCT T TTCCTTCT TCCT T TTCCTTCT T TTCCTTCT T TTCCTTCT T TTCCTTCT T TTCCT T TTCT	GACATGAAGC GGCTCGGTC CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGCTCTCACC CTGCTCTCACC CTGCTCTCACC CTGCTCTCACC CTGCTCTCACC CTGCTCTCACC CTGCTCACC CTGCTCACC CTGCTCACC CTGCTCACC CTGCTCACC CTGCACACC CTGCACACC CTTCACACC CTGCACACC CTGCACACC CTGCACACC CTGCACACC CTTCCAAAAC CGCACACCAC CTTCCAAAAC CGCACACCAC CTTTACACG CTCTCAAAAC CGCACACC CTTCCAAAAC CGCACACC CTTCCAAAAC CGCACACC CTTCTCAAAAC CGCACACC CTTTACACC CTTCTCAAAAC CGCACACC CTTTACACC CTTCTCAAAAC CGCACACC CTTTTACACC CTTTTACACC CGCACACC CTTTTACACC CGCACACC CTTTTACACC CTTTTACACC CTTTTACACC CTTTTACACC CTTTTACACC CTTTTACACC CTTTTTACACC CTTTTTTTC CTTTTTTC CTTTTTC CTTTTTTC CTTTTTT	ACATGCAAGA AGAGCCCCT CGAGCCGGG AACGCCGCAG GGGAGCGCC CATCTGGCA TGCCCCACC CATTTGGCAG TTGACAAGTA TCCACTGGAG TTGACAAGTA TCCACTGGAG ATGGTACAAGTA TCCACTGGAG AGAGCACAAG TGGTATATG AAAAACAAAG AAAAAACAAAG AAAAAACAAA TACTGCATGAA AAAAACAAAG TACTGATTATA AAAACCAAAG AAAAACCAAAG AAAACCAAAG AAAAACCAAAG AAAAACCAAAG AAAAACCAAAG AAAAACCAAAG AAAAACCAAAG AAAAACCAAAG AAAAACCAAAG AAAAACCAAAG AAAACCAAAG AAAACCAAG AAAACCAAG AAAACCACACAC AAACCACACAC AAACCACACAC AAACCACACAC AAACCCCGCT	GCGTCCAGCT CTGGGCAGC CCGGGCATCC GGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTTC CACTGGCCAG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CAGGGCCATCCCC 51 CAAAATTGAC CATCAGAGTG CGAAACACAA AAACAACAA AAAACAACAA AAAACAACAA	120 180 240 300 360 420 480 540 660 720 840 900 936 60 120 180 240 360 420 480 540 660 720 780
505560657075	I HATGGAGCCAA GCCTCGCCTT GCCCCCGAGGGGGGGGGAGGAGGAGGAGGAGGAAGAAGGGAAGAA	11 GCCACAGCCA TAAAATGCCA TAAAATGCCA TAGAAATAA GTGAGGCA TGGGTGGGC TGGGAGAATAA TGTCACACTC TGCTACAACTC TGCTACACTC TGCTACACTC TGGTACACCC ACCATTACACTC GGGAGGAGC 171 DNA S CID ACCACTC TACAACTC TACAACTC TACAACTC TACAACTC TACAACTC CAACAGCCAA CAACACCAACTA CAACAACTA GAACAGCCAA GAACAGCCAA GAACAGCCAA GAACAGCCAA GAACACCAACTA GAACAACTA CAACAACTA CAAC	21 ACCCACAATO A GGACGCCCC C GCGGGCCCCC C GCGGGCCCAC C TACCATTGCA C CAACCTTACC C TACCATTGCA C CAACCTTACA C CAACCTTACA C CAACCTTACA C CAACCTTACA C CAACCTTACA C CAACCTTACA C CAACCTTACA C CAACGCAA C CAACCCTGCA C CAGCCCCGCA C CAGCCCCGCA C CAGCCCTGCA C CAGCCCTGCA C CAGCCCTGCA C CACCCAACCA C ATCATCACT C AGTTAGAAT T GAACAGCA T GAACAGAAA T GACACCTCAT T GCCACCCCT A CACACCAACAA T GTTGACCCT T TTCCTTGTC T TTCCTTCT T TTCCTTCT T TTCCTTCTTC T TTCCTTCTTC T TTCCTTCT T TTCCTTCT T TTCCTTCT T TTCCTTCTTC T TTCCTTCTTC T TTCCTTCT T TTCCTTCT T TTCCTTCTTC T TTCCTTCT T TTCCTTCTTC T TTCCTTCT T TTCCTTCT T TTCCTTCT T TTCCTTCT T TTCCTTCT T TTCCTTCT T TTCTTCT T TTCCTTCT TCCT T TTCCTTCT T TTCCTTCT T TTCCTTCT T TTCCTTCT T TTCCT T TTCT	GACATGAAGC GGCTCGGTC CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGCTCTCACC CTGCTCTCACC CTGCTCTCACC CTGCTCTCACC CTGCTCTCACC CTGCTCTCACC CTGCTCACC CTGCTCACC CTGCTCACC CTGCTCACC CTGCTCACC CTGCACACC CTGCACACC CTTCACACC CTGCACACC CTGCACACC CTGCACACC CTGCACACC CTTCCAAAAC CGCACACCAC CTTCCAAAAC CGCACACCAC CTTTACACG CTCTCAAAAC CGCACACC CTTCCAAAAC CGCACACC CTTCCAAAAC CGCACACC CTTCTCAAAAC CGCACACC CTTTACACC CTTCTCAAAAC CGCACACC CTTTACACC CTTCTCAAAAC CGCACACC CTTTTACACC CTTTTACACC CGCACACC CTTTTACACC CGCACACC CTTTTACACC CTTTTACACC CTTTTACACC CTTTTACACC CTTTTACACC CTTTTACACC CTTTTTACACC CTTTTTTTC CTTTTTTC CTTTTTC CTTTTTTC CTTTTTT	ACATGCAAGA AGAGCCCCT CGAGCCGGG AACGCCGCAG GGGAGCGCC CATCTGGCA TGCCCCACC CATTTGGCAG TTGACAAGTA TCCACTGGAG TTGACAAGTA TCCACTGGAG ATGGTAACA TCCACTGCAG AACACAAAG AACAAAAGCAAA AAAAACAAA AAAAACAAA AAAAACAAA TACTGCAT AATGCAAT AATGCAAT AATGCAAT AATGCAAT AATGCAAT ATACTGGCAT ATACTGCAT CAC ATCCGCTGCT	GCGTCCAGCT CTGGGCAGC CCGGGCATCC GGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGCT GACTCTTTC CACTGGCAGC CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGAGCCC CTGCCTCTTC CGCCATCCCC 51 CAAAATTGAC CAAAACCACA CAAAACCACA CAAAAACCACA CAAAAACCACA CACGGTCATC CACTGGTCATT CTGCACCTTTG CTGCACTTTG CTGCACCTTTG CTGCAGCAGAGGG CACTGGTCAAT CCTTATTAGT CTGCACCTTTG CTGCCCTTTG CTGCCCTTTG CTGCCCTTTG CTGCCCTTTG CTGCCCTTTG CTCCCCTTTG CTCCCTTTG CTCCCCTTTG CTCCCCTTTG CTCCCCTTTG CTCCCTTTG CTCCTTTG CTCCCTTTG CTCCTCCTTTG CTCCTTTG CTCCTTTG CTCCTTTG CTCCTTTG CTCCTTTG CTCCTTTTTC CTCCTTTTTTTT	120 180 240 300 360 420 480 600 660 720 780 840 900 936
505560657075	I I ATGGGCCAA GCCTCGCCTT GGCCCCCGGG GGGTCGCCC ACACCACCCT ACACCACCCT ACACCACCCT ACACCACCCT ACACCACCACCC ACACCACCACCACCACCACCACACCAC	11 GCCACAGCCA TAAAATGCCA TAAAATGCCA CACCCGGAGC CCCCGGAGC CCCCGGAGC TGGAAAATA TGTGAGAACTC TGTTACATCT TGTTACATCT TGTACAACTC TGGTACAACTC TAATTAAACTC CTACAACTACAACTC CAACTCAACTC AACTTACACACCC TTCCTTTAACCC TTCCTTTAACCC TTCCTTTAACCCC TTCCTTTAACCCC TTCCTTTAACCCC TTCCTTTAACCCCC TACATTAACACCCC TACATTAACACCCCCCCCCCCCCCCCCCCCCCCCCCCC	21 A ACCCACAATO A GAAGGCCCCC C GCGGGCCCAG C CAGGGCCCAG C CAGGCCCAG C CAGCACAGA C CAACATACA C CTATAGCT C CAGCCAGGAC C CACCTGGAC C CACCTGGAC C CAGCAGGAA A CGCACAGGA A CGCACAGGA C CAACATACA C TAAAACACA C TAAAACACA C TAAAACACA C TAAAACACA C TAAAACACA C ATCATCAGAA A ACCCAAACA A CACCAACAA A CACCAACAA C ATCATCAGTT C C AGTTAGAAT C CACACCAA C ATCATCAGTT T CACACCACA C T CACACCAA C T CACACCACA C T CACACCACA C T CACACCACA C T CACACCACA C T CACACCACA C T CACACCACA C T CACACCACA C T CACACCACA C T CACACCACA C T CACACCAC C T C C C C C C C C C C C C C C C C C	GACATGAAGC GGCTCGGTC CTGACTCGGTC CTGACTCGGTC CTGACTCGGTC CTGACTCCGGTC CTGACTCTACGCTC CTGACTCTACGCTC CTGACTCTACGCTC CTGACTCACGCTC CTGACTCACGCT CTGACTCACGCT CTGACTCACGCT CTGACTCACGCT CTGACTCACGCT CTGACTCACCT CTGACTCACCT CTGACT CTGACTCACCT CTGACT CTGACT CTGACT CTGACTCACCT CTGAC	ACATGCAAGA AGAGCCCCCCCCCCCCCCCCCCCCCCCCC	GCGTCCAGCT CTGGGCAGC CCGGGGATCC GGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTTC GACTCTTTC CCACGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCACAGGGCCAG CCAGAGGCC CTGCCTCTTC CGCCATCCCC 51 1 2 CAAAATTGAC CAAAACAGA ACAACAGA ACAACAGAA ACAACAGA ACAACACAA ACATATTAGT CTCAAGAGGCT ACGCCATCCCC CCTTATTAGT CTCAAGAGAG TCTCACTTG AGACCATTG AGACCATTA	120 180 240 300 360 420 480 540 660 720 840 900 936 60 120 180 240 360 420 480 540 660 720 780
505560657075	I HATGGAGCCAA GCCTCGCCTTGGCAGCACCCTAGCAGCACCCTAGCAGCACCCTAGCACCCTAGCAGATTTGGATCCTCAGAGGATGATTGGATCATAGACAAAAAAAA	11 GCCACAGCCA TAAAATGCCA TAAAATGCCA CACCCGGAGC CGGGGAGC TGGGAGAGCA TGGTAGAACTA TGTCACACTC TGCTACAACC TGCTACAACC TGCTACAACC TGCTACAACC TGCTACAACC TGCTACAACC TGCTACAACC TGCTACAACC TGCTACAACC TGCTACAACC TGCTACAACC TGCTACAACC TGCTACAACC TGCTACAACC TGCTACACC TGCTACACC TGCTACACC TGCTACACC TGCTACACC TACTACACC TACTACACC TACTACACC TACTACACC TCCTTTAA TCCAAACTA TTCCAAACTA TTCCAAACTA TTCCAAACTA TTCCAAACTA TACTACACC TTCCTCTC TACTACACC TTCCTCTCT TACTACACC TTCCTCTCT TACTACACC TTCCTCTCT TACTACACC TTCCTCTCT TACTACACC TTCCTCTCT TACTACACC TTCCTCTCT TACTACACC TTCCTCTCT TACTACACC TTCCTCTCT TACTACACC TTCCTCTCT TACTACACC TTCCTCTCT TACTACACC TTCCTCTCT TACTACACC TTCCTCTCT TACTACACC TTCCTCTCT TACTACACC TTCCTCTCT TACTACACC TTCCTCTCT TACTACACC TTCCTCTCT TACTACACC TTCCTCTCT TTCCTCTCT TTCCTCTCT TTCCTCTCTCT TTCCTCTCT TTCTTCT TTCCTCTCT TTCCTCTCT TTCCTCTCT TTCCTCTCT TTCCTCTCTCT TTCCTCTCTCT TTCCTCTCTCT TTCCTCTCTCT TT	21 ACCCACAATO A GAACGACCCC C GCGGGCCCCC C GCGGGCCCCC C GCGGCCCCC C CACCTTGC C CACCTTGC C CACCTTGC C CACCTTGC C CACCTTGC C CACCTTGC C CACCTGC C CACCTGC C CACCTGC C CACCTGC C CACCTGC C C TAAACACC C TAAACACC C TAAACACC C ATCACCTC C AGTTAGAAT A ACCCAAACA T GAACAGAA T GAACACAA T GCACTCGT A CACCACCAT T GCCACTGC T TTCCCTTGG T TTCCCTTGT C TTCCATTAC C TTCCATT	GACATGAAGC GACATGAAGC GACATGAAGC GACATCAGG CTGACCCG CTGACCCG CTGACCCGG CTGACCCG CTGACCCG CTGACCCG CTGACCCG CTGACCCG CTGACCCG CTGACCACC CTGACCACC CTGACCACC CTGACACCC CTGACACCC CTGACACCC CTACATGC CTACATGC CTGACACCC CTGACACCC CTGCACACCC CTGCACACCC CTGCACACCC CTGCACACCC CTTGCACACCC CTGCACACCC CTTTCCAAAAC CTGCACACCC CTTTCCAAAAC CTCCACACCC CTTTTACAAGC CTACTACACC CTACTAC	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCGAGCGGG AACGCCGAGCGGG ACGCCGACCGGG GGGAGCGCAC CCTTCTGGCA TCGCCACC CCTTTTGGCA ATGGTACAAGT ATCACTGGAT ACCCTTACAG AAGAAACTAA GAAAAACCAA TGACTGGAT TGACTGGAT ATGACTGGAT ATGACTGGAT ATGACTAGGAT ATGACTAGGAT TACTGGAT TTTGGAT TTTCGATTG	GCGTCCAGCT CTGGGCAGC CCGGGCATCC GGGACGGCC AGCTACTGGG TTTACTGCT GACTCTTTC GACTCTTTC CACTGGCAGC CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTC CCACTGCCCC 51 CCACTGCTCTTC CGCCATCCCC 4 CACTGGCAGCCC CCACCCCC CACTGCCCC CCACCCCC CCACCCCC CCACCCCC CCACCCCC CCACCCCC CCACCCCC CCACCCCC CCACCCCC CCACCCCCC	120 180 240 300 360 420 480 560 660 720 780 840 900 936
505560657075	I HATGGAGCCAA GCCTCGCCTT GCCCCCGAGGGAGAAACACAAGAAAAAAAAAA	11 GCCACAGCCA TAAAATGCCA TAAAATGCCA TAGAAATAA GGCACGGGCC TGGGCGGGC TGGGGCGGCC TGGTGGCACATCACCCC TCCTCACATCCC TCCTCACATCCC TCCTCACATCCC TCCTCACATCCC TCCTCACATCCC TCCTCACATCCC TCCTCACATCCC TCCTCACATCCC TCCTTCACATCCC TCCTTCACATCCC TCCTCACATCCCC TCCTCACATCCCC TCCTTCACATCCCC TCCTCACACCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	21 ACCCACAATO A GAACGACCE C GEGGGCCCCC C GCGGGCCCAC C CACCTTACCT C TACCATTGCC C CACCCTTACCT C TACCATTGCA C CAACCTTACA A CTCTAGACT C CAACCTTACA A CTCTAGACT C CAACCTTACA C CAACCTTACA C CAACCTTACA C CAACCTTGAA C CAACCTGAA C CAACCTGAA C CAACCTGAA C CAACCTAGAC C ATCATCAC C AGTAGACAC C ATCATCAC C AGTAGACA T GAACGACA T GAACCAACA T GAACACAA T GTAGACAC T TTCCTTCT T TTCCTTCT C TGCCATGAC T TTCCTTCT C TGCCATGAC T TTCCTTCT C TGCCATGAC T TTCCTTCT C TGCCATGAC T TTCCTTCT C TGCCATGAC T TTCCTTCT C TGCCATGAC T TTCCTTCT C TGCCATGAC T TTCCTTCT C TGCCATGAC T TTCCTTCT C TGCCATGAC T TTCCTTCT C TGCCATGAC T TTCCTTCT C TGCCATGAC T TTCCTTCT C TGCCATGAC T TTCCTTCT C TGCCATGAC T TTCACACA A ACTCACCCT C T TTCTTCAAA A ACTCACCCT T TTCTTCAAA A ACTCACCCT T TTCTTCAAA A ACTCACCCT T TTCTTCAAA A ACTCACCCT T TTCTTCAAA A ACTCACCCT T TGTTTCAAAA A ACTCACCCT T TGTTTCAAAA A ACTCACCCT T TGTTTCAAAA A ACTCACCCT T TGTTTCAAAA A ACTCACCCT T TGTTTCAAAA A ACTCACCCT T TGTTTCAAAA A ACTCACCCT T TGTTTCAAAA A ACTCACCCT T TGTTTCAAAA A ACTCACCCT T TGTTTCAAAA A ACTCACCCT T TGTTTCAAAA A ACTCACCCT T TGTTTCAAAA A ACTCACCCT T TGTTTCAAAA A ACTCACCCT T TCTTTCAAAA A ACTCACCCT T TCTTTCAAAA A ACTCACCCT T TCTTTCAAAA A ACTCACCCT T TCTTTCAAAA A ACTCACCCT T TCTTCAAAA T TCACCT T TCTTCTTCAAAA A ACTCACCCT T TCTTCTTCT TCTTCTTCT TTCTTCTTCT TTCTTCTTC	GACATGAAGC GGCTCGGTC CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGCTCTCACG CTGCTCTCAC CTGCTCTCACG CTGCTCTCACG CTGCTCTCACG CTGCTCTCACG CTGCTCACG CTGCTCACG CTGCTCACG CTGCTCACG CTGCACG CTCCACG CTGCACG CTGCACG CTGCACG CTCCACG ATGCAAGA AGAGCCCCCCCCCCCCCCCCCCCCCCCCC	GCGTCCAGCT CTGGGCAGC CCGGGGATCC GGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTTC GACTCTTTC CCACGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCACAGGGCCAG CCAGAGGCC CTGCCTCTTC CGCCATCCCC 51 1 2 CAAAATTGAC CAAAACAGA ACAACAGA ACAACAGAA ACAACAGA ACAACACAA ACATATTAGT CTCAAGAGGCT ACGCCATCCCC CCTTATTAGT CTCAAGAGAG TCTCACTTG AGACCATTG AGACCATTA	120 180 240 300 360 420 480 600 660 720 780 840 900 936	

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	TTTGGCATAA	AAAGGACTAT	AGCTTCAAAA	GTGTCTCTTG	GTGCTGTGTA	CTTCTTTATG	1260
_	AATGGAACCT	ATGGACTTGC	TTTTTTTTTT	GGAACCTCCT	TEATTETTAA	TOCACAACCT	1320
5	GCATATACCA	TCGGGACTGT	TOTALOUTE		2001101100	OLOGRAPHICE:	
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		CAGTCCCTCA					1440
	ATTITCCAGG	TTATTGATAA	GAAACCCAGT	ATAGATAACT	TTTCCACAGC	TGGATATAAA	1500
	CCTGAATCCA	TAGAAGGAAC	TGTGGAATTT	AAAAATGTTT	CTITCAATTA	TCCATCAAGA	1560
	CCATCTATCA	AGATTCTGAA	AGGTCTGAAT	CTCAGAATTA	ACTOTOGAGA	GACACTOGOC	1620
10	TTGGTCGGTC	TCAATGGCAG	TOCCONCRO	*CCC#*CMCC	ACCUTOMON.	CACCETATAT	
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	AGTAACAATA	TCAAGTATGG	ACGAGATGAT	GTGACTGATG	AAGAGATGGA	GAGAGCAGCA	1860
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15	CCCCAAAAAG	GAGCTCAAAT	CACTCCACCC	CACAAACACA	CCATCCCAAT	TOCTOCTOCO	
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20	TCGGTCTCAA	TGGCAGTGGG	AAGAGTACGG	TAGTCCAGCT	TCTGCAGAGG	TTATATGATC	360
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	ACCADAGA	CELEGGE	GITAGICANG	MGCCIGIIII	GIICGGGACC	ACCATCAGTA	480
	ACAATATCAA	GIAIGGACGA	GATGATGIGA	CTGATGAAGA	GATGGAGAGA	GCAGCAAGGG	540
	AAGCAAATGC	GTATGATTTT	ATCATGGAGT	TTCCTAATAA	ATTTAATACA	TTGGTAGGGG	600
	AAAAAGGAGC	TCAAATGAGT	GGAGGGCAGA	AACAGAGGAT	CGCAATTGCT	CGTGCCTTAG	660
35	TTCGAAACCC	CAAGATTCTG	ATTITACATO	ACCCUACCEC	TOCOCOCAT	TCACAAACCA	720
	BCTCACCTCT	TCAACCTCCA	CTCC16110	ADDCINCOIC	1000010071	TGACCTAATT	
							780
	TCACCTCAAG	TGGAGAATCG	CTGACCTTGA	ACCAGCGCCC	TTCGACAGCT	CTGGCCCCTC	840
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45	1	11	1	1	1	1	
45	1 GAGAAGCCCT	11 CTTCCCTTTA	21 	 AAAAAAGGCT	[GCTTCTCGCA	 GAGTGGAAAG	60
45	I GAGAAGCCCT CCCCGGTCCC	11 CTTCCCTTTA CATCCCACCA	21 AAAAAAAAAA AAACCATTTG	AAAAAAGGCT ACAAGCAGGA	[GCTTCTCGCA CAACGAAGAG	 GAGTGGAAAG GCAGAAGGAT	120
45	1 GAGAAGCCCT CCCCGGTCCC CTGGGCCTGT	11 CTTCCCTTTA CATCCCACCA GCGCGACGCC	21 AAAAAAAAA AAACCATTTG CCGGGGGACG	AAAAAAGGCT ACAAGCAGGA AGGCTCATGG	CAACGAAGAG GAAGTTTCG	GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG	
45	1 GAGAAGCCCT CCCCGGTCCC CTGGGCCTGT	11 CTTCCCTTTA CATCCCACCA GCGCGACGCC	21 AAAAAAAAA AAACCATTTG CCGGGGGACG	AAAAAAGGCT ACAAGCAGGA AGGCTCATGG	CAACGAAGAG GAAGTTTCG	GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG	120 180
	1 GAGAAGCCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG	11 CTTCCCTTTA CATCCCACCA GCGCGACGCC TCAAGCACCA	21 AAAAAAAAAA AAACCATTTG CCGGGGGACG CAGCGCCTTG	AAAAAAGGCT ACAAGCAGGA AGGCTCATGG GGCTACGGCC	GCTTCTCGCA CAACGAAGAG AGAAGTTTCG TGGTGACCCT	GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGACGGCG	120 180 240
	I GAGAAGCCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGCOOGGAGC	11 CTTCCCTTTA CATCCCACCA GCGCGACGCC TCAAGCACCA GCATCTTCTC	21 AAAAAAAAA AAACCATTTG CCGGGGGACG CAGCGCCTTG CGCCGTGGCA	AAAAAAGGCT ACAAGCAGGA AGGCTCATGG GGCTACGGCC TTCCAGTGCC	GCTTCTCGCA CAACGAAGAG AGAAGTTTCG TGGTGACCCT CGTGCAGCGC	GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGACGGCG CGCCTGGAAC	120 180 240 300
45 50	1 GAGAAGCCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGCGGGGAGC CTGCCCTACG	11 CTTCCCTTTA CATCCCACCA GCGCGACGCC TCAAGCACCA GCATCTTCTC GCCTGGTCTT	21 AAAAAAAAA AAACCATTTG CCGGGGGACG CAGCGCCTTG CGCCGTGGCA CTTGCTGGTG	AAAAAAGGCT ACAAGCAGGA AGGCTCATGG GGCTACGGCC TTCCAGTGCC CCGGCGCTCG	GCTTCTCGCA CAACGAAGAG AGAAGTTTCG TGGTGACCCT CGTGCAGCGC CGCTCTTCCT	GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGACGGCG CGCCTGGAAC CCTGGGCTAC	120 180 240 300 360
	1 GAGAAGCCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGCGGGAGC CTGCCCTACG GTGCTGAGCG	11 CTTCCCTTTA CATCCACCA GCGCGACGCC TCAAGCACCA GCATCTTCTC GCCTGGTCTT CACGCACGTG	21 AAAAAAAAAA AAACCATTTG CCGGGGGACG CAGCGCCTTG CCCCTTGGCA CTTGCTGGTG GCGCCTGCTC	AAAAAAGGCT ACAAGCAGGA AGGCTCATGG GGCTACGGCC TTCCAGTGCC CCGGCGCTCG ACCGGATGCT	GCTTCTCGCA CAACGAAGAG AGAAGTTTCG TGGTGACCCT CGTGCAGCGC CGCTCTTCCT GCTCCAGCGC	GAGTGGAAAG GCAGAAGGAT GCCGGTGCTG GCTGACGGCG CGCCTGGAAC CCTGGGCTAC CCGCGCGAGT	120 180 240 300 360 420
	1 GAGAAGCCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGCGGGGAGC CTGCCCTACG GTGCTGAGCG TGCGGATCGG	11 CTTCCCTTTA CATCCACCA GCGCGACGCC TCAAGCACCA GCATCTTCTC GCCTGGTCTT CACGCACGTG CGCTGCGCGG	21 AAAAAAAAA AAACCATTG CCGGGGGACG CAGCGCCTTG CCCGTGGCA CTTCCTGGTG GCGCCTGCTC CTCCCTGGTG	AAAAAAGGCT ACAAGCAGGA AGGCTCATGG GGCTACGGCC TTCCAGTGCC CCGGCGCTCG ACCGGATGCT TGCAGGCAAA	GCTTCTCGCA CAACGAAGAG AGAAGTTTCG TGGTGACCCT CGTGCAGCGC CGCTCTTCCT GCTCCAGCGC TCAGCGCGCC	GAGTGGAAAG GCAGAAGGAT GCCGGTGCTG GCTGACGGCG CGCCTGGAAC CCTGGGCTAC CCGCGCGAGT CGCCGCGCGCTC	120 180 240 300 360
	1 GAGAAGCCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGCGGGGAGC CTGCCCTACG GTGCTGAGCG TGCGGATCGG	11 CTTCCCTTTA CATCCACCA GCGCGACGCC TCAAGCACCA GCATCTTCTC GCCTGGTCTT CACGCACGTG CGCTGCGCGG	21 AAAAAAAAA AAACCATTG CCGGGGGACG CAGCGCCTTG CCCGTGGCA CTTCCTGGTG GCGCCTGCTC CTCCCTGGTG	AAAAAAGGCT ACAAGCAGGA AGGCTCATGG GGCTACGGCC TTCCAGTGCC CCGGCGCTCG ACCGGATGCT TGCAGGCAAA	GCTTCTCGCA CAACGAAGAG AGAAGTTTCG TGGTGACCCT CGTGCAGCGC CGCTCTTCCT GCTCCAGCGC TCAGCGCGCC	GAGTGGAAAG GCAGAAGGAT GCCGGTGCTG GCTGACGGCG CGCCTGGAAC CCTGGGCTAC CCGCGCGAGT CGCCGCGCGCTC	120 180 240 300 360 420 480
50	1 GAGAAGCCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGCGGGGAGC CTGCCCTACG GTGCTGAGCG TGCGGATCGG GCGCCCTCA	11 CTTCCCTTTA CATCCACCA GCGCGACGCC TCAAGCACCA GCATCTTCTC GCCTGGTCTT CACGCACGTG CGCTGCGCGGG CCTGGGTGGC	21 AAAAAAAAA AAACCATTIG CCGGGGGACG CAGCGCCTIGC GCCCTGGTG GCGCCTGGTG CCCCCGGTG CCCCCGGTG CGTGGCGCTG	AAAAAAGGCT ACAAGCAGGA AGGCTCATGG GGCTACGGCC TTCCAGTGCC CCGGGGTCG ACCGGATGCT TGCACGCAAA CTCGGGGGCG	GCTTCTCGCA CAACGAAGAG AGAAGTTTCG TGGTGACCCT CGTGCAGCGC CGCTCTTCCT GCTCCAGCGC TCAGCGCGCC CCTTTTACGA	I GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGACGGCG CGCCTGGAAC CCTGGGCTAC CCGCGCGCGCTC GCCGCGCGCTC GTGCGCGCCC	120 180 240 300 360 420 480 540
	I GAGAAGCCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGCGGGAGC CTGCCCTACG GTGCTGAGCG TGCGGATCGG GCGCCCTCA ACCGGGAGCG	11 CTTCCCTTTA CATCCCACCA GCGCGACGCC TCAAGCACCA GCATCTTCTC GCCTGGTCTT CACGCACGTG CCTGCGGGGC CCTGCGGGGC CCGCCTTCGC	21 AAAAAAAAA AAACCATTIG CCGGGGGACG CAGCGCTIGG CCCTGGTG GCGCCTGGTG CTCCCTGGTG CGTGGCGCTG CGAGCGCCTG	AAAAAAGGCT ACAAGCAGGA AGGCTCATGG GGCTACGGCC TTCCAGTGCC CCGGCGCTCG ACCGGATGCT TGCACGCAAA CTCGGGGGG TGCCTCGGCC	GCTTCTCGCA CAACGAAGAG AGAAGTTTCG TGGTGACCCT CGTGCAGCGC CGCTCTTCCT GCTCCAGCGCC TCAGCGCGC CCTTTTACGA GCAACCGCAG GCAACCGCAG	I GAGTIGGAAAG GCAGTAGGAT GGCGTGCTG GCTGACGGC CGCCTGGAAC CCGCGCGAGT CGCCGCGCTC GTGCGCGCC CTGCGCCGCC CTGCGCCGCC	120 180 240 300 360 420 480 540
50	I GAGAAGCCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGCGGGAGC CTGCCTACG GTGCTGAGCG TGCCGATCGG GCGCCCTCA ACCGGGAGCG GAGCTGCCGC	11 CTTCCCTTTA CATCCACCA GCGGGACGCC TCAAGCACCA GCATCTTCTC GCCTGGTCTT CACGCACGTG CCTGGGTGGC CTGGGTGGC CGGCCTTCGC	21 AAAAAAAAA AAACCATTIG CCGGGGGACG CAGCGCTTGC CTTCGCTGGTG CGCCTGGTG CGTGGCGCTG GCAGCGCCTG CAACCAGGCC	AAAAAAGGCT ACAAGCAGGA ACAGCTCATGG GGCTACGGCC TTCCAGTGCC CCGGCGCTCG ACCGCATGCT TGCACGCAAA CTCGGGGGG TGCCTCGGCC AAGGCSTCGG	GCTTCTCGCA CAACGAAGAG AGAAGTTTCG TGGTGACCCT CGTGCAGCGC CGCTCTTCCT GCTCCAGCGC TCAGCGCGC CCTTTTACGA GCAACCGCAG ACGTGCAGGA ACGTGCAGGA	I GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGACGGCG GCCTGGAAC CCTGGGCTAC CCGCGCGAGT CGCCGCGGCTC CTGCGCCGCC CTGCGCCGCG CCTCCTGAAG	120 180 240 300 360 420 480 540 600 660
50	1 GAGAAGCCT CCCCGGTCCC CTGGGCTGT GACCTGCAGG GGCCGGGAGG CTGCCCTAGG GTGCTGACGG GGCCCCTCA ACCGGGAGGG GATCTGAAGG	11 CTTCCCTTTA CATCCACCA GCGGACGCC TCAAGCACCA GCATCTTCTC GCCTGGTCTT CACSCACGTG GCTGGGGG CCTGGGTGGC CGGCCTTGGC TGGTGCCGTGC CTGGTGGC CTGGTGCCTTGC CTCAGTCGC	21 AAAAAAAA AAACCATTIG CCGGGGGACG CAGCGCCTGCTG CCCCTGGTG CTCCCTGGTG CTCCCTGGTG CTCCCTGGTG CAGCGCCTG CAACCAGCCC CAACCAGCCC CAACCAGCCC CATTIGGGCGTGTTGGGCGCTGTTTGGGCGTGTTTGGGCGTGTGGGCGTGTGGGCGTGTGGGCGTGTGGGCGTGTTTGGGCGGTGTTTGGGCGGTGTTTGGGGGG	AAAAAAGCT AAAAAAGCT AACAAGAAGAA AGGCTCATGG GGCTACGGCC TTCCAGTGCC CCGGGGTCG ACCGGATGCT TGCACGCAAA CTCGGGGGG TGCCTCGGC TAGGTCTGCC TGGATCTTGA	CATTCTCGCA GCATCAGAGA GAAGATTCG GTGCAGCGC CGCTCTTCCG GCTCCAGCGC CCTTTTACGA GCACCGCGG CCTTTTACGA GCACCGCAG ACGTCGAGAG TAGCAGTTGT	I GAGTIGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGACGGCG CGCCTGGAAC CCTGGGCTAC CGCGGCAGT CGCCGCGCTC GTGCGCGCC CTGCGCCGCC CTGCGCCGCC CTCCTGAAG TATCATT	120 180 240 300 360 420 480 540 600 660 720
50	1 GAGAAGCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGGGGGAGC CTGCCCTACG TGGGGATCGG GGCCCCTCA ACCGGGAGCG GACTGCCGC GACTGCACG CTTCTGAAGG	11	21 MARARARA ARCCATTIG CCGGGGGACG CAGCGCCTIG CGCCTGGCA CTCCTGGTG CGCCCTGGTG CGCCCGGTGCC CACCAGGCC CACCAGGCC CACCAGGTGC CACCAGGTGC	I AAAAAGCT ACAGCAGA AGGCTCATGG GGCTACGGC TTCCAGTGCC CCGGGGTCG ACCGCATGCT TGCACGCAA AGGGTCGG TGCCTCGGC AAGGGTCTGACTCTGA CTATCTCCAG CTATCTCAG CTATCAG CTATCTCAG CTATCTCAG CTATCTCAG CTATCAG CTATCTCAG CTATCTCAG CTATCAG CTATCTCAG CTATCTCAG CTATCAG CTATCTCAG CTATCTCAG CTATCAG CTATCTCAG CTATCTCAG CTATCTCAG CTATCAG CTATCTCAG CTATCAG CTATCAG CTATCTCAG	CATCTCCCA GAGAGATTCG GAGAGGTTCG GGTGACCGT GGTCACGGC GCTCTTCCT GCTCAGGGC CCTTTTAGCA GCAACCGCAG ACGTGCAGGA TAGCAGTTGT TAGCTTTTCT	I GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCCCTGGAAC CCCGCGCTAC CCGCCGCTC CTGCGCCTC CTGCGCGCC CCTCCTGAAG TATCATCATT	120 180 240 300 360 420 480 540 600 660
50	1 GAGAAGCCT CCCCGGTCCC CTGGGCCTGT GACCTGCAGG GGCGGGAGG CTGCCCTAGG GTGCTGAGGG TGCGGATGG GGCCCCTCA ACCGGGAGG GAGCTGCGG GATCTGAAGG CTTCTGAATT TTCTGGAAAA	11 CTTCCCTTTA CATCCACCA GCGGACCCC GCGGACCCC GCATCTTCTC GCTGGTCTT CACCCACGTG CGCTGCGCG CCTGGGTGGC CGGCCTTCGC CTGGTCGCCTT CTCATCCCAT TTACATCTGT TCTATTTGGA	21 MAAAAAAA AAACCATTTG CCGGGGGACG CAGCGCCTTG CGCCTGGTG CTCCCTGGTG CGTGCCCTG CAACCAGGCC GGTGTTGCGC CACCCGATGC ACCAGGCCAACCAACCAACCAACCAACCAACCAACCA	I AAAAAAGCT ACAGGCTCATGG GGCTCATGG GGCTCATGG CCGGCGCTCG ACCGGATCCT TGCAGGCAAACCTCGGCCTGGCCT	CAACGAAGAG AGAAGTTTCG CAACGAAGAG AGAAGTTTCG TGGTGACCCT CGTGCAGGGC CGCTCTTCCT GCTCCAGGGC CCTTTTACGA GCAACGCAG ACGTGCAGGA TAGCAGTTGT TTAGTTTTCT TTAGTAAAGC	I GAGTGGAAAG GCAGAAGGAT GCCGCAGCTGACGCC CCCCCGCAGT GCCCCCCCCCC	120 180 240 300 360 420 480 540 600 660 720
50	1 GAGAAGCCCT CCCCGGTCCC CCCGGTCCC CTGGGCCTGT GACCTGCACG GGCOGGAGC GTGCTGACG GTGCTGACG ACCGGATCGG GAGCTGCCGC GAGCTGCAGC CATCTGAAGG CTTCTGAATA CCACTGAATA GCAACTGAAT	11 CTTCCCTTTA CATCCCACCA GCACCACCA GCACCACCAC GCACTTCTCTC CACCCACGTG CCTCGGCGGG CCTGGGTGGC CGGCCTTCGC TGGGCCGTG TCTACACCTGT TCTACTCTGT TCTATTTGGA TGGCAAAAGA	21 AAAAAAAAA AAACCATTIG CCGGGGGACG CAGCGCCTTG GCCTGGTG GCCCTGGTG GCGCCTGCTG GCAGCGCCTG GCAGCGCCTG GCAGCGCCTG CAACCAGGCC CACCGATGC ACACGAGCACA ACACGAGCACA ACACGAGCACA ACACGAGCACAGACAA ACACGAGCACAGACAA ACACGAGCACAGACAAA ACACGAGACAAA GAATATTAAAA	I AAAAAAGCT ACAGGACAGAAAAAAAAGCTACGGACAGAAAACGCACAAAACGCACAAAACCCCAGCACAAACCCAGAACCAGAACCAGAACCAGAACCAGAACCCAGAACCCAGAACCCAGAACCCAGAACCCTCAGACCAGAACCCTCAGACCCAGATCTTTTTTTT	CAACGAAGA AGAAGTTCC CAACGAAGAA AGAAGTTCC TGGTGACCCT CGTCCAGCCC CGCTCTTCCT GCTCCAGCCC CCTTTAGGA GCAACCGCAG ACGTCCAG TAGCAGTTGT TTAGTTTTCT AAAGTAAAGC	I GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGGCTAC CCGCGCGAGT CGCCGCGCCCCTGGGCCGCCCTGGGCCGCCCTGGCCGCGCCCTGGAGT TATCATCATT GCAGCTGAAA CACAGAGCAT TCCAAAAGAA	120 180 240 300 360 420 480 540 600 660 720 780
50	1 GAGAAGCCCT CCCCGGTCCC CCCGGTCCC CTGGGCCTGT GACCTGCACG GGCOGGAGC GTGCTGACG GTGCTGACG ACCGGATCGG GAGCTGCCGC GAGCTGCAGC CATCTGAAGG CTTCTGAATA CCACTGAATA GCAACTGAAT	11 CTTCCCTTTA CATCCCACCA GCACCACCA GCACCACCAC GCACTTCTCTC CACCCACGTG CCTCGGCGGG CCTGGGTGGC CGGCCTTCGC TGGGCCGTG TCTACACCTGT TCTACTCTGT TCTATTTGGA TGGCAAAAGA	21 AAAAAAAAA AAACCATTIG CCGGGGGACG CAGCGCCTTG GCCTGGTG GCCCTGGTG GCGCCTGCTG GCAGCGCCTG GCAGCGCCTG GCAGCGCCTG CAACCAGGCC CACCGATGC ACACGAGCACA ACACGAGCACA ACACGAGCACA ACACGAGCACAGACAA ACACGAGCACAGACAA ACACGAGCACAGACAAA ACACGAGACAAA GAATATTAAAA	I AAAAAAGCT ACAGGACAGAAAAAAAAGCTACGGACAGAAAACGCACAAAACGCACAAAACCCCAGCACAAACCCAGAACCAGAACCAGAACCAGAACCAGAACCCAGAACCCAGAACCCAGAACCCAGAACCCTCAGACCAGAACCCTCAGACCCAGATCTTTTTTTT	CAACGAAGA AGAAGTTCC CAACGAAGAA AGAAGTTCC TGGTGACCCT CGTCCAGCCC CGCTCTTCCT GCTCCAGCCC CCTTTAGGA GCAACCGCAG ACGTCCAG TAGCAGTTGT TTAGTTTTCT AAAGTAAAGC	I GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGGCTAC CCGCGCGAGT CGCCGCGCCCCTGGGCCGCCCTGGGCCGCCCTGGCCGCGCCCTGGAGT TATCATCATT GCAGCTGAAA CACAGAGCAT TCCAAAAGAA	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50	1 GAGAAGCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGCGGGAGC CTGCCCTACG TGGGATCGG GACCTGCACG ACCGGGAGCG GACTGCCGC CTTCTGATT TTCTGGAAAA TATAACACTC	II CTTCCCTTTA CATCCACCA GCGCACCCC GCGCACCCC GCATCTTCTC GCCTGGTCTT GCTCCCCGGCCTTCGC CGGCCTTCGC CGGCCTTCGC TGGTCCCCGG CTCAGTCCCCA TTACATCTGT TCTATTTGGA TGGCAAAAGGA CAAGCATGAA	21 MARARARA ARACCATTIG CCGGGGGACG CAGCGCCTIG CGCCTGGCA CTCCCTGGTG CCCCTGGTG CACCGGCCTG CACCGAGCC CACCGATGC ACAGGAGCAG CACCGATGC ACAGGAGCAG GAATATTARA AGAGTGGCAG	I AAAAAAGCT ACAGCAGGA AGGCTCATGG GGCTACGGC CCGGGGTCG ACCGGATGCT TGCACGCAAA CTCGGGGCG TGCCTCGGCC AAGGCGTCGG CTATCTCCAG CAGATCCTTA TGTTTCTTTG CAAATTCCTTA	CONTINUES OF THE PROPERTY OF T	I GAGTGGAAAG GCAGAAGGAT GGCGGTGCCGCCCCCCCCCC	120 180 240 300 360 420 480 540 660 720 780 840 900 960
50	1 GAGAAGCCCT CCCCGGTCCC CTGGGCCTGT GACCTGCAGG GGCGGGAGC CTGCCGATCGG GGGCCCCTCA ACCGGGAGCG GATCTGAAGG CTTCTGAATT TTCTGGAAAA GCAACTGAAT TATAACACTC AAGGGCCAGT	11 CTTCCCTTTA CATCCACCA GCGGACCCC TCAAGCACCA GCATCTTCTC GCTGGTCTT CACGCACGTG CGCTGCGCG CGTGCGCGG TGGGCCTGG TGGTCCCTG TTACATCTGT TCAATTTGGA TGGCAAAAGA CAAGCATTAGA CAAGCATAGA ACTACAGCAT	21 AAAAAAAAA AAACCATTTG CCGGGGGACG CAGCGCCTTGCC CTCCCTGGTG CGCGCTGCTC CTCCCTGGTG CGAGCGCCTG CAACCAGGCC GGTGTTGCGC CACCCGATGC CACCCGATGC CACCGATGC CACCGATGC CACCGATGC GGTTGCACAAA	AAAAAAGGCT ACAAGGAGGA AGGCTCATGG GGCTACGGCC CCGGCGCTCG ACCGGATCCT TGCAGGCAAA CTCGGGGGG TGCCTCGGCC TGGCTCGGCC TGGATCTTGA CTATCTCCAG CAGATCCTTA TGTTTCTTTG CAAATTTCAT TATGTCAACA	CALCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	I GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCCTGGACGCGAGT GCCCGCGAGT GCCCGCGCGCC CTGCGCCGCC CTGCGCCGCGC CTCCGCAGAGT TCCAAAAGAA TTTCAATCCG GACTCACAGGCAGT GCACCACAGGCAGT GCACCACAGGCAT TCCAAAAGAA TTTCAATCCG GACTCACAGG	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020
50	1 GAGAAGCCT CCCCGGTCCC CCCGGTCCC CTGGGCCTGT GACCTGCACG GGCGGGAGCG GGCGCCCTCA ACCGGATCGG GGGCCCTCA ACCGGAGCG GATCTGAAGG CTTCTGAATA TTTTCTGAAAAA TATAACACTC AAGGCCAGT ATCAGGTCTA	11 CTTCCCTTTA CATCCACCA GCACCACCA GCACCACCA GCACACTC GCACACTG GCACGTGCGCGG CTGGGTGGC GGCCTTCGC TGGCCTGG TTGTCCCTG TTGTCCCTG TTGTCCCTG TCTATTTGGA ACTATCTGT TCTATTTGGA ACTACACCAT ACTACACCAT ACTACAGCAT CTGAAGGAGAA	21 AAAAAAAAA AAACCATTIG CCGGGGGACG CCGGGGGCAC CTTGCTGGTG CGCCTGCTC CTCCCTGGTG CGACCGCCTG CAACCAGGCC CACCCGATGC ACACGAGCAC ACACGAGCAC CAACTGATTAAA AGAGTGCACAA TACGGTGATT	I AAAAAAGGCT ACAGGCTCATGG GGCTCATGG GGCTCGGCCCC ACCGGATGCT TGCAGGCAGCT TGCAGGCAGCT TGCATCTTTA CTATCTCCAG CAGATCTTTA TATGTCATCAT TATGTCACAT TATGTACATCTTCAT CAAATTTCAT TATGTACACTCTTCATCCCTGTTCTTCACCTCTTCTTTCACACTCTTCTTCACCTCTTCTT	CAACGAAGAG GCATCTCTCCCA GCTCCAGGGC CGCTCTTCCT GCTCCAGGGC CCTTTAGGA GCAACGCCAG ACGTCCAGG TTAGCAGTTTT TTAGTTTTCT AAAGTAAAGC ACGTCGCAG CAACGCAGC ACGTCGACAG ACGTCGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACTTGTATAC GAAAAGAGAAA	I GAGTIGGAAAG GCAGAAGGAT GGCGGTGCTG GCCTGGACGCC CGCGCGCGCCC CTGGGCCGCC CTGGGCCGCC CTGGGCCGCG CCTCCTGAAG CACAGAGCAT TCCAAAAGAA TTTCAATCGG GACTCACAGT TTCATCTGTT	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080
50	1	II CTTCCCTTTA CATCCACCA GCGGACGCC GCGCGTCTC GCCGGCCTTCG CCCGGCCTTCGC CGCCTGGTCGC CGGCCTTCGC TGGTGCCGG CTCAGTCCCA TACATCTGC TACATCTGT TCTATTTGA TGGCAAAAGA ACTACAGCAT CTGAAGGAGA CTGAAGGAGA	21 MARARARA ARCCATTTG CCGGGGGACG CAGCGCCTTG CGCGTGGCA CTTCCTGGTG GCGCTGCTC CTCCTGGTG GCACGCCCTG CAACCAGGCC CACCAGTGCC ACCAGGCCG GGTATTGCGC ACCAGGAGCAG GAATATTARA AGAGTGGCAG GTTGCACAAA TACGGGGATATACACAAA TACGGTGATTA	I AAAAAAGCT ACAGCAGGA AGGCTCATGG GCCTAGGCC CCGGGGTCG ACCGGATCCT TGCAGGCAAA CTCGGGGGCTAG AGGGGTCGG AGGGTTCTT TGTTTTTTTT TGTTTTTTTTTT	CAACGAAGAG GCATCTCTCCCA GCTCCAGGGC CGCTCTTCCT GCTCCAGGGC CCTTTAGGA GCAACGCCAG ACGTCCAGG TTAGCAGTTTT TTAGTTTTCT AAAGTAAAGC ACGTCGCAG CAACGCAGC ACGTCGACAG ACGTCGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACTTGTATAC GAAAAGAGAAA	I GAGTIGGAAAG GCAGAAGGAT GGCGGTGCTG GCCTGGACGCC CGCGCGCGCCC CTGGGCCGCC CTGGGCCGCC CTGGGCCGCG CCTCCTGAAG CACAGAGCAT TCCAAAAGAA TTTCAATCGG GACTCACAGT TTCATCTGTT	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020
50 55	1	II CTTCCCTTTA CATCCACCA GCGGACGCC GCGCGTCTC GCCGGCCTTCG CCCGGCCTTCGC CGCCTGGTCGC CGGCCTTCGC TGGTGCCGG CTCAGTCCCA TACATCTGC TACATCTGT TCTATTTGA TGGCAAAAGA ACTACAGCAT CTGAAGGAGA CTGAAGGAGA	21 MARARARA ARCCATTTG CCGGGGGACG CAGCGCCTTG CGCGTGGCA CTTCCTGGTG GCGCTGCTC CTCCTGGTG GCACGCCCTG CAACCAGGCC CACCAGTGCC ACCAGGCCG GGTATTGCGC ACCAGGAGCAG GAATATTARA AGAGTGGCAG GTTGCACAAA TACGGGGATATACACAAA TACGGTGATTA	I AAAAAAGCT ACAGCAGGA AGGCTCATGG GCCTAGGCC CCGGGGTCG ACCGGATCCT TGCAGGCAAA CTCGGGGGCTAG AGGGGTCGG AGGGTTCTT TGTTTTTTTT TGTTTTTTTTTT	CAACGAAGAG GCATCTCTCCCA GCTCCAGGGC CGCTCTTCCT GCTCCAGGGC CCTTTAGGA GCAACGCCAG ACGTCCAGG TTAGCAGTTTT TTAGTTTTCT AAAGTAAAGC ACGTCGCAG CAACGCAGC ACGTCGACAG ACGTCGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACTTGTATAC GAAAAGAGAAA	I GAGTIGGAAAG GCAGAAGGAT GGCGGTGCTG GCCTGGACGCC CGCGCGCGCCC CTGGGCCGCC CTGGGCCGCC CTGGGCCGCG CCTCCTGAAG CACAGAGCAT TCCAAAAGAA TTTCAATCGG GACTCACAGT TTCATCTGTT	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080 1140
50	1 GAGAAGCCT CCCCGGTCCC CCCGGTCCC CCCGGTCCC CTGGGCCTGT GACCTCACG GGCGGGGGG GGCCCTCA ACCGGGATCGG GGGCCCTCA ACCGGGACGG GGCCTCCTGATT TTCTGGAAAA CCACTGAAT TATAACACTC AAGGGCCAGT ATCAGGTCTA ATAAACACCA TATACCTCTA ATAAACACCA TATACCTTTA	11 CTTCCCTTTA CATCCACCA GCGGCACCCC GCGCCTCTCAC GCACCACTG GCCTGGTCTT CACCACCATG GCTGGTGGC GGCCTTGGC TGGCCATG TTACATCTGT TCTATTTGGA TCTATTTTGA ACTACACCAT TGGCAAAAGA ACTACAGCAT TTAAAAAATA	21 MARARARA AACCATTIG CCGGGGGACG CAGCGCCTTG GCCGTGGCA CTTCCTGGTG GCGCGCTGCTC CTCCCTGGTG CAGCGCCTG CAGCGCCTG CACCGGTGC CACCGGTGC CACCGGTTGCC CACCGGTTGCC CACCGGTTGCC CACCTGGTTGCC CACCTGGTTGCC CACCTGGTTGCC CACCTGGTTGCC CACCTGGTTACA ACAGTGCCACAAA AGAGTGGCAGA TACGGTGGTTTTAAACATTGGTA	I AAAAAAGCT ACAGCAGGA AGGCTCATGG GCCTAGGCC CCGGGGTCG ACCGGATCCT TGCAGGCAAA CTCGGGGGCTAG AGGGGTCGG AGGGTTCTT TGTTTTTTTT TGTTTTTTTTTT	CAACGAAGAG GCATCTCTCCCA GCTCCAGGGC CGCTCTTCCT GCTCCAGGGC CCTTTAGGA GCAACGCCAG ACGTCCAGG TTAGCAGTTTT TTAGTTTTCT AAAGTAAAGC ACGTCGCAG CAACGCAGC ACGTCGACAG ACGTCGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACTTGTATAC GAAAAGAGAAA	I GAGTIGGAAAG GCAGAAGGAT GGCGGTGCTG GCCTGGACGCC CGCGCGCGCCC CTGGGCCGCC CTGGGCCGCC CTGGGCCGCG CCTCCTGAAG CACAGAGCAT TCCAAAAGAA TTTCAATCGG GACTCACAGT TTCATCTGTT	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080
50 55	1 GAGAAGCCT CCCCGGTCCC CCCGGTCCC CCCGGTCCC CTGGGCCTGT GACCTCACG GGCGGGGGG GGCCCTCA ACCGGGATCGG GGGCCCTCA ACCGGGACGG GGCCTCCTGATT TTCTGGAAAA CCACTGAAT TATAACACTC AAGGGCCAGT ATCAGGTCTA ATAAACACCA TATACCTCTA ATAAACACCA TATACCTTTA	11 CTTCCCTTTA CATCCACCA GCGGCACCCC GCGCCTCTCAC GCACCACTG GCCTGGTCTT CACCACCATG GCTGGTGGC GGCCTTGGC TGGCCATG TTACATCTGT TCTATTTGGA TCTATTTTGA ACTACACCAT TGGCAAAAGA ACTACAGCAT TTAAAAAATA	21 MARARARA AACCATTIG CCGGGGGACG CAGCGCCTTG GCCGTGGCA CTTCCTGGTG GCGCGCTGCTC CTCCCTGGTG CAGCGCCTG CAGCGCCTG CACCGGTGC CACCGGTGC CACCGGTTGCC CACCGGTTGCC CACCGGTTGCC CACCTGGTTGCC CACCTGGTTGCC CACCTGGTTGCC CACCTGGTTGCC CACCTGGTTACA ACAGTGCCACAAA AGAGTGGCAGA TACGGTGGTTTTAAACATTGGTA	I AAAAAAGCT ACAGCAGGA AGGCTCATGG GCCTAGGCC CCGGGGTCG ACCGGATCCT TGCAGGCAAA CTCGGGGGCTAG AGGGGTCGG AGGGTTCTT TGTTTTTTTT TGTTTTTTTTTT	CAACGAAGAG GCATCTCTCCCA GCTCCAGGGC CGCTCTTCCT GCTCCAGGGC CCTTTAGGA GCAACGCCAG ACGTCCAGG TTAGCAGTTTT TTAGTTTTCT AAAGTAAAGC ACGTCGCAG CAACGCAGC ACGTCGACAG ACGTCGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACTTGTATAC GAAAAGAGAAA	I GAGTIGGAAAG GCAGAAGGAT GGCGGTGCTG GCCTGGACGCC CGCGCGCGCCC CTGGGCCGCC CTGGGCCGCC CTGGGCCGCG CCTCCTGAAG CACAGAGCAT TCCAAAAGAA TTTCAATCGG GACTCACAGT TTCATCTGTT	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080 1140
50 55	1 GAGAAGCCT CCCCGGTCCC CCCCGGTCCC CTGGGCGGGGGGGG	11 CTTCCCTTTA CATCCACCA GCGGACGCC GCAGCACCA GCATCTTCTC GCCTGGTCTT GCCTGGTCGT GCTGGCGGG CCTGGGTGGC CTCGGTGGC CTCAGTGCCAT TACATCTGT TCTATTTGGA ACTACAGCAT CTGAAGGAGAA ACTACAGCAT TTAAAAAAATA 174 DNA Se	21 MANANANA ANACCATTTG CCGGGGGACG CAGCGCCTTG CGCGTGGCA CTTCCTGGTG CGCCTGCTC CTCCCTGGTG CACCAGGCC CACCAGTTGCCA ACACAGGCC GGTATTGCAC ACAGGAGCAG GATTATTANA AGACTGGCAA TACGGTGATT ATGACCTTTT AACATTGGTA TUEnce	I AAAAAAGGCT ACAGGCAGGAAGGCTCATGGCCC CCGGGGTCG ACCGGATCCT TGCACGCAAA CTCGGGGGG TGGATCTTGA CTATCTCAG CAGATCTTATTTTTTTT TGTTTTTTTTTT	CAACGAAGAG GCATCTCTCCCA GCTCCAGGGC CGCTCTTCCT GCTCCAGGGC CCTTTAGGA GCAACGCCAG ACGTCCAGG TTAGCAGTTTT TTAGTTTTCT AAAGTAAAGC ACGTCGCAG CAACGCAGC ACGTCGACAG ACGTCGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACTTGTATAC GAAAAGAGAAA	I GAGTIGGAAAG GCAGAAGGAT GGCGGTGCTG GCCTGGACGCC CGCGCGCGCCC CTGGGCCGCC CTGGGCCGCC CTGGGCCGCG CCTCCTGAAG CACAGAGCAT TCCAAAAGAA TTTCAATCGG GACTCACAGT TTCATCTGTT	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080 1140
50 55	1 GAGAAGCCT CCCCGGTCCC CTGGGGCTGT GACCTGCACG GGCGGGAGCG GGCGCCTCA ACCGGAGCG GGCCCCTCA ACCGGAGCG GATCTGAAG CTTCTGATTT TTCTGGAAA GCAACTGAAT ATAACACTC ATCAGGTCTA ATCAGGTCTA SEQ ID NO: Nucleic AC	11 CATCCCTTTA CATCCCACCA GCACCTCCACCA GCACACTCC TCAAGCACCA GCACTTCTCC GCTGGTGCT CACGCACGTG CCTGGGTGGC CGGCCTTGGC TGGTGCCCTG TGGTGCCTG TTCAATCCCA TTCAATCTGT TCTATTTTGGA ACTACAGCAT CTGAAGGAGA CTCCTGAGTT TTAAAAAATA 174 DNA Sei id Accessio	AAAAAAAAA AAACCATTTG CCGGGGGACG CAGGGCTTGGG CTTGCTGGTG GCGCTGCTG CTCCCTGGTG GCAGCGCCTG CAACCAGGCC CACCAGGCCTG CAACCAGGCC CACCGATTG CACCGATTG CACCGATTG CACCGATTG CACCGATTG AACAGTGCAA AACATTGAAA AACATTGTA AACATTGTA Quence n #: NM_032	I AAAAAAGGCT ACAGGCAGGAAGGCTCATGGCCC CCGGGGTCG ACCGGATCCT TGCACGCAAA CTCGGGGGG TGGATCTTGA CTATCTCAG CAGATCTTATTTTTTTT TGTTTTTTTTTT	CAACGAAGAG GCATCTCTCCCA GCTCCAGGGC CGCTCTTCCT GCTCCAGGGC CCTTTAGGA GCAACGCCAG ACGTCCAGG TTAGCAGTTTT TTAGTTTTCT AAAGTAAAGC ACGTCGCAG CAACGCAGC ACGTCGACAG ACGTCGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACTTGTATAC GAAAAGAGAAA	I GAGTIGGAAAG GCAGAAGGAT GGCGGTGCTG GCCTGGACGCC CGCGCGCGCCC CTGGGCCGCC CTGGGCCGCC CTGGGCCGCG CCTCCTGAAG CACAGAGCAT TCCAAAAGAA TTTCAATCGG GACTCACAGT TTCATCTGTT	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080 1140
50 55	1 GAGAAGCCT CCCCGGTCCC CCCGGTCCC CCCGGTCCC GACCTCACG GGCGGGAGCG GGCGCCCTCA ACCGGAGCG GGCCCCTCA ACCGGAGCG GACCTGAGC CATCTGAAGG CTTCTGAATT TTCTGAAAAA TATAACACTC AAGGCCAGT ATTAACTT ATAACACTC ATTACCTTA ATAACAGCA TATTTCTTTA Seq ID NO: Nucleic Ac Coding seq	11 CTTCCCTTTA CATCCACCA GCACCACCA GCACACTC GCACACTC GCACACTG GCACACTG GCTGGTGGC GGGCCTTCGC TGGTGCCGGG CTCAGTGCCTG TTGACACTGT TCTATTTGGA ACTACTGT TCTATTTGGA ACTACAGCAT TTACAGCAT	AAAAAAAAA AAACCATTTG CCGGGGGACG CAGGGCTTGGG CTTGCTGGTG GCGCTGCTG CTCCCTGGTG GCAGCGCCTG CAACCAGGCC CACCAGGCCTG CAACCAGGCC CACCGATTG CACCGATTG CACCGATTG CACCGATTG CACCGATTG AACAGTGCAA AACATTGAAA AACATTGTA AACATTGTA Quence n #: NM_032	I AAAAAAGGCT ACAGGCAGGAAGGCTCATGGCCC CCGGGGTCG ACCGGATCCT TGCACGCAAA CTCGGGGGG TGGATCTTGA CTATCTCAG CAGATCTTATTTTTTTT TGTTTTTTTTTT	CAACGAAGAG GCATCTCTCCCA GCTCCAGGGC CGCTCTTCCT GCTCCAGGGC CCTTTAGGA GCAACGCCAG ACGTCCAGG TTAGCAGTTTT TTAGTTTTCT AAAGTAAAGC ACGTCGCAG CAACGCAGC ACGTCGACAG ACGTCGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACTTGTATAC GAAAAGAGAAA	I GAGTIGGAAAG GCAGAAGGAT GGCGGTGCTG GCCTGGACGCC CGCGCGCGCCC CTGGGCCGCC CTGGGCCGCC CTGGGCCGCG CCTCCTGAAG CACAGAGCAT TCCAAAAGAA TTTCAATCGG GACTCACAGT TTCATCTGTT	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080 1140
50 55 60 65	1 GAGAAGCCT CCCCGGTCCC CTGGGGCTGT GACCTGCACG GGCGGGAGCG GGCGCCTCA ACCGGAGCG GGCCCCTCA ACCGGAGCG GATCTGAAG CTTCTGATTT TTCTGGAAA GCAACTGAAT ATAACACTC ATCAGGTCTA ATCAGGTCTA SEQ ID NO: Nucleic AC	11 CATCCCTTTA CATCCCACCA GCACCTCCACCA GCACACTCC TCAAGCACCA GCACTTCTCC GCTGGTGCT CACGCACGTG CCTGGGTGGC CGGCCTTGGC TGGTGCCCTG TGGTGCCTG TTCAATCCCA TTCAATCTGT TCTATTTTGGA ACTACAGCAT CTGAAGGAGA CTCCTGAGTT TTAAAAAATA 174 DNA Sei id Accessio	AAAAAAAAA AAACCATTTG CCGGGGGACG CAGGGCTTGGG CTTGCTGGTG GCGCTGCTG CTCCCTGGTG GCAGCGCCTG CAACCAGGCC CACCAGGCCTG CAACCAGGCC CACCGATTG CACCGATTG CACCGATTG CACCGATTG CACCGATTG AACAGTGCAA AACATTGAAA AACATTGTA AACATTGTA Quence n #: NM_032	I AAAAAAGGCT ACAGGCAGGAAGGCTCATGGCCC CCGGGGTCG ACCGGATCCT TGCACGCAAA CTCGGGGGG TGGATCTTGA CTATCTCAG CAGATCTTATTTTTTTT TGTTTTTTTTTT	CAACGAAGAG GCATCTCTCCCA GCTCCAGGGC CGCTCTTCCT GCTCCAGGGC CCTTTAGGA GCAACGCCAG ACGTCCAGG TTAGCAGTTTT TTAGTTTTCT AAAGTAAAGC ACGTCGCAG CAACGCAGC ACGTCGACAG ACGTCGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACGTCAGCAG ACTTGTATAC GAAAAGAGAAA	I GAGTIGGAAAG GCAGAAGGAT GGCGGTGCTG GCCTGGACGCC CGCGCGCGCCC CTGGGCCGCC CTGGGCCGCC CTGGGCCGCG CCTCCTGAAG CACAGAGCAT TCCAAAAGAA TTTCAATCGG GACTCACAGT TTCATCTGTT	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080 1140
50 55	1 GAGAAGCCT CCCCGGTCCC CCCGGTCCC CCCGGTCCC GACCTCACG GGCGGGAGCG GGCGCCCTCA ACCGGAGCG GGCCCCTCA ACCGGAGCG GACCTGAGC CATCTGAAGG CTTCTGAATT TTCTGAAAAA TATAACACTC AAGGCCAGT ATTAACTC AAGGCCAGT ATTAACTC AATTACTTTA Seq ID NO: Nucleic Ac Coding seq	11 CTTCCCTTTA CATCCACCA GCACCACCA GCACACTC GCACACTC GCACACTG GCACACTG GCTGGTGGC GGGCCTTCGC TGGTGCCGGG CTCAGTGCCTG TTGACACTGT TCTATTTGGA ACTACTGT TCTATTTGGA ACTACAGCAT TTACAGCAT	21 AAAAAAAAA AAACCATTTG CCGGGGACG CAGGGCCTTG GCCGTGGCA CTTGCTGGTG GCGCCTGCTC CTCCCTGGTG CAACCAGGCC CAACCAGGCC CACCCGATGC AAACAAGCAG GAATATTAAA AAACTGGACAA TACGAGCAGTAT AACATTGGACAAA TACGAGTGATT AACATTGGTA Quence n #: NM_032 .2422 21	AAAAAAGGCT ACAAGGAGGA AGGCTCATGG GGCTACGGCC CCGGCGCTCG ACCGGATCCT TGCAGGCAAA CTCGCGGGCGT TGCACTCAAA CTCGCGGCCT TGCATCTCAG TGCATCTCAG CCAGATCCTTA TGTTTCTTTG CAAATTTCAT TATGTCAACA CCTGTTCTTG GAATGAGTAG TTTTT Z11.5	CAACGAGGGCCCGCTCTTCCTGCTCCAGGGCCCCTTTTACGAGGACTCTTTACGAGGCCCCCTTTTACGAGGCCCCCTTTTACGAGCAGGCCCCTTTTACGAGCAGGCAG	I GAGTIGGAAAG GCAGAAGGAT GGCGGAGTGCTG GCCCTGGACGCC CTGCGCGCGCC CTGCGCCGCC CTGCGCCGCC CTGCGCCGAAC ACACAGAGAA TITCAATCCG GACTCAAAGAA TITCAATCCG GACTCACAGT TTCAATCCG TTCATCGCTGGT TTCATCGCT TTCATCGCT TTCATCGCT TTCATCGCT TTCATCGCT TTCATCGCT TTCATCGCT TTCATCTGGT TGTTTTGAAT	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080 1140
50 55 60 65	1 GAGAAGCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGCOGGAGC GTGCTGACG GTGCTGACG GTGCTGACG GGGCCCTCA ACCGGGAGCG GAGCTGCGGC GATCTGAAGG CTTCTGATTT TTCTGGAATA TATAACACTC AACAGCCAGT ATCAGGTCTA ATAACAGCA TATTGCTTTA ATAACAGCA TATTGCTTTA CAGGCCAGT ATCAGGTCTA ATAACAGCA TATTGCTTTA CAGGCCAGT CAGGCCAGT CAGGCCAGT ACCGGTCTA ATAACAGCA TATTGCTTTA CAGGCCAGT CAGCCAGT CAGGCCAGT CAGCCAGT CAGGCCAGT CAGCCAGT 11 CTTCCCTTTA CATCCCACCA GCACCACCA GCACCACCAC GCACTTCTCC GCACCACGTG GCACGACGTG GCACGACGTG CCTGGGTGGC GGCCTTGGC GGGCCTTGGC TGGGCGTG TCTAGTCCCA TTACATCTGT TCTATTTGGA AAGAAAGA CAGCATGAA CTCGAGGGAG TTAAAAAATA 174 DNA Sei did Accessio uence: 152. 11	21 MARARARAA AACCATTTG CCGGGGGACG CCTGGCGG CTTGCTGGTG GCGCTGCTG CTCCCTGGTG GCAGCGCCTG CAACCAGGCC CACCAGGCC CACAAA AGAGTGCACAA AGAGTGCACAA AGAGTGCACAA AGAGTGCACAA AGAGTTGCACAAA AGAGTGGCAG CTTCCACAAA CACTTTT AACATTGGTA CCGTTTT AACATTGGTA CCGTTTT CACCATTT CACCACAC CACCAC CACCAC CACCAC CACCAC CACCAC	AAAAAAGGCT ACAAGGAGGA AGGCTCATGG GGCTACGGCC CCGGCGCTCG ACCGGATCCT TGCAGGCAAA CTCGGGGGCT TGCACGCAAA CTCGGGGCT TGCATCTTGA CTATCTCCAG TGATCTTTG CAAATTTCAT TATGTCAACA CCTGTTCTTG GAATTAGATTA TATGTCAACA CCTGTTCTTG GAATTAGATTA	CATCTCTCGCA GCACGAGGGG GGAGGTCTCCT GCTCCAGGGC CCTCTTCCT GCTCCAGGGC CCTTTTACGA GCAACCGCAG TAGCAGGTGT TTAGTTTTCT TAGCAGGTC AAAGTAAAGC ACGTGTATAC CAAAAAAAAAA	I GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGGACGCC CGCCTGGGCTAC CCGCGCAGT GCCCCCGCGCC CTGCGCCGCC CTGCGCCGCAGT TCCACAAAGAA TTTCAATCCG GACTCACAAAGAA TTTCAATCCG TTCATCAGT TCCATCAGT TCC	120 180 240 300 360 420 480 540 660 720 840 900 1020 1080 1175	
50 55 60 65	1 GAGAAGCCT CCCCGGTCCC CCCGGTCCC CCCGGTCCC CCCGGTCCC GACCTCACG GGCGGGGGGG GGCCCCTCA ACCGGGACCG GGGCCTCGCACCG GACCTGAGC GACCTGAGC CATCTGAAGG CTTCTGAATT TTCTGAAAGA CCACTGAAT TATAACACTC AAGGGCCAGT ATTACTTTA Seq ID NO: NCcleic Ac CCding seq 1 GGCTCGGGGGGG GGCTCGGGGG GGCTCGGGGGGGGGG	11 CTTCCCTTTA CATCCACCA GCGGCACCAC GCGCGACCAC GCATCTTCTC GCCGGCTCTT CACCACCATG GCTGGTCGT CGTGGCCGG CTGGTGGCCGG CTCGGTGCCCTG TGTGCCCTG TTACATCTGT TCTAATTTGGA ACTACACCAT TTACATCTGT TTAAAAAATA 174 DNA Sei did Accessio uence: 152. 11	21 MARARARAA AACCATTTG CCGGGGACG CAGGGCCTTG GCCGTGGCA CTTGCTGGTG GCAGCGCTGCTC CTCCCTGGTG CAGCGCCTG CACCAGGGC CACCCGATGCA ACAGGGCC GAATATAAA AGAGTGGCAG TAGCACAAA TACGGTGATT AACATTGGTA quence n #: NM_032 .2422 21 GAGGCCGATAC	AAAAAAGGCCCC	CTTCTCGCA GCAGGAGGG GCAGGAGGG GGTCAGCGC TCAGCGGGC TCAGCGGGC TCAGCGGGC TCAGCGGGC TCAGCGGGC TCAGCGGGC TTAGCGAG ACGTGCAGGA ACGTGCAGGA ACGTGCAGGA ACGTGCAGGA ACGTGCAGGA ACGTGTATAC AAAGAAAAAAAAA 41 AGGGCGCCCCG	GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGACGCGC CCTGGGCTAC CCGCGCGAGT CGCCGCGCCC CTGCGCCGCC CTCCTGAAG TATCATCATT GCAGCTGAAA CACAGAGCAT TCCAAAAGAA TTCAATACCG GACTCACAGT TTCATCAGT TTCATCAGT TTCATCTGGT TTCATCTGGT TGTTTTGAAT \$1	120 180 240 300 360 420 480 540 660 720 780 900 91020 1080 1140 1175
50 55 60 65	1	11 CTTCCCTTTA CATCCACCA GCGGACGCC GCGGACGCC GCACACT GCACGACACT GCACCACGT GCTGCGCGG CCTGGGTCGT CGTGGCCGG CTCGGTCGC CTGGTCGCCGG CTCAGTCCCA TACATCTGT TCTATTTGA TGGCAAAAGA ACTACAGCAT TTAAAAAATA 174 DNA Se id ACCESSIO uence: 152. 11 CCCCCCGCGCCGC CCGCCGCCGC CCTCCCCCCC CTTCCCCCCCC	21 MARARARA AACCATTIG CCGGGGGACG CAGCGCCTTG CGCGTGGCA CTTCCTGGTG GCGCTGCTC CTCCCTGGTG CGCGCGCCC CACCCGATGC ACACCAGGCC GGTATTGCACAAA AACAGGGCAAA AACAGGGCAAA AACAGGGCAAA AACAGGGCAAA AACAGGGCAAA AACAGGGACAG GAATATTAAA AGACTTGCACAAA TACGGCGATGC ###################################	AAAAAAGGCCCCGG	CONTINUES OF THE PROPERTY OF T	I GAGTGGAAAG GCAGAAGGAT GCCGCTCCATCTGGACCCCC CTCCACACGCC CTCCACACGCC CTCCACACGCC CTCAAAAGAA TTCAAAAGAA TTCAAAATCCC GACTCAAAAGAA TTCATCATT CAAAAAGAA TTCAATCATT CAAAAAGAA TTCAATCATT CAAAAAGAA TTCAAAATCCC GACTCACAGT TTCATCTGT TCATCTGG CTCCATCTGG CCCCATCTGACCGC TCCATCTGG CTCCATCTGG TCATCTG CTCATCTG CTCATCTG CTCATCTG CTCATCTG CTCATCTG CTCATCTG CTCATCTG CTCATCTG CTCCATCTG CTCATCTG TTCTTTTTTTTTT	120 180 240 300 360 420 480 540 560 720 840 900 1020 1080 1140 1175
50 55 60 65	1 GAGAAGCCT CCCCGGTCCC CTGGGCCTGTCCC CTGGGCCTGTCACG GGCOGGAGC GGCGCCCTCA ACCGGAGCG GAGCTGCGGC GAGCTGCGGC GATCTGAAGG CTTCTGATTT TTCTGGAATA ATAACACTC ATCAGGTCTA Seq ID NO: Nucleic Ac Coding seq 1 GGTTGGGGG GGCTTGGGGC TATCTTGGCC TATCTTGGCC	11 CTTCCCTTTA CATCCCACCA GCACCACCA GCACCACCA GCACACTC CACCACAGG CACCACGTG CCTCGACGCAGG CCTGGGTGGC CGGCCTTCGC TGGGCCGTG CTCAGTCCCAC TTACATCTGT TCTATTTGGA AAGAAAGA CTCCTGAGGTG TTAAAAAATA 174 DNA Sei did ACCESSio uence: 152. 11 CCGCGGGCGG TGGTCCCCCCC TCGTCCCCCCC TCGCTCCCCCCT TCAGCTGTT TCAGTTTTCAGCATT TTAAAAATA TTAAAAAATA TTAAAAATA TTAAAAATA TTAAAAATA TTAAAAATA TTAAAAATA TTAAAAATA TTAAAAATA TTAAAAATA TTAAAAATA TTAACACTT TTAAAAATA TTAAAAATA TTAACACTT TTAACACT TTAACACT TTAACACT TTA	21 MARARARAA AACCATTTG CCGGGGGACG CCGGGGGCCTTG GCCGTGGCA CTTGCTGGTG GCGCTGCTC CTCCCTGGTG GCAGCGCCTG CAACCAGGCC CACCGATTGC ACACGAGCA CACCGATTGCA ACAGGACAG GTTGCACAAA AGAGTAGCAG GTTGCACAAA AGAGTAGCAGT ACACTGGTAT AACATTGGTA TACGGTGATT AACATTGGTA QUENCE n #: NN_032 .2422 21 GAGGCGGATA GGGCGCCCCCT TTGAAGTCAC	AAAAAAGCCCCCCCACACGGCAGCACCCCGCCGCCGCCCGCCCCGCCCCGCCCCCC	CALCACACA ACACACACACACACACACACACACACACA	GAGTGGAAAG GCAGAAGGAT GCCGGAGTGCTG GCTGACGGCC CCCCGCAGTC GCCCCGCAGT GCCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTCCCCCCCC	120 180 240 300 360 420 480 540 660 720 780 900 91020 1080 1140 1175
50 55 60 65 70	1 GAGAAGCCT CCCCGGTCCC CCCCGGTCCC CCCCGGTCCC CCCCGGCCGG	11 CTTCCCTTTA CATCCACCA GCGGACGCC GCGGACGCC GCACCACGG GCATCTTCTC GCCGGTCGT GCTGGGGGG GCCTTGGC GGCCTTGGC GGCCTTGGC TGGTCGCGG GCCTTGGC TGGTCGCGG TCAGTCCCGA TTACATCTGT TCTAATTTGGA ACTACAGCAT TTAAAAAATA 174 DNA Se id Accessio uence: 152. 11 CCGCCGGGCGG TCGCGGCGCG TCGCTGCGCG TCAGTGTCGCACG TCGCTGCGCGCG TCGCTGCTGC	21 MARARARAA AAACCATTTG CCGGGGACG CAGGGCCTTG GCCGTGGCA CTTGCTGGTG GCAGCGCTGCTC CTCCCTGGTG GCAGCGCTG CAACCAGGCC CACCGATTGC CACCGATGC ACACGAGCA CACCGATGC ACACGAGCA ACAGGAGCAG TTGCACAAA AGAGTGGCAAA AGAGTGGCAG TUGACCAGGAGCAG TUGACCAGGAGCAG TUGACCAGAGCAGAGAAA AGAGTGGCAAAA AGAGTGGCAAAA TACGGTGATTA AACATTGGTA TUGACCATTT AACATTGGTA TUGACCAGAGCAGAGAGAAAAAAAAAAAAAAAAAAAAAAA	AAAAAAGGCTAAGGAGAAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	COCCACCACA	GAGTGGAAAG GCAGAAGGAT GGCGGCTCC CCCCGCGCTC GTGCGCCCC CTCCTGAAC CCTCCTGAAC CCTCCTGAAC CCTCCTGAAC CCTCCTGAAC CCTCCTGAAC CCTCCTGAAC CACAGAGCAT TCCAAAAAGAA TTCCAATT TCATCTGGT TTCATCTGGT TTCATCTGGT TTCATCTGGT TCCTCTGAAT CCCAACAGGCAT TCCAACAGGCAT TCCAACAGGCAT TCCACCTCTT TGGCACCCCCTCTT TGGCCACCCTCTT TGGCCACCCCTCTT TGGCCACCCCCTCTT TGGCCACCCCCTCTT TGGCCACCCCCTCTT TGGCCACCCCCTCTT TGGCCACCCCCCTCTT TGGCCACCCCCCTCTT TGGCCACCCCCCTCTT TGGCCACCCCCCTCTT TGGCCACCCCCCTCTT TGGCCACCCCCCTCTT TGGCCACCCCCCCTCTT TGGCCACCCCCCCTCTT TGGCCACCCCCCCTCTT TGGCCACCCCCCCTCTT TGGCCACCCCCCCTCTT TGGCCACCCCCCCTCTT TGGCCACCCCCCCTCTT TGGCCACCCCCCCTCTT TGGCCACCCCCCCCCTCTT TGGCCACCCCCCCCCC	120 180 240 300 360 420 480 540 660 720 780 840 960 1080 1140 1175
50 55 60 65	1 GAGAAGCCT CCCCGGTCCC CCCCGGTCCC CCCCGGTCCC CCCCGGCCGG	11 CTTCCCTTTA CATCCACCA GCGGACGCC GCGGACGCC GCACCACGG GCATCTTCTC GCCGGTCGT GCTGGGGGG GCCTTGGC GGCCTTGGC GGCCTTGGC TGGTCGCGG GCCTTGGC TGGTCGCGG TCAGTCCCGA TTACATCTGT TCTAATTTGGA ACTACAGCAT TTAAAAAATA 174 DNA Se id Accessio uence: 152. 11 CCGCCGGGCGG TCGCGGCGCG TCGCTGCGCG TCAGTGTCGCACG TCGCTGCGCGCG TCGCTGCTGC	21 MARARARAA AAACCATTTG CCGGGGACG CAGGGCCTTG GCCGTGGCA CTTGCTGGTG GCAGCGCTGCTC CTCCCTGGTG GCAGCGCTG CAACCAGGCC CACCGATTGC CACCGATGC ACACGAGCA CACCGATGC ACACGAGCA ACAGGAGCAG TTGCACAAA AGAGTGGCAAA AGAGTGGCAG TUGACCAGGAGCAG TUGACCAGGAGCAG TUGACCAGAGCAGAGAAA AGAGTGGCAAAA AGAGTGGCAAAA TACGGTGATTA AACATTGGTA TUGACCATTT AACATTGGTA TUGACCAGAGCAGAGAGAAAAAAAAAAAAAAAAAAAAAAA	AAAAAAGGCTAAGGAGAAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	COCCACCACA	GAGTGGAAAG GCAGAAGGAT GGCGGCTCC CCCCGCGCTC GTGCGCCCC CTCCTGAAC CCTCCTGAAC CCTCCTGAAC CCTCCTGAAC CCTCCTGAAC CCTCCTGAAC CCTCCTGAAC CACAGAGCAT TCCAAAAAGAA TTCCAATT TCATCTGGT TTCATCTGGT TTCATCTGGT TTCATCTGGT TCCTCTGAAT CCCAACAGGCAT TCCAACAGGCAT TCCAACAGGCAT TCCACCTCTT TGGCACCCCCTCTT TGGCCACCCTCTT TGGCCACCCCTCTT TGGCCACCCCCTCTT TGGCCACCCCCTCTT TGGCCACCCCCTCTT TGGCCACCCCCTCTT TGGCCACCCCCCTCTT TGGCCACCCCCCTCTT TGGCCACCCCCCTCTT TGGCCACCCCCCTCTT TGGCCACCCCCCTCTT TGGCCACCCCCCTCTT TGGCCACCCCCCCTCTT TGGCCACCCCCCCTCTT TGGCCACCCCCCCTCTT TGGCCACCCCCCCTCTT TGGCCACCCCCCCTCTT TGGCCACCCCCCCTCTT TGGCCACCCCCCCTCTT TGGCCACCCCCCCTCTT TGGCCACCCCCCCCCTCTT TGGCCACCCCCCCCCC	120 180 240 300 360 420 480 540 760 780 840 960 1020 1140 1175
50 55 60 65 70	1 GAGAAGCCCT CCCCGGTCCC CCCGGTCCC CCCGGTCCC GGCGGGGGGG GGCCCCTCA ACCGGAGCG GGCCCCTCA ACCGGAGCG GGCCCCTCA ACCGGAGCG GATCTGAAG CTTCTGATT TTCTGGAAA GCAACTGAAT ATAACACTC AACAGCCAGT ATCAGTCTA Seq ID NO: Nucleic Ac Coding seq 1 GGCTGGGGGG TATCTGGCC TATCTTGCCC TATCTTGCCC TATCTTGCCC TATCTTGCCC TATCTTGCCC TATCTTGCCC TATCTTGCCC TATCTTGCCC TATCTTGCCC TATCTTGCCC TATCTTGCCC TATCTTGCCC TATCTTGCCC TATCTTGCCC TATCTTGCCC TATCTTGCCC TATCTTGCCC TATCTTGCCC TATCTTGCCC TATCTTCCTC TAGCCC TATCTTCCTC TAGCCC TATCTTCCTC TAGCCC TATCTTCCTC TAGCCC TATCTTCCTC TAGCCC TATCTTCCTC TAGCCC TATCTTCCTC TATCTTCCTC TAGCCC TATCTTCCTC TAGCCC TATCTTCCTC TAGCCC TATCTTCCTC TAGCCC TATCTTCCTC TAGCCC TATCTTCCTC TAGCCC TAGCCC TATCTTCCTC TAGCCC TATCTTCCTC TAGCCC TATCTTCCTC TAGCCC TATCTTCCTC TAGCCC TATCTTCCTC TAGCCC TATCTTCCTC TAGCCC TATCTTCCTC TAGCCC TATCTTCCTC TAGCCC TAGCCC TAGCCC TACCTCC TAGCCC TACCTCC TACCTC TAGCCC TACCTC TAGCCC TACCTC TAGCC TAGCCC TACCTC TAGCC TACCTC TAGCC TACCTC TAGCC TACCT TAGCC TACCT TAGCC TACCT TAGCC TAGCC TACCT TAGCC TACCT TAGCC TACCT TAGCC TACCT TAGCC TACCT TAGCC TACCT TAGCC TACCT	11 CATCCCTTTA CATCCCACCA GCACCTCCACCA GCACACTCCCAC GCACACTTCCC GCACGTCTCACCACGCACCTC CACCACGTG CGCTGGTGCCCGG CGCCCTTCGC TGGTGCCCTG TGGTGCCCTG TCAGTCCCA TTACATCTGT TCTATTTTGGA ACTACAGCAT CTGAAGGAGA TTAAAAAATA ATACAGCAT TTAAAAAATA 174 DNA Sei id ACCESSIO uence: 152. 11	21 MARARARA AACCATTIG CCGGGGGCCC CAGCGCCTTIG GCCGTGGCA CTTGCTGGTG GCGCTGCTG CTCCCTGGTG GCAGCGCCTG CAACCAGCCC CACCCGATGC AACCAGCCC CACCGATTG CACCGATTG AACATTAAA AGAGTGGCAG GAATATTAAA AGAGTGGAT ATACCTTTT AACATTGTA QUENCE n #: NM_032 .2422 21 GAGGCGGATA CGGCGCCCCC CCAGAGCCCCC CCAGAGCCCCCC CAGAGCCCCCCC CCAGAGCCCCCCC CCAGAGCCCCCCC CCAGAGCCCCCCC CCAGAGCCCCCCC CCAGAGCCCCCCC CCAGAGCCCCCCC CCAGAGCCCCCCC CCAGAGCCCCCCCC	AAAAAAGGCTAGGGAGGAGGAGGAGGAGGAGGGGGGGGGG	CALCAGTACA AGAGGAGGA GAACGAGGA GAACGAGGA GCAACGCAG GCTCTACGCGC GCTCAGCGC CCTTTTACGA GCAACCGCAG ACGTCAGGA TAGGTGAGGA TAGGTTTTT TAGTTTTCT TAGATAAGC CAACAGTAAA CATTGTATACA AAAAAAAAAA	GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGACGCCG CCTCGGACCCC CTGCGCCGCC CTGCCCCGCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTCCCCCCCC	120 180 240 300 360 420 480 540 960 1020 1080 1140 1175
50 55 60 65 70	1 GAGAAGCCT CCCCGGTCCC CTGGGCCTGTCCC CTGGGCCTGTCACG GGCOGGAGC GGCGCCTCA ACCGGAGCG GAGCTGCGGC GAGCTGCGGC GAGCTGCGGC GATCTGAAGG CTTCTGATTT TTCTGGAATA ATAACACTC AAGGCCAGT ATAACAGTCT AAGGCCAGT ATAACAGTCT ATAACAGTCT ATAACAGTCT ATAACAGTCT ATAACAGTCT 1 GGCTGGGGG GGCCGGTGGGGG TATCTGGCC TAGTTGGCC TAGTTCCTG TAAGCTCCGG CCCAGGGCCAG CCCAGGGCCAG CCCAGGCCCAGCCC CTGTTCCTGCC TAAGCTCCGG CCAGGGCCAG	11 CTTCCCTTTA CATCCACCA GCACCAC GCACCAC GCACACTC TCAAGCACCA GCACTTCTCC GCTGGTGGTGC GCGGCGTGGC GGCCTTGGC TGGGCGGG CTCAGTCCCA TTACATCTGT TCTATTTGGA AAGAAAGA AAGCATGAA ACTACAGCAT TTAAAAAATA 174 DNA Sei did ACCESSio uence: 152. 11 CCGCGGGCGG TGGTGCCCCC TGGGGCACCG TGGGGCACCG TGGGGCACCG TGGGGCACCG TGGGGCACCG TGGGGCACCG TGGGGCACCG TGGGGCACCG TGGGGCACCG	21 MARARARAA AACCATTTG CCGGGGGACG CCGGGGGCTGGGA CTTGCTGGTG GCGCTGGTG GCGCTGGTG GCGCTGGTG GCAGCGCTTG CAACCAGGCC CACCGATGC ACAGGACAG GTTGTTGGGC ACAGGAGCAG GTTGCACAAA AGAGTAGCAG GTTGCACAAA AGAGTAGCAG TACGGTGATT AACATTGGTA TACGGTGATT ACATTGGTA TGGGCGCCCCC CAGGGCCCCC CAGGGGCCCCC CAGGGGGCCCCC CAGGGGCCCCC CAGGCCCCCC CAGGGGCCCCC CAGGGGCCCCC CAGGGGCCCCC CAGGGGCCCCC CAGGGGCCCCC CAGGGGCCCCC CAGGGCCCCC CAGGGCCCCC CAGGGCCCCCC CAGGGCCCCCC CAGGCCCCCC CAGGGCCCCCC CAGGCCCCCC AGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCCC CAGGCCCCCC CAGCCCCCCC CAGCCCCCCC CAGCCCCCC CAGCCCCCCC CAGCCCCCCC CACCCCCCC CACCCCCCC CACCCCCCCC	AAAAAAGGCTAAGGAAGAAGAGAAGAGAGAGAGAGAGAGA	CALCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	GAGTGGAAAG GCAGAAGGAT GCCGCACCC CCCCCCCCCC	120 180 240 300 360 420 480 540 660 780 900 960 1080 1140 1175
50 55 60 65 70	1 GAGAAGCCCT CCCCGGTCCC CCCCGGTCCC CCCCGGTCCC CCCCGGCCGG	11 CTTCCCTTTA CATCCACCA GCGGACGCC GCGGACGCC GCACCACTG GCACCACGGGCCTTCGC CGGCGTCGC CGGCCTTCGC CGGCCTTCGC TGGTCGCCGG CTCAGTCCCAC TTACATCTGT TCTAATTTGGA ACTACACCAT TTAAAAAATA LTA DNA Se id Accessio uence: 152. 11 CCGCCGGCCGC TCGCCTCGC TCGCTGCCCGC TCGCCTGCCCCC TCGCTGCCCCC TCGCTGCCCCC TCGCTCCTCCC CTGCGCCTTCGC CTGCGCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCCC CTGCGCCCTCCC CTGCGCCCTCCC CTGCGCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCACCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCTTCGCCTTCGCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCGCCCTTCCCTTCCTTCCTTCTT	21 MARARARAA AACCATTTG CCGGGGACG CAGGGCCTTG GCCGTGGCA CTTGCTGGTG GCAGCGCTGCTC CTCCCTGGTG GCAGCGCCTG CAACCAGGCC CACCGATGC ACACGATGC ACACGAGCC CACCGATGC ACACGAGCA ACAGGAGCAG TTGCACAAA AGAGTGGCCTT AACATTGGTA Quence #: NM_032 _21 GAGGGCGGATA CGGCGCCCC CAGAAGTCCCCC CAGAAGAGCAA TGTGTGATGATAA AGAGTGCCTTT AACATTGGTA TTGACTAA CGCCCCCC CAGAAGAGCAA TGTGTGATGAA TGATGTATGATCAA TGTGTGATGAA TGATGATCACA TGTGTGATGAA	AAAAAAGGCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	COCCACAGAG AGAGGGGCCCCGGCCCCGGCCCCGGCCCCGGCCCCGGCCCCGGCCCC	GAGTGGAAAG GCAGAAGGAT GCOGGTGCTG GCTGACGCC CCTCTGGACC CCTGGGCTAC CCGCCGCTC GTGCGCCTC GTGCGCCTC GTGCGCCGC CCTCCTGAAG TATCATCATT GCAGCTGAAA CACAGAGCAT TCCAAAAGAA TTCAATCCG GACTCACAGT TTCATCTGGT TGTTTTGAAT 51 GGGAGGGAGC CCTCCATCTGC CCACCCTCTT TGGGCACCAC AGGTGCTGCA ACGAGCCAC AGGTGCTGCA ACGAGCCAC AGGTGCTCA ACGAGCCCAC AGGTGCTCAC AGGTGCCAC AGGTGCCCAC GGTGCCCAC AGGTGCCCAC AGGTGCCCAC AGGTGCCCAC AGGTGCCCAC AGGTGCCAC	120 180 240 300 360 420 480 540 960 1020 1080 1140 1175
50 55 60 65 70	1 GAGAAGCCT CCCCGGTCCC CTGGGGCTGT GACCTGCACG GGCGGGGGGG GGCCCCTCA ACCGGATCGG GGGCCCCTCA ACCGGAGGG GATCTGAAGG CTTCTGATTT TTCTGGAAA GCAACTGAAT ATAACACTC AACAGCCAGT ATCAGTTA Seq ID NO: Nucleic Ac Coding seq 1 GGCTTGGGGG TATCTTGCCC TATCTTGCCC TAGCTCCTTACCC TAGCGCCAGG TAGCGCCAGG	11 CATTCCCTTTA CATCCCACCA GCACCTCCACCA GCACACTCCCAC GCACACTCC GCACACTCCCCCCCCCC	21 AAAAAAAAA AAACCATTIG CCGGGGGCCC CAGGGCCTTIG GCCGTGGCA CTTGCTGCTG GCGCTGCCA CTTGCTGCTG GCAGCCCTG CAACCAGCCC CACCCGATTGC AACCAGCCC AACCGATTGCA AACATTTAAA AGAGTGATT ATGACCTTTT AACATTTGTA QUENCE n #: NM_032 .2422 21 GAGGGCGGATA GGGCGGGATA CGGCAGCCCCC CCCAGCCCCCC CAGAGAGCAA TGTGTAATGA AAGGTGCATT AAGAGTGATA AAGGTGATA AAGGTGATA AAGGTGATA AAGTTGATA AAGGTGATT AAGAGTAAC TTGAAGTAAA AAGTTGATGA AAGGTGCATT TGGACAATTTT AAGAGTAATTAAA AAGGTGCATT TGGACAATTT TGGACAATTT TGGACAATTT TGGACAATTT TGGACAATTT TGGACAATTT TGGACAATTT TGGACAATTT TGGACAATTT TGGACAATTT TGGACAATTT TGGACAATTT TGAACAATTT TGGACAATTT TGACAATTT TGGACAATTT TGGACAATTT TGGACAATTT TGGACAATTT TGGACAATTT TG	AAAAAAGGCTAGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	GCTTCTCGCA GCTTCTCGCA CAAGGAGGAG AGAAGTTTCG TGGTGACCCT GCTCCAGCGG GCTCTTCCT GCTCCAGCGG CCTCTCGCG CCTCAGCGCGC CCTTTTAGGA ACGCAGG TAGCAGTGT TAGTTTTCT TAGTTTTCT TAGAAAGCAGAAG CCTTTGTAGA AAAAAAAAAA	GAGTGGAAAG GCAGAAGGAT GCGGTGCTG GCTGACGCC CCCCCCCCCC	120 180 240 300 360 420 480 540 660 780 900 960 1080 1140 1175
50 55 60 65 70	1 GAGAAGCCT CCCCGGTCCC CTGGGGCTGT GACCTGCACG GGCGGGGGGG GGCCCCTCA ACCGGATCGG GGGCCCCTCA ACCGGAGGG GATCTGAAGG CTTCTGATTT TTCTGGAAA GCAACTGAAT ATAACACTC AACAGCCAGT ATCAGTTA Seq ID NO: Nucleic Ac Coding seq 1 GGCTTGGGGG TATCTTGCCC TATCTTGCCC TAGCTCCTTACCC TAGCGCCAGG TAGCGCCAGG	11 CATTCCCTTTA CATCCCACCA GCACCTCCACCA GCACACTCCCAC GCACACTCC GCACACTCCCCCCCCCC	21 AAAAAAAAA AAACCATTIG CCGGGGGCCC CAGGGCCTTIG GCCGTGGCA CTTGCTGCTG GCGCTGCCA CTTGCTGCTG GCAGCCCTG CAACCAGCCC CACCCGATTGC AACCAGCCC AACCGATTGCA AACATTTAAA AGAGTGATT ATGACCTTTT AACATTTGTA QUENCE n #: NM_032 .2422 21 GAGGGCGGATA GGGCGGGATA CGGCAGCCCCC CCCAGCCCCCC CAGAGAGCAA TGTGTAATGA AAGGTGCATT AAGAGTGATA AAGGTGATA AAGGTGATA AAGGTGATA AAGTTGATA AAGGTGATTA AAGGTGATA TTGAACATTTT AAGAGTAAA TTGAACATTTT TGAACAATTT TGGACAATTT TGGACAATTT TGGACAATTT TGAACAATTT TTT TTT TTT TTT TTT TTT TTT TTT	AAAAAAGGCTAGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	GCTTCTCGCA GCTTCTCGCA CAAGGAGGAG AGAAGTTTCG TGGTGACCCT GCTCCAGCGG GCTCTTCCT GCTCCAGCGG CCTCTCGCG CCTCAGCGCGC CCTTTTAGGA ACGCAGG TAGCAGTGT TAGTTTTCT TAGTTTTCT TAGAAAGCAGAAG CCTTTGTAGA AAAAAAAAAA	GAGTGGAAAG GCAGAAGGAT GCGGTGCTG GCTGACGCC CCCCCCCCCC	120 180 240 300 360 420 480 540 560 720 1020 1020 1140 1175
50 55 60 65 70	1 GAGAAGCCCT CCCCGGTCCC CCCGGTCCC CCCGGTCCC GGCGGGGGGG GGCCGCTGACGGGGGGGGGG	11 CTTCCCTTTA CATCCACCA GCACCACCA GCACCACCA GCACACTC GCACACCACGTC GCACGACGTC CACCACGTG CCTGGTCGCCGG CTGGTGCCCGG CTCGTCTGC TGGTGCCTG TTGATCTGAC TTACATCTGT TCTATTTGGA ACTACACCAT TTACACCAT TTACACCAT TTACAGCAT TTAAAAATA 174 DNA Sei did ACCEBSio ouence: 152. 11 CCGCCGGCGCG TGGGTGCCCTGG TCTGGTGTGCCCC CTGCTGTGTGCCCC CTGCTGTGGCCCC CTGGGCCCCC CTGGGCCCCC CTGGGCCCCC CTGGGCCCCC CTGGCCCCC CTGGCCTCCC CCCATCTGCC CCCATCTGCC CTCACTTCGCCC CTGGCCTCC CCCATCTGCC CTCACTCTGCC CTGCTCCCCC CTGGCCCCC CTGGCCCCC CTGGCCCCC CTGCGCCCC CTGCTCCC CCCATCTGCC CTCACTCTGCC CTCACTTGCC CTCACTTCTGC CTCACTTGCC CTCACTTCTGC CTCACTTGCC CTCACTCTGCC TCACTCTCC CTCACTCTCC CTCACTCTCC CTCACTCTCC CTCACTCTCC CTCACTCTCC CTCACTCTCC CTCACTCTCC CTCACTCTCC CTCACTCTCC CTCACTCTCC CTCACTCTCC CTCACTCTCC CTCACTCTCC CTCACTCTCC CTCACTCTCC CTCACTCTCC CTCACTCTCC CTCACTCTCC CTCACTCTC CTCACTCTC CTCACTCTC CTCACTCTC CTCACTCTC CTCACTCT CTCAC	21 MARARARAA AACCATTTG CCGGGGACG CAGGGCCTTG GCCGTGGCA CTTGCTGGTG GCAGCGCCTG GCAGCGCCTG GCAGCGCCTG CAACCAGGCC CACCCGATGC ACACGAGCA CACCGATGC ACACGAGCA CACCGATGC ACACGAGCA CACCGATGC ACACGAGCA CACCGATGC ACACGAGCA CACCGATGC ACACGAGCA CACCCGATGC ACACGAGCA CACCCGATGC ACACGACCAC CCCAGAGAGCAA AGCTGCCTT TGGACAAAA AGCTGCCTT TGGACACCCCC CAGAGAGCAA AGGTGCCCCT TGGACACATGT TGGACACATGT TGGACACTT TGGACACATGT TGGACACATGT TGGACACATGT TGGACACATGT TGGACACATGT TGGACACATGT TGGACACATGT TGGACACATGT TGGACACATGT TGGACACATGT TGGGGACATTCA	I AAAAAAGGCT ACAGGCAGGAGGAGGATCTTG AAAAAGGCTCAGGCCCCAAAGGCAGGGATCGT TGCACGGACGGATCTT TGCACGCAAAGCCTCAAAGCCTCAAAGCCTCAAAGCCTCAAAGCCTCAAATTCATTC	CACAGAGCACAGAGAGCACACAGAGACACAGAGACACAGAGACACAGAGACACAGAGACACAGAGACACAGAGACACACAGAGACACACAGAGACCACAGAGACACACAGAGACACACAGAGACACACAGAGACACACAGAGACACACAGAGACACACAGAGACACACAGAGACACACAGAGACACACACAGAGACACACACAGAGACACACACAGAGACACACACAGAGACACACACAGAGACACACACAGAGACACACACAGAGACACACACAGAGACACACACAGAGACACACACAGAGACACACACAGAGACACACAGAGACACACACAGAGACACACACAGAGACACACACAGAGAC	GAGTGGAAAG GCAGAAGGAT GGCGGGTGCTG GCTGACGCGC CCTCGGACCCCC CTGCGCCACC CTGCGCCACC CTGCGCCACC CTGCCCGCG CCTCCTGAAG TATCATCATT CCAAAAGGA TTCAAAACAA TTCAAACCA GACTCACAGT TTCATCTGGT TGTTTTGAAT \$1 GGGAGGGAGC CCACCCTCTT TGGGCACCA AGGTGCTCA AGGTGCTCA AGGTGCCA AGGTGCTCA AGGTGCTCA AGGTGCTCA AGGTGCCCA AGGTGCCCA AGGTGCCCA ACGTACGCCA ACGTACGCCCA ACGTACGCCCA ACGTACGCCCA ACGTACGCCCA ACGTACGCCCA ACGTACGCCCA ACGTACGCCCA ACGTACGCCCA ACGTACGCCCA ACGTACGCCCA ACGTACGGCCCA ACGTACGCCCA ACGTACGCCCA ACGTACGGCCCA ACGTACGGCCCA ACGTACGGCCCA ACGTACGGCCCA ACGTACGGCCCA ACGTACGGCCA ACGTACGGCCA ACGTACGGCCCA ACGTACGGCCA ACGTACGGCCCA ACGTACGGCCA ACGTACGGCCCA ACGTACGGCCA ACGTACGGCCA ACGTACGGCCA ACGTACGGCCA ACGTACGGCCA ACGTACGGCCA ACGTACGGCCA ACGTACGGCCA ACGTACGGCCA ACGTACGCCA ACGTACGGCCA ACGTACGGCCA ACGTACGGCCA ACGTACGGCCA ACGTACGCCA ACGTACGGCCA ACGTACGCCA GTACGCCA ACGTACCA ACGTACGCCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACCA ACGTACA ACGTACCA ACGTACCA ACGTACA ACGTACCA ACGTACA ACGTA	120 180 240 300 360 420 480 660 780 840 960 1020 1140 1175
50 55 60 65 70	1 GAGAAGCCT CCCCGGTCCC CCCCGGTCCC CCCCGGTCCC CCCCGGTCCC CCCCGGCCGG	11 CATCCCTTTA CATCCACCA GCGGACGCC GCGGACGCC GCACCACGG GCACCACT GCCGGGCGTCGC CGGCCTTCGC CGGCCTTCGC CGGCCTTCGC TGGTCGCCGG CTCAGTCCCAC TTACATCTGT TCTAATTTGGA ACTACACCAT TTAAAAAATA 174 DNA Se id Accessio uence: 152. 11 CCGCCGGCGCG TCGCGCGCC TCGCTCTCGC TCGCCTTCGC TCGCTCTCGC TCGCCTTCGC TCGCCTTCGC TCGCCTTCGC TCGCCTTCGC TCGCCCTTCGC TCTCACCTTCC CCCCCGCCCC TCTCACCTTCC CCCCCGCCCC TCTAATGCC TCTAATGCCT TCTAATGCCT TCTAATGCCT TCTAATGCCT TCTAATGCCT TCTCCCCCCGCCCC CCCCCGCCCCC TCTAATGCCT TCTAATGCCT TCTCACCCCCCCCCC	21 MARARARAA AACCATTTG CCGGGGACG CAGGGCCTTG GCCGTGGCA CTTGCTGGTG GCGCCTGCTC CTCCCTGGTG GCAGCGCCTG CACCCGATGC CACCCGATGC CACCGATGC CACCGATGC CACCGATGC ACACGGACGC GAGTGGCACAA AGAGTGGCAA AGAGTGGCAAA TAGACTTTT AACATTGGTA Quence #: NM_032 _2422 21 GAGGGCGGATA CGGGGCCCCC CAGAGAGCAA TTGTGATGAA TTGTGATGAA TTGTGATGAA TTGTGATGAA TTGTGATGAA TTGTGATGAA TTGTGATGAA TTGTGATGAA TTGTGATGAA TTGTGTATGAA TGAGCAATGT TGGACAATGT TGGACAATGT TGGGCAACTCCC CGGGACGCCCCC CAGAGAGCAA ATGTGTGATGAA ATGTGTGATGAA ATGTGGCTAA TTGGGGATTCAG CGGGACATCAG CGGGACATCAG CGGGACATCAG CGGGACATCAG CGGGACATCAG ATCGTGGCTAA	AAAAAAGGCTA ACAAGCAGGA AGGCTCATGG GGCTACGGCC CCGGGGCTCG TGCACGCAAA CTCGGGGCTCG TGCACGCAAA CTCGGGGCTCG AAGGCGTCGG CTACTCCAG CAAATTCAT TATGTCAACA CTCTACCAG AAAAAGCCCCC CCAGCCCCGG CAGACCTCGG CCAGCCCCGG CAACTTTGCT TCTTTTT 211.5	COCCACAGAGA AGAGAGAGAGAGAGAGAGAGAGAGAGAGA	GAGTGGAAAG GCAGAAGGAT GCOGGTGCTG GCTGACGCC CCTCGGACC CCTCGGACC CCTCGCACC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTCCCCCCC CTCCCCCCCC	120 180 240 300 420 480 600 660 780 840 960 1080 1140 1175
50 55 60 65 70	1 GAGAAGCCT CCCCGGTCCC CTGGGGCTGG GACCTGCAGG GGGGGGGGG GGGCCCTCA ACCGGGAGGG GAGCTGCAGG GATCTGAAGG CTTCTGATT TTCTGGAAAA GCAACTGAAT ATAACAGTC AACAGGCAGT ATCAGGTCTA Seq ID NO: Nucleic Ac Coding seq 1 GGCTGGGGGG GGCTGGGGG TATCTGTCTT TATCTTGCC TATCTTGCCCCAG CCAGGCCAG ACGGCAGGAGGA CCAGTGCGGG GATCTCCGGG CCAGGCCAGG	11 CATTCCCTTTA CATCCCACCA GCATCTCTCC TCAAGCACCA GCATCTTCTC GCCTGGTGCT GCCTGGTGGCGGG GGCCTTCGC TGGTGCCGTG TGGTGCCTG TGGTGCCTG TGGTGCCTG TGGTGCCTG TCAATCCAC TTCAATCGA TTCAATCGA TTCAATCGA TTAAAAAATA 174 DNA Sei id ACCESSio uence: 152. 11 CCGCGGGCGG TCAGCTGTCC TCAGCTGTCC TCAGCTGTCC TCAGCTGTCC TCAGCTGTCC TCAGCTGCCGC TCAGCTGCCGC TCAGCTGCC TCGGCCTCG TCAGCTTCGC TCAGCTTCC TGGGCCTTGG TCACTCGCC TCACCTGCCC TCACCTGCCC TCACCTGCCC TCCCCCCCCC TCCCCCCCCC TCCCCCCCCC	21 MARARARAA AMACCATTIG CCGGGGGACG CCGGGGGCCTIG GCGCTGGGG GCGCCTGGGG GCGCCTGGGG GCGCCTGGGG GCGCCCGGGGGCCGG CACCCGATGG ACAGGGCCT GCAGGGCGGG GAATATTAAA AGAGTGCAT ATACCTTTT ACATTGGA QUENCE n #: NM_032 .2422 21 GAGGCGGATA GCGCCCCC CCAGAGGCAG GCCAGCCCCC CCAGAGGCAG TTGAAGGCAAT TGGGCATTGAAG AGGTGCAT AGGTGCAT AGGTGCAT GCGGGCCCCC CCAGAGGCAA TGTGTGATGA AAGCTGCCTT TGGACAATGT GGGGAGTCAG AAGCTGCCTT TGGACAATGT GGGGAGTCAG ATCGTGGCTAG AGGAGGTAA AGGAGGTAGGAATGT	AAAAAAGGCTAGGGAGAGAGAGAGAGAGAGAGAGAGAGAG	GCTTCTCGCA GCTTCTCGCA CAAGGAAGAG AGAAGTTTCG TGGTGACCCT GCTCCAGCGC GCTCTCTCCT GCTCCAGCGC GCTCTCAGCGC CCTTTTAGGA CACGCAG CAACCGCAG CAACCGCAG CAACCGCAG CAACCGCAG CAACTGCAC CAAGTACAC AGGGGCCCCG ATCCACGAG ACTGTCCCACAG ACCAGTCCCA ACCGCAGC ACCGCAGCAG ACCGCAGCAG ACCGCAGGAG ACCGCAGGAG ACCGCAGGAGA ACCGCAGGAGA ACCGCAGGAGA ACCGCAGGAGA ACCGCAGGAGA ACCGCAGGAGA ACCGCACGAGAG ACCGCACGAGAG ACCGCACGAGAG ACCGCACGAGAG ACCGCCCCG ACCCCACGAG CACAGCAC CACAGCAC CACAGAGAC CACAGAGAC CACTCCAGAAG ACCGCCCC CACAGAGAC CACTCCCAC CACAGAC CACTCCCAC CACAGAC CACTCCCC ACCGCCCC CACAGAC CACTCCCC ACCGCCCC CACAGCAC CACTCCC CACAGAC CACTCCC CACAGAC CACTCCC CACAGAC CACTCCC CACAGC CACAGC CACAGC CACTCCC CACAGC CACTCCC CACAGC CACTCCC CACAGC CACTCC CACAGC CACTCC CACAGC CACTCC CACAGC CACTCC CACAGC CACTCC CACAGC CACTCC CACAGC CACTCC CACAGC CACTCC CACAGC CACTC CACAGC CACTC CACAGC CACTC CACAGC CACTC CACAGC CACTC CACAGC CACTC CACAGC CACA	GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGACGGCC CCTGGGCTAC CCGCCGCGCTC GTGCGCCGCC CTGCCCCGCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTCCCCCCCC	120 180 240 300 360 420 480 540 660 720 780 840 960 1080 1140 1175
50 55 60 65 70	1 GAGAAGCCCT CCCCGGTCCC CCCGGTCCC CCCGGTCCC GGCGGGGGG GGCGCGGGGGGGG	11 CTTCCCTTTA CATCCACCA GCACCACCA GCACCACCA GCACACTC GCACACACTG GCACGACTC CACCACGTG CCTGGCGCGG CTGGTGGCCGG CTCGGTGGCCTG CTCAGTCCTGC TGGTGCCTG TGTACACTGT TCTATTTGGA ACTACTGT TTAAAAAATA 174 DNA Sei did ACCEBSio ouence: 152. 11 CCGCGGGCGG TCGGCTTGG TCTGTTGGCTAG TCTGGCTAG TCTGGCTAG TCTGGCTGC TCTGGTGCCTG TCTGCTGCC TTGGCTTGG CTGGTTGGCCCTGGGCCCC CTGGGCCCCG CTGGGCCCCG CTGGGCCCCC CTGGGCCCCC CTGGGCCCCC CTGGGCCCCC CTGGCCCCCCC CTGGCCCCCCC CTGGCCCCCCC CTGCTCCACCC CTGCTCCACCC CTGCTCCCCCC CTGGCCCCCC CTGCGCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCC CTGCTCCCCCC TGCTCCCCCC TGCTCCCCCC TGCTCCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCC CTGCTCCCCCC CTGCTCCCCC CTGCTCCCCC CTCCCCCCC CTCCCCCC CTCCCCCC CTCCCCCC	21 AAAAAAAAA AAACCATTTG CCGGGGACG CAGGGCCTTG GCCGTGGCA CTTGCTGGTG GCAGCGCCTG GCAGCGCCTG CAACCAGGCC CACCCGATGC ACACGGACAG GAATATTAAA AGAGTGGCAG ACAGGGCAG GAATATTAAA AGAGTGGCAG ACAGGGCAG GAATATTAAA AGAGTGGCAG CACCCGATGC ACACGGACAG CACCCGATGC ACACGGACAG CACCCGATGC CACCCGATGC CACCCGATGC CACCCCCC CAGAGAGCAA AGAGGCAAA AGGCGCCCCC CAGAGAGCAA AAGCTGCCTT TGGACAAAT AGGACAATGT TGGGACATTC CGGGGAGTCAG ATCGTGCCTA AAGGACACACC CAGACACCCC CAGACACCCCC CAGACACCCCC CAGACACCCCC CAGACACCCCC CAGACACCCCC CAGACACCCCC CAGACACCCCC CAGACACCCCC CAGACACCCCC CAGACCCCCC CAGACACCCCC CAGACCCCCC CAGACCCCCC CAGACCCCCC CAGACCCCCC CAGACCCCCC CAGACCCCCCC CAGACCCCCC CACACCCCCC CAGACCCCCCC CAGACCCCCCC CAGACCCCCCC CAGACCCCCCC CAGACCCCCCC CAGACCCCCCC CAGACCCCCCC CAGACCCCCCC CAGACCCCCCC CAGACCCCCCCC	AAAAAAGGCT ACAGCAGGA AGGCTCATGG GGCTACGGCC CCGGGGTCG TGCACGCCC AAGGCGTCGG TGCACGGCCC AAGGCGTCGG TGGATCTTA TGTTCTTTC CAAATTTCTTT GAATTCAT CCAAGTCCA 211.5 31 AAAAGGCCCC CCAGCCCCGG CACGCAGGGG CCAGGGAGG CCAGGGAGG CCAGGGAGG CCAGGGAGG CCAGGGAGG CCAGGGAGG CCAGGCAGG	CACAGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	GAGTGGAAAG GCAGAAGGAT GCAGAAGGAT GCAGAAGGAT GCAGACGCC CCTGGGCTAC CCGCCGCGCC CCTCCTGAAG TATCATCATT CCAAAAGAA TTCAAACAT TCCAAAAGAA TTCAATCAT TCTTTGAAT \$1 GGGAGGGAGC CCTCCTCTGAA \$31 CGGACTGCAC CCTCATCTGA CCACCTCTT TGGCACCAC AGGTGCTAC AGGTGCTACA AGGTGCTACA AGGTACCAC CCACCTCTT TGGCACCCAC CCACCTCTT TGGCACCCAC AGGTGCTACA AGGTACGCCA AGGTGCTACA AGGTACGCCA CCTCCTTTGAA ACGTAGGGGT ATGCCCTTCG TTCCAAAGCA CCTCCTTCGA AGGTACCAC CCTCCTTCGA ACGTACGCCA CCTCCTTCGA ACGTACGGCT ATGCCCTTCG TTCCAAAGCA CCTCCTTCGA ACGTACGCGT ATGCCCTTCG TTCCAAACA CCCCCCTCTT AGGCACAGGGGT ATGCCCTTCG TTCCCAACGG TTCCCAACGG TTCCCAACGG TTCCCAACGGGT ATGCCCTTCG TTCCCAACGGGT TCCCAACGGGT CCAACGGGT TCCCAACGGGT TCCCAACGGGT TCCCAACGGGT TCCCAACGGGT TCCCAACGGGT TCCCAACGGGT TCCCAACGGGT TCCCAACGGGT TCCCAACGGGT TCCCAACGAGGGT TCCCAACGAGGGT TCCCAACGAGGAGC TCCCCTTCGA TCCCAACGAGGAGC TCCCTTCGA TCCCAACGAGCA TCCCAACGAC TCCCAACCAC TCCCAACGAC TCCCAACGAC TCCCAACGAC TCCCAACGAC TCCCAACGAC TCCCAACC	120 180 240 300 420 480 600 660 780 840 960 1080 1140 1175
50 55 60 65 70	1 GAGAAGCCCT CCCCGGTCCC CTGGGGCTGT GACCTGCACG GGCGGGGGGG GGCCCTCA ACCGGATCGG GGCCCCTCA ACCGGATCGG GATCTGAAG CTTCTGATTT TTCTGGAAA GCAACTGAAT TATAACACTC AAGGCCAGT ATCAGGTATA Seq ID NO: Nucleic Ac Coding seq 1 GGCTCGGGGG TATCTTGCC TATCTTGCC TATCTTGCC TATCTTGCC TAGGTCCGG CCAGGCCAG ACGGACGGA ACGGACGGA ACGGACGG	11 CATTCCCTTTA CATCCCACCA GCATCTTCTC CTCAAGCACCA GCATCTTCTC GCCAGTGCTCTC CACGCACGTG CGCTGGTGGCCGG CGCCGTGGCCGG CGCCGTGGCCGG CTCAGTCCCA TTACAACATCTGT TCTATTTGGA TGCAACACACA ACTACAAC ACTACATCTGT TTAAAAAATA 174 DNA Se id Accessio uence: 152. 1 CCCGCGGGCGG TGCTGGCTGC TGCTGGTTGC TGCTGGTTGC TGCTGGCTG	21 MARARARAA AACCATTTG CCGGGGGGCGC CAGGGCCTTTG GCCGTGGCA CTTGCTGGTG GCGCTTGCC CTCCCTGGTG GCAGCCCTG CAACCAGCCC CACCAGGCCCTG CAACCAGCCC CACCAGGCC AACCAGCCC CACCAGGCC CACCAGGCC CACCAGGCC CACCAGGCC CACCAGGCC CACCAGGCC CACCAGGCC CACCAGGCC CACCAGGCC CACCAGGCC CACCAGGCCCCCC CAGAGGCAGAACAGGCAGCACCCCCC CAGAGGCAGCACCCCCC CAGAGGCAACAGGCAGCACCCCCC CAGAGGGCAGCACCCCCC CAGAGGCAACAGGCAACAGGCACCCCCCC CAGAGGCAACACGCCCCCC CAGAGGCAACACGCCCCCCC CAGAGGCAACACGCCCCCC CAGAGGCAACACGCCCCCCC CAGAGGCAACACGCCCCCCCC	AAAAAAGGCTA ACAAGCAGGA AGGCTCATGG GCCTACGGCC CCGGGGCTCG ACCGCACAAC ACGCCCCACACACACACACACACACA	CATTOTOGOA CARGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	GAGTGGAAAG GCAGAAGGAT GCOGGTGCTG GCTGACGCGC CCCTCGGACC CCTGCGCCGCC CTGCGCCGCC CTGCCCGCC CTGCCCCCC CTGCCCCCC CTGCACAGC TATCATCATT CCAAAAGAA TTCAATATCCG GACTCACAGT TTCATCTGT TCATCTGGT TCATCTGGT TCATCTCGT TCATCTCGT CCACCTCTT TCGGCACCAC CACCTTCTT TCGGCACCAC CCACAGTGCC ACGTACGCCAC ACGTACGCCA GCTCCTTGCA ACGTACGCCA GCTCCTTGCA ACGTACGCCA GCTCCTTGCA GCCCCCTTTGCA ACGTACGCCA GCTCCTTCGC GCCCCCTTTGCA ACGTACGCCA GCTCCTTCGC GCCCCCCTTTGCA ACGTACGCCA GCTCCTTCGC GCCCCCCTTTGCA ACGTACGCCA GCTCCTTCGC GCCCACCTTTGCA TCGCCCACCA GCCCCCTTTGCA TCGCCCACCAC GCCCCCCTTTCCC TCGCCCACCAC TCCCTTCGC TCCCCCCTTCCC TCGCCCACCTTCTCC TCGCCCACCAC TCCCTTCCC TCCCCTTCCC TCTCCCTTCCC TCCCCCC	120 180 240 300 360 420 480 660 720 780 840 960 1020 1140 1175
50 55 60 65 70	1 GAGAAGCCCT CCCCGGTCCC CTGGGGCTGT GACCTGCACG GGCGGGGGGG GGCCCTCA ACCGGATCGG GGCCCCTCA ACCGGATCGG GATCTGAAG CTTCTGATTT TTCTGGAAA GCAACTGAAT TATAACACTC AAGGCCAGT ATCAGGTATA Seq ID NO: Nucleic Ac Coding seq 1 GGCTCGGGGG TATCTTGCC TATCTTGCC TATCTTGCC TATCTTGCC TAGGTCCGG CCAGGCCAG ACGGACGGA ACGGACGGA ACGGACGG	11 CATTCCCTTTA CATCCCACCA GCATCTTCTC CTCAAGCACCA GCATCTTCTC GCCAGTGCTCTC CACGCACGTG CGCTGGTGGCCGG CGCCGTGGCCGG CGCCGTGGCCGG CTCAGTCCCA TTACAACATCTGT TCTATTTGGA TGCAACACACA ACTACAAC ACTACATCTGT TTAAAAAATA 174 DNA Se id Accessio uence: 152. 1 CCCGCGGGCGG TGCTGGCTGC TGCTGGTTGC TGCTGGTTGC TGCTGGCTG	21 MARARARAA AACCATTTG CCGGGGGGCGC CAGGGCCTTTG GCCGTGGCA CTTGCTGGTG GCGCTTGCC CTCCCTGGTG GCAGCCCTG CAACCAGCCC CACCAGGCCCTG CAACCAGCCC CACCAGGCC AACCAGCCC CACCAGGCC CACCAGGCC CACCAGGCC CACCAGGCC CACCAGGCC CACCAGGCC CACCAGGCC CACCAGGCC CACCAGGCC CACCAGGCC CACCAGGCCCCCC CAGAGGCAGAACAGGCAGCACCCCCC CAGAGGCAGCACCCCCC CAGAGGCAACAGGCAGCACCCCCC CAGAGGGCAGCACCCCCC CAGAGGCAACAGGCAACAGGCACCCCCCC CAGAGGCAACACGCCCCCC CAGAGGCAACACGCCCCCCC CAGAGGCAACACGCCCCCC CAGAGGCAACACGCCCCCCC CAGAGGCAACACGCCCCCCCC	AAAAAAGGCTA ACAAGCAGGA AGGCTCATGG GCCTACGGCC CCGGGGCTCG ACCGCACAAC ACGCCCCACACACACACACACACACA	CATTOTOGOA CARGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	GAGTGGAAAG GCAGAAGGAT GCAGAAGGAT GCAGAAGGAT GCAGACGCC CCTGGGCTAC CCGCCGCGCC CCTCCTGAAG TATCATCATT CCAAAAGAA TTCAAACAT TCCAAAAGAA TTCAATCAT TCTTTGAAT \$1 GGGAGGGAGC CCTCCTCTGAA \$31 CGGACTGCAC CCTCATCTGA CCACCTCTT TGGCACCAC AGGTGCTAC AGGTGCTACA AGGTGCTACA AGGTACCAC CCACCTCTT TGGCACCCAC CCACCTCTT TGGCACCCAC AGGTGCTACA AGGTACGCCA AGGTGCTACA AGGTACGCCA CCTCCTTTGAA ACGTAGGGGT ATGCCCTTCG TTCCAAAGCA CCTCCTTCGA AGGTACCAC CCTCCTTCGA ACGTACGCCA CCTCCTTCGA ACGTACGGCT ATGCCCTTCG TTCCAAAGCA CCTCCTTCGA ACGTACGCGT ATGCCCTTCG TTCCAAACA CCCCCCTCTT AGGCACAGGGGT ATGCCCTTCG TTCCCAACGG TTCCCAACGG TTCCCAACGG TTCCCAACGGGT ATGCCCTTCG TTCCCAACGGGT TCCCAACGGGT CCAACGGGT TCCCAACGGGT TCCCAACGGGT TCCCAACGGGT TCCCAACGGGT TCCCAACGGGT TCCCAACGGGT TCCCAACGGGT TCCCAACGGGT TCCCAACGGGT TCCCAACGAGGGT TCCCAACGAGGGT TCCCAACGAGGAGC TCCCCTTCGA TCCCAACGAGGAGC TCCCTTCGA TCCCAACGAGCA TCCCAACGAC TCCCAACCAC TCCCAACGAC TCCCAACGAC TCCCAACGAC TCCCAACGAC TCCCAACGAC TCCCAACC	120 180 240 300 360 420 480 540 660 720 780 840 960 1080 1140 1175

					TTCTGGATCC		900
					CAGGTGGCTC		960
	CAAGCTGCGG	CCAGCCTGCC	CAGGTGGCAT	GCATGCTGTG	GTCAGCTGTG	TGGCAGGGCC	1020
5	GCTGCCCTG	CCCCCCAAGA	CCAAAGCCACA	ACGCAAAGGG	TCCTGGGCAG GTGGAAGTGC	AGGAGCUGAG TCATCA A CCC	1080
-	CCAGTGGGGC	ACCGTCTGTG	ACCACAGGTG	GAACCTCATC	TCTGCCAGTG	TOTTOTOTO	1200
	TCAGCTGGGC	TTTGGCTCTG	CTCGGGAGGC	CCTCTTTGGG	GCCCGGCTGG	GCCAAGGGCT	1260
	AGGGCCCATC	CACCTGAGTG	AGGTGCGCTG	CAGGGGATAT	GAGOGGACCC	TCAGCGACTG	1320
10	CCCTGCCCTG	GAAGGGTCCC	AGAATGGTTG	CCAACATGAG	AATGCTGCTG	CTGTCAGGTG	1380
10	CAATGTCCCT	AACATGGGCT	TTCAGAATCA	GGTGCGCTTG	GCTGGTGGGC	GTATCCCTGA	1440
					CCACGCTGGG		1500
	TOCCATOCAT	CCCTACAACC	CCGAAGCCAT	GGTGGCCTGC	CGACAGCTCG ACGCCAAGGG	GCCTGGGTTT	1560
	GCTGATGAGT	GGGGTGCGCT	GCTCAGGCAC	PERCECCE	CTCCACCACT	GCCAGAGGCA	1620 1680
15	CGGGCCGGTG	CACTGCTCCC	ACGGTGGCGG	GCGCTTCCTG	GCTGGAGTCT	CCTGCATGGA	1740
	CAGTGCACCA	GACCTGGTGA	TGAACGCCCA	GCTAGTGCAG	GAGACGGCCT	ACTTGGAGGA	1800
	CCGCCCGCTC	AGCCAGCTGT	ATTGTGCCCA	CGAGGAGAAC	TGCCTCTCCA	AGTCTGCGGA	1860
						AGATCTACAA	1920
20						GGCACCAGTG	1980
20	CEACAGGCAT	COTCACAGCA	TIGAGGICTT	CACCCACTAC	GACCTCCTCA	CTCTCAATGG	2040
	AGGACTGCAG	OGGGGCTACG	CATCTCCCAA	CTTCGGGGAA	CAGGACACAA	CTGTAGGCTG	2100 2160
	CTGGGACACC	TACCGGCATG	ACATTGATTG	CCAGTGGGTG	GATATCACAG	ATGTGGGCCC	2220
~~	CGGGAATTAT	ATCTTCCAGG	TGATTGTGAA	CCCCCACTAT	GAAGTGGCAG	AGTCAGATTT	2280
25	CTCCAACAAT	ATGCTGCAGT	GCCGCTGCAA	GTATGATGGG	CACCGGGTCT	GGCTGCACAA	2340
	CTGCCACACA	GGGAATTCAT	ACCCAGCCAA	TGCAGAACTC	TCCCTGGAGC	AGGAACAGCG	2400
					CTAGCTGCTG		2460
	CACTGCCAAG	CCCCACCAAC	GCCATGCCCT	TCACAGAGTC	CCAACTCAGA	ATCACCAATC	2520
30	CAGATGGTAT	TGCTCCCTCA	GGATGGCTCT	GGGCCTTCCCC	CTARGECCO	GTGGCCTATG	2580 2640
	GAATATGTCC	TCCAGGCTTT	GCTCAGCTGA	GCTCCTCTTC	TGTAAGGAAA	CCCAGTCATC	2700
	CCTGAATCTT	GCCACAGAGA	TCCGGGATTC	AGGAGCTCTC	AGTTTCTTAG	GGATGGACTA	2760
	TGGCCCAGTC	CCCCATCTAA	GTGGTGCTTT	GCAAATGTCT	TGGAGGAGTA	TAGGACAGAG	2820
35	GACCAAAATA	CACAGCAGGT	AGTGTTAGCT	CTCTGCTAGG	AGCTCAAAGC	AACACAACTT	2880
33	GTATCAAAAT	CACAACTGGC	AGAGAAGCTG	GTGGATCCAA	TCCTTTCTTC	ATCTGTTGTT	2940
						TTACCACACA TTGCCTGATG	3000 3060
						AATGGCCAGA	3120
	TAGGGCCTTC	CTACAGAGCA	GCAAGAGTAG	GCCAAGCAGA	AAGACTGCTG	AGGTAACACG	3180
40	GACCCCAGCC	CCTGTCAGGG	CCTCTGCCAA	GGAAATAATA	TGGACCATTT	ACCTGGCAGG	3240
	CAGTCTGCTC	TCTCTCAGGA	TCACCACGCA	TCTCAGGATT	GGTCTAAACT	TCAAGTCTCA	3300
	ACCAAGTGTC	TGAAGTGAAC	TTTGCATTGA	TITITAAATA	GCCATGGAAA	GAACATCAAA	3360
	CAAGCCACTC	ATCTCTACAG	AGATAAGAAA	ACAACTTTCC	CACACCAACA	GACAGAAGAC	3420
	CONCERCE DE	2010110000	********	7001011100			
45	CGTGGAGAAA	TCAGAAGGGG	GAACAGTCAG	TTTAGTTAAG	GATGGAACCT	GGGAAAGGCC	3480
45	CGTGGAGAAA ACCATTCCTG	TCAGAAGGGG CTTGATGGGG	GAACAGTCAG CTCTGATTTG	TTTAGTTAAG CTCTTGCTCA	GATGGAACCT AGTGGAATAA	GGGAAAGGCC AACCCCATGG	3480 3540
45	CGTGGAGAAA ACCATTCCTG TCTTCTTGAC	TCAGAAGGGG CTTGATGGGG ATGATTCTTG	GAACAGTCAG CTCTGATTTG ATCTTTTCTC	TTTAGTTAAG CTCTTGCTCA CACTGAGACA	GATGGAACCT AGTGGAATAA CACTTAAGTG	GGGAAAGGCC AACCCCATGG ATGATCCTTA	3480 3540 3600
45	CGTGGAGAAA ACCATTCCTG TCTTCTTGAC	TCAGAAGGGG CTTGATGGGG ATGATTCTTG	GAACAGTCAG CTCTGATTTG ATCTTTTCTC	TTTAGTTAAG CTCTTGCTCA CACTGAGACA	GATGGAACCT AGTGGAATAA CACTTAAGTG	GGGAAAGGCC AACCCCATGG	3480 3540
	CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA	TCAGAAGGGG CTTGATGGGG ATGATTCTTG ACCCTAATGC	GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT	TTTAGTTAAG CTCTTGCTCA CACTGAGACA	GATGGAACCT AGTGGAATAA CACTTAAGTG	GGGAAAGGCC AACCCCATGG ATGATCCTTA	3480 3540 3600 3660
45 50	CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO:	TCAGAAGGGG CTTGATGGGG ATGATTCTTG ACCCTAATGC 175 DNA Se	GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT Quence	TITAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT	GATGGAACCT AGTGGAATAA CACTTAAGTG	GGGAAAGGCC AACCCCATGG ATGATCCTTA	3480 3540 3600 3660
	CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac	TCAGAAGGGG CTTGATGGGG ATGATTCTTG ACCCTAATGC 175 DNA Seid Accession	GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT Quence n #: NM_001	TITAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT	GATGGAACCT AGTGGAATAA CACTTAAGTG	GGGAAAGGCC AACCCCATGG ATGATCCTTA	3480 3540 3600 3660
	CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac	TCAGAAGGGG CTTGATGGGG ATGATTCTTG ACCCTAATGC 175 DNA Seid Accession uence: 234.	GAACAGTCAG CTCTGATTTG ATCTTTCTC CAATAAAAGT Quence n #: NM_001 .1130	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT	GATGGAACCT AGTGGAATAA CACTTAAGTG GGACTGCTAC	GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAAA	3480 3540 3600 3660
50	CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding sequ	TCAGAAGGGG CTTGATGGGG ATGATTCTTG ACCCTAATGC 175 DNA Seid Accession	GAACAGTCAG CTCTGATTTG ATCTTTCTC CAATAAAAGT Quence n #: NM_001 .1130 21	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2	GATGGAACCT AGTGGAATAA CACTTAAGTG	GGGAAAGGCC AACCCCATGG ATGATCCTTA	3480 3540 3600 3660
	CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding sequil	TCAGAAGGG CTTGATGGG ATGATTCTTG ACCCTAATGC 175 DNA Seid Accession Lence: 234.	GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT Quence n #: NM_001 .1130 21	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2	GATGGAACCT AGTGGAATAA CACTTAAGTG GGACTGCTAC	GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAAA	3480 3540 3600 3660
50	CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding sequ 1 j GGAAGCAGGG TCAAGTTGGC	TCAGAAGGGG CTTGATGGGG ATGATTCTTG ACCCTAATGC 175 DNA Seid Accession Leence: 234. 11 CGGGGCCTCT CAAATTGACA	GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT quence n #: NM_001 .1130 21 GGTGCCGGTC AGAGGGAGAG	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2 31	GATGGAACCT AGTGGAATAA CACTTAAGTG GGACTGCTAC 41	GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAAA	3480 3540 3600 3660 3665
50	COTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding sequ 1 GAAGCAGGG TCAAGTTGGC ACGGTACTGGC ACGGTACTGGC	TCAGAAGGG CTTGATGGGG ATGATTCTTG ACCCTAATGC 175 DNA Seid Accession uence: 234. 11 1 CGGGGCCTCT CAAATTGACA GCCCTGTTTC	GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT Quence n #: NM_001 .1130 21 GGTGGCGGTC AGAGCGAGAG CCCCTCCTCG	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2 31	GATGGAACCT AGTGGAATAA CACTTAAGTG GGACTGCTAC 41 I TGGGAGGCGG TTCCATCCCG GCCAGGGTCC	GGGAAAGGCC AACCCATGG ATGATCCTTA AAAAAAAAAA	3490 3540 3600 3660 3665
50	COTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding seq 1 GGAAGCAGGG TCAAGTTGGC ACGGTACTGGC ACGGTACTGG	TCAGAAGGG CTTGATGGGG ATGATTCTTG ACCCTAATGC 175 DNA Sei did Accession uence: 234. 11	GAACAGTCAG CTCTGATTTG CAATAAAAGT quence n #: NM_001 .1130 21 GGTGCCGGTC AGAGGGAGAG CCCTCCTCG CAGGCCCGGC	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2 31 GGGAACTCGG GTATACTGGG GCCCCGGAGA CTGGACCCGACG	GATGGAACCT AGTGGAATAGT GGACTGCTAC 41 TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TTGCTGGCGC	GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA 51 CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATGGAGA	3490 3540 3600 3660 3665 60 120 180 240
50	COTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding sequ j GGAAGCAGGG TCAAGTTGGC ACCGTACTGG ACTTCCAAAA	TCAGAGGGG CTTGATGGGG ATGATTCTTG ACCCTAATGC 175 DNA Seid Accession uence: 234. 11 CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCCGCTC GGTGGAAAAG	GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT quence n #: MM_001 .1130 21 GGTGCCGGTC AGAGGGAGAG CCCCTCCTGC CAGGGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2 31 GGGAACTCGG GTATACTGCG GCCCCGAGA CTGACCGGAC CGCACTACGG	GATGGAACCT AGTGGAATAA GGACTGCTAC 41	GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAAA	3490 3540 3660 3665 3665 60 120 180 240 300
50	COTGGGGAAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding seq I GGAAGCAGGG TCAAGTTGAC ACGGTTCCCAG ACCAGTTGAC ACCAGTTGAC ACCAGTTGAC	TCAGAGGGG CTTGATGGGG ATGATTCTTG ACCCTAATGC 175 DNA Seid Accession Luence: 234. 11 CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCGCTC GGGGAGAGGTG GGGAGAGGTG	GAACAGTCAG CTCTGATTTG CAATAAAAGT Quence n #: NM_001 .1130 21 GGTGCGGGTC AGAGGGAGAG CCCCTCCTCG CACGGCCGGA ATCGGAGAGG GTGGGGCTTA	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2 31 GGGAACTCGG GTATACTGCG GCCCCGGGA CTGACCGGAC GCACGTACGG GCACGTACGA GCACGTACGA GCACGTACGA GCACGTACGA GCACGTACGA GCACGTACGA GCACGTACGA GCACGTACGA GCACGTACGA GCACGTACGA	GATGGAACAT AGTGGAATAA CACTTAAGTG GGACTGCTAC 41	GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAAA	3490 3540 3660 3665 3665 60 120 180 240 300 360
50	COTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding seq 1 GGAAGCAGGG TCAAGTTGGC ACGGTACTGGC ACTTCCAAAA ACAAGTTGAC TGTGTGCCCAG	TCAGAAGGG CTTGATAGGG ATGATTCTTG ACCCTAATGC 175 DNA Sei did Accession uence: 234. 11 GGGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCGGCTC GGTGGAAAAG GGGAGGTG TACTGCCATC	GAACAGTCAG CTCTGATTTG CAATAAAAGT Quence n #: NM_001 11130 21 GGTGCCGGTC AGAGGGAGAG CCCCTCCTCG CAGGCCCGGG ATCGCAGAGG ATCGCAGAGG CCCCTCCTCG CAGGGCCGGG ATCGCAGAGG ATCGCAGAGG CCCCAGAGAGGT CGAGAGATCT	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2 31 GGGAACTCGG GTATACTGGG GCCCCGGAGA CTGACCCGAG GCACGTACGG GCACGTACGG GCACGTACGG CTGACCCGAC GCACGTACGG CTCTCCCTTAA	GATGGAACCT AGTGGAATAA GGACTGCTAC 41 TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TGGCTGGCAG AGTTGTGTAC CCTGGACACT GGAGGTTAAC	GGGAAAGGCC AACCCCATGG ATGATCCCTTA AAAAAAAAA 51 CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATGGAGA AAAGCCAGAA GAGACTGAGG	3490 3540 3600 3660 3665 60 120 180 240 300 360 420
50	COTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding sequ GGAAGCAGGG TCAAGTTCGC ACCGTACTGG GGGTTCCCAG GGGTTCCCAG GGTTCCAAAA ACAAGTTGAC TTGTCAAGCT	TCAGAGGGG CTTGATGGGG ATGATTCTTG ACCCTAATGC 175 DNA Seid Accession uence: 234. 11 CGGGGCCTCT CGAGGGCCTCT GGCCCCGCTC GGTGGAAAAG GGGAGAGGTG TACTGCCATC	GAACAGTCAG CTCTGATTTG CAATAAAAGT Quence n 8: MM_001 .1130 21 GGTCCCGGTC AGAGGGAGAG CCCCTCCTCG CAGGGCCGGG ATCGGAGAGGG ATCGGAGAGAGG TGGGCCTTA CGAGAGATC CATCACACAG	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2 31 GGGAACTCGG GTATACTGCG GCCCCGGAGA CTGACCCGAC CTGACCCGAC CTGACCCGAC CTCGCTTAA AAAATAAACT	GATGGAACCT AGTGGAATAA CACTTAAGTG GGACTGCTAC 41	GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAAA	3490 3540 3660 3665 3665 60 120 180 240 300 360
50 55 60	COTGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding seq I GGAAGCAGGG TCAAGTTGGC ACGGTACTGGC ACTCCAAAA ACAAGTTGAC TGTCAAGGT TGTCAAGGT TGTCAAGGT TGTCAAGGT TGTCAAGGT TGTCAAGAGT TGACCCAAGA TTGTCAA	TCAGAAGGGG CTTGATAGGGG ATGATTCTTG ACCCTAATGC 175 DNA Sei did Accession uence: 234. 11 GGGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCGGCTC GGTGGAAAAG GGGAGGTGT TACTGCCATC GCTGGATGTC TCTCAAGAAAA CTATCTGTTC	GAACAGTCAG CTCTGATTTG CAATAAAAGT Quence n #: NM_001 .1130 21 GGTGCCGGTC AGAGGCAGAG CCCTCCTCG CAGGCCCGGG ATCGGAGAG GTGGCGCTTC CTGAGAGAGT CTACACAG TTCATGGATC CAGGTCCCGG TTCATGATC CAGGTCCCCT CTGAGAGATCT ATTCACACAG TTCATGGATC CAGGTCCTCC	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2 31 GGGAACTCGG GTATACTGGG GCCCCGAGA AGAAATCCG CTGACCCGAC AGAAATCAC CTCTGCTTAA AAATAAACT CTCTTGCTTAA AGGGCCTACC AGGGCCTACC	GATGGAACCT AGTGGAATAA CACTTAAGTG GGACTGCTAC 41 TGGGAGGCCG TTCCATCCCG GCCAGGGTCC TCGCTGGCAC AGTTGTGAC CTACCTGGCTT CACTGGCTT CACTGGCTT TTCTGCCAT TTTCTGCCAT TTTCTGCCAT TTTCTGCCAT TTTCTGCCAT TTTCTGCCAT TTTCTGCCAT	GGGAAAGGCC AACCCCATGG ATGATCCCTTA AAAAAAAAA 51 CAACATTGTT ACCCGGGGCC GCCTTCTTGCA ATTGAATTGT ATTGAATTTC CCTCTTCTCCC TCTCTTCCCG	3490 3540 3660 3660 3665 60 120 180 240 300 360 420 480
50	COTGGGGAAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding seq I I CAGGACGAGG GGAACCAGGG TCAAGTTGGC ACGGTTCCCAG ACTTCCAAAA ACAAGTTGAC TGTGCCCAG TTGTCAAGCT TCCACCAAGA TCATCAAGAT TCATCAAGAT TCATCAAGAT	TCAGAAGGGG CTTGATAGGGG ATGATTCTTG ACCCTAATGC 175 DNA Seid Accession uence: 234. 11 GGGGGCTCT CAAATTGACA GCCCTGTTTC GCCCCGGTTC GTGGAAAAG GGGAGAGGTG TACTGCCATC CTCAAGAAA CTATCTGTTC AGGACTTAAA	GARCAGTCAG CTCTGATTTG CAATAAAAGT Quence n #: NM_001 .1130 21 GGTGGGGTG AGAGGGAGAG ATCGGAGAGG GTGGGGGGTA TCAAGAGATT TTCAACACAG TTCATGGATG CAGTGGTGCAGAGG CCCTCTGGATGCACACAGAGT CAGGGGTGCACACACACACACACACACACACACACACACA	TTTAGTTAAG CTCTTGCTCA TGCTCATTAT 798.2 31 GGGAACTCGG GTATACTGCG GCCCCGGGA CTGACCGGAC GCACGTACGG GCACGCACGG GCACGTACGG GCACGCACGG GCACGTACGG GCACGTACGG	GATGGAACAT AGTGGAATAA CACTTAAGTG GGACTGCTAC 41	GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAAA	3480 35400 3660 3665 3665 60 120 180 240 360 420 480 540 660
50 55 60	COTGGGGAAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding seq I GGAAGCAGGG TCAAGTTGAC ACGGTTCCAGG ACTTCCAGAA ACTACTTCAGAC TTGTCCACAGA TCTTCAAGAT TCACCAGGA TCATCAAGAG TCATCAAGAG TCATCAAGAG TCATCCAAGAG TCATCCAAGAG TCATCCAAGAG TCATCCACAGA TCATCCAAGAG TCATCCAACAGA	TCAGAAGGG CTTGATAGGG ATGATTCTTG ACCCTAATGC 175 DNA Sei did Accession uence: 234. 11 CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCGCTC GGTGGAAAAG GGAGGAGGTG TACTGCCATC GCTGGATGTC TCTCAAGAAA CTATCTGTTC AGACCTTAAA TGGACTTAGCC	GAACAGTCAG CTCTGATTTG CAATAAAAGT Quence n #: NM_001 .1130 21 GGTGCCGGTC AGAGGGAGAG CCCCTCCTCG CAGGGCCGGG ATCGGAGAGG TTCAACACAG TTCAACACAG TTCAACAGAG TTCATGGATTC CAGGGTGCTCC CCCTCAGATTC CAGGAGATTTAACACAGA CAGGTGCTCC CCCTCAGAATC CAGCTGCTCC CCCTCAGAATC CAGAGCTTTTG AGAGCTTTTG AGAGCTTTTG AGAGCTTTTG AGAGCTTTTG AGAGCTTTTG AGAGCTTTTG AGAGCTTTTG	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2 31	GATGGAACCT AGTGGAATAA CACTTAAGTG GGACTGCTAC 41 TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TCGCTGGCACCT CGCTGGCACCT CACTGGCATTTTTTTGTCC TACTGGCATT TTTTGGCATT TTTCGCCATT TTCAGCAGT TGCAGAGGCGT TGGAGAGCT TACAGAGGGG TGGTACTTAC	GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA 51 CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATGGAGA AAAGCCAGAA AGAGCCAGAA TTTGAATTTC CCTCTTCCCC TCTCATCGGG CCATCAAGG ACCCATCAAGG	3480 3540 3660 3665 3665 60 120 180 240 360 420 480 540 660 720
50 55 60	COTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding seq I GGAAGCAGGG TCAAGTTGGC ACGGTACTGG ACTTCCAAGA ACTACTAGAA ACAAGTTGAC TGGTCCCAG TTGTCAAGGT TGCACCAAGA TCATCAAGAG TCCTCCACCG TTGTCAAGAG TCCTCCACCG TTGGTCAAGAT TGGTCAAGACT TGGTCAAGACT TGGTCAAGAGT TGGTCAAGAG	TCAGAAGGGG CTTGATAGGGG ATGATTCTTG ACCCTAATGC 175 DNA Sei did Accession uence: 234. 11 CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCCGCTC GGTGGAAAAG GGGAGGTGT TACTGCCATC GCTGGATGTC TCTCAAGAAA CTATCTGTTC AGACCTTAACA TGGACTAGCC GTGGTACCGA	GAACAGTCAG CTCTGATTTG CAATAAAAGT Quence n #: NM_001 .1130 21 GGTGCCGGTC AGAGGCAGAG CCCCTCCTCG CAGGCCCGGG ATCGGAGAG GTGGCGCTTCTTCG AGAGGATCT ATTCACACAG TTCATGGATTC CAGCTCTTCC CCTCAGAATTC AGACTTTTC AGAGCTTTCAGAGCTTTCAGAGCTTTTC AGAGCTTTTC	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2 31 GGGAACTCGG GTATACTGGG GCCCCCGAGA GCACGTACGG AGAAATCCG CTGACCCGAC AGAAATCAG CTCTGCTTAA AAAATAAACT CCTCTGCTTCT AGGGCCTACC TGCTTATTAA GAGTCCCTGCT TGCTTCTTAAAACT TCCTCTCTGCTTCT AGGGCCTACC TGCTTATTAA	GATGGAACCT AGTGGAATAA CACTTAAGTG GGACTGCTAC 41 TGGGAGGCCG TTCCATCCCG GCCAGGGTCC TCGCTGGCAC AGTTGTTAC CCTGGACACT TACCTGGTT CACTGGCAT TTTCTGCCAT CACAGAGGGG CACAGAGGGG CCAGAGGGGC CCCGCATAAC CTACTGCAT CCTGCAATAT CTGCAAATAT	GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA 51 CAACATTGTT ACCCGGGGCC GCCTTCTTGCA TTCATGGAGA AAAGCCAGAA AGGACTGAGG CATCCTAATA TTTGAATTTC CCTCTTCTCCC TCTCTTCCCC TCTCTTCCCC ACCCATGAGG ACCCATGAGG ACCCATGAGG ACCCATGAGG ACCCATGAGG	3480 35400 3660 3665 60 120 180 240 300 360 420 480 540 600 660 720
50 55 60 65	COTGGGGAAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding seq I I GGAAGCAGGG TCAAGTTGGC GGGTTCCCAG ACTTCCAAAA ACAAGTTGAC TTGTCCCAGG TTGTCCCAGG TTGTCCAGGA TCATCAAGAT	TCAGAAGGG CTTGATAGGG ATGATTCTTG ACCCTAATGC 175 DNA Seid Accession uence: 234. 11 GGGGCTCT CAAATTGACA GCCCTGTTTC GCCCCGCTC GGTGGAAAAG GGGAGAGGTG TACTGCCATC TCTCAAGAAA TGACTTACA AGACTTACCA TGGCTTACCGA TGGTGTACCGA TGGTGTACCGA CTGGAGCCTG	GARCAGTCAG CTCTGATTTG CAATAAAAGT QUENCE n #: NM_001 .1130 21 GGTGGGGTC AGAGGGGGGG ATGGGGGTG ATGGGGCTGA ATGAGAGATT CAAGAGATT ATCACACAG TTCATGGATG CAGGGTTTTG GAGGCTTTTG GAGGCTTTTG GAGGCTTTTG GCTCCTGAATC AGAGCTTTTG GCTCCTGAATC AGAGCTTTTG GCTCCATCT	TTTAGTTAAG CTCTTGCTCA TGCTCATTAT 798.2 31 GGGAACTCGG GTATACTGCG GCCCCGAGA CTGACCGGAC GCACGTACGG GCACGTACGG GCACGTACGG GCACGTACGG GCACGTACGG TGCATATAAACT AGAGCCTACG TCCTCTTATAA GAGTCCCTGT TCCTTCCTTGA GGGCTACGG TCCTTCCTGGAGA TTCCTCCTGGG TTCCTTCCTGGAGAT TCCTCCTGGG	GATGGAACCT AGTGGAATAA CACTTAAGTG GGACTGCTAC 41	SGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA 51 CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATGGAGA AAAGCCAGAA GAGACTAGAT ATTGAATTTC CCTCTTCCCC TCTCATCGGG CCTCTCATCAGG ACCCATGAGG TATTCCACAGG ACCCATGAGG TATTCCACAGG CGGGCCCTTAT	3480 3540 3660 3660 3665 60 120 180 240 300 360 420 480 540 660 720 780 840
50 55 60	COTGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding seq I GGAAGCAGGG TCAAGTTGGC ACGGTACTGG ACTTCCAAAA ACAAGTTGAC TGTGCACCAGGA TCATCAAGAG TCATCAAGAG TCATCAAGAG TCTCCACCG TAGGACACT TAGGACCACCA	TCAGAAGGGG CTTGATAGGGG ATGATTCTTG ACCCTAATGC 175 DNA Sei did Accession uence: 234. 11 GGGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCGCTC GGTGGAAAAG CGGAGGGTG TACTGCCATC GCTGAGAAA CTATCTGTTC AGACCTAAAA TGACTAACA TGGCTAGCC GTGGTACCGA CTGGAGCTGG TTCTCAGACAT GGGGGCCTGTTTCTCAGACAT TGGACTACCA CTGGAGCCTG TTCTGAGACT GTGGTACCGA CTGGAGCCTG TTCTGAGATT GTGGCCAGCA	GAACAGTCAG CTCTGATTTG CAATAAAAGT Quence n #: NM_001 .1130 21 GGTGCCGGTC AGAGCGAGAG CCCCTCCTCG CAGGCCCGGG ATCGCAGAGG ATCGCAGAGG TTCACACAG TTCACACAG TTCACACAG GCTCCTCGTAGAGGCTCCCCCCCCCC	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2 31 GGGAACTCGG GTATACTGCG GCCCCGAGA GCACGTACCG GCACGTACCG GCACGTACCG AGAAAATCAC CCTCTGCTCT AAAATAAACT CCTCTGCTCT TCCTCTGCTCT TCCTCTCTGCTCT TCCTCTCTGCT TCCTCTGCTCT TCCTCTGCTCT TCCTCTGCTCT TCCTCTGGATT TCCGGATCTT TCGCTGATTA	GATGGAACCT AGTGGAATAA CACTTAAGTG GGACTGCTAC 41 I TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TGGCTGGCACACT TTTCTGGCAC CACTGGCAT TACCTGGAT TTTCTGCCAT CACAGAGGGG TCGTACTTAC CTGCAATAT GGTGACTCCC TGGCAATAT GGTGACTCCAAGCCAAG	GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA 51 CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATGAGG AAAGCCAGAA GAGACTGAGG CATCCTAATA TTTGAATTTC CCTCTTCCCC TCTCTTCCCC ACCCATGAGG ACCCATGAGG CCGCCCTAT GGGACCCCAG GGGACCCCAGT TTCCCCAAGT	3480 35400 3660 3665 60 120 180 240 300 360 420 480 540 600 660 720
50 55 60 65	COTGGAGAAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding seq I GAAGCAGGG TCAAGTTGGC ACGGTTCCCAG ACTTCCACA ACTACCAAGA TCATCAAGAT TCCACCAAGA TCATCAAGAT TCCACCAAGA TCATCAAGAT TCCACCAAGA TCATCAAGAT TCCTCAAGAT TCCTCAAGAT TCCACCAAGA TCATCAAGAT TCCTCAAGAT TCCTCGAGAA ATGAGAGATT TCGTGGACAT TCGTGGACAT TCCTTGGACAT TCCCTGGAGAA ATGAGGTGGT	TCAGAAGGGG CTTGATAGGGG ATGATTCTTG ACCCTAATGC 175 DNA Seid Accession Lence: 234. 11 GGGGCCTCT CAGATTGACA GGCCTGTTTC GCCCCGCTC GGTGGAAAAG GGGAGAGGTG TACTGCCATC TCTCAAGAAA TGACTACGCATC TGGGTGCAGAAA TGGACTAGAA TGGACCAGGA TTCTGAGATT	GARCAGTCAG CTCTGATTTG CAATAAAAGT QUENCE n #: MM_001 .1130 21 GGTGCGGGTC AGAGGAGGAGG ATCGGAGGGGGGG ATCGGAGGAGG TTCATGGAGGG TTCATGGAGGG CCCTCTGAGAGG TCAGGAGT TTCATGAATC AGAGCTTTTG GCTCCTGAATC AGAGCTTTTG GCTCCTGAATC AAAGTTGTAC TTAATCTTCTA AAAAGTTGTAC	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2 31	GATGGAACCT AGTGGAATAA A1 I GGACTGCTAC GGACGCCG TCCATCCACCG GCCAGGGTCC TCGCTGGCACCT CACTGGATTAAC CTACCTGGT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCAATATAC TGCGAATATAC TGCGAATTAC TGCGAATTAC TGCGAATTTAC TGCGAATTTAC TGCGAATTTAC TGGAATTTAC TGGAATTTAC TGGAATTTAC TGGAATTTAC TGGAATTTAC TGGAATTTAC TGGAATTTAC TGAAGATGGA TGAAGATGGA	GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAAA	3480 3540 3660 3660 3665 60 120 180 240 360 420 480 660 660 720 780 840 900
50 55 60 65	COTGGGGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding seq I GGAAGCAGGG TCAAGTTGAC ACGGTTCCAGA ACTACTCGAC ACGTTCCAGA ACTTCCAGA ACTTCCAGA ACTTCCAGA TTGTCAGACT TGCACCAGGA TCATCAGAGA TCATCAGAGA TCATCAGAGA TCATCAGGG TAGCAGACT TGGTGACCT TGGTGACCT TGGTGACCT TGGTGACCT TCCCTCGGGGA ATGAGGTGGT GACCGAAT	TCAGAAGGGG CTTGATAGGGG ATGATTCTTG ACCCTAATGC 175 DNA Sei did Accession uence: 234. 11 CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCTCGAAAAG GGGAGAGGTG TACTGCTATC GCTGGATCTC TCTCAAGAAA CTATCTGTTC AGACCTTAAA TGGACTAGCC GTGGTACCGA CTCGAGCCTG GTGGCAGGA AGATTTTAGT GTGGCCAGGA AGATTTTAGT GCTGCACTAC	GAACAGTCAG CTCTGATTTG CAATAAAAGT Quence n #: NM_001 .1130 21 GGTGCGGGTC AGAGGCAGGG ATCGGAGAGG TCCAGGCCTGG ATCAGAGAGTCT ATTCACACAG TCAGGAGAGT CAGGTGCTCCTGC CAGGCTGTCCTGGTAAAGGTTTTG GCTCCTGAAAT AGAGTTTTG ACCAGGTCT GTTACTTCAA AAAGTTGTAC AAAGTTGTAC AAAGTTGTACACAGAGCAGCTCT ACCAGGTCT ACCAGGTCT ACCAGGTCT ACCAGGTCT AAAGTTGTACACAGA AAAGTTGTACACAGACCTCT AAAGTTGTACACAGACCTCT ACACAGCTCT AAAGTTGTACACAGACCTCT ACACAGCTCT ACAGCTCT ACACAGCTCT ACACAGCTCT ACACAGCTCT ACACAGCTCT ACACAGC	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2 31 GGGAACTCGG GTATACTCGG GCCCCCGAGA CTGACCCGAGA CTGACCCGAGA CTGACCCGAGA CTGACCCGAGA AGAAATACACT CCTCTGCTTAA AAAATAAACT TCCTCTGCTCT AGGGCCTACC TGCTTATTAA TCCTCTGGGT TCCTCTGGGT TCCCCTGGGT TCCCCTGGGT TCCCCTGGAGA CTCCCCTGGAGA AGAGTCTT TCCCCTGGAGA TCCCCTGAGATCT TCCCCTGGAGATCT TGCCTGATTA CTCCCCTGGAGATCT TGCCTGATTA	GATGGAACCT AGTGGAATAA CACTTAAGTG GGACTGCTAC 41 TGGGAGGCGG TTCCATCCGG GCCAGGGTCC TCGCTGGCAC AGTTTGTTAC CACTGGCAT TTTCTGCCAT CACTGGCAT TTTCTGCAT CACTGGCAT TTTCTGCAT CACTGGCAT TTTCTGCAT CACTGGCAT TTTCTGCAT CACTGGCAT TTTCTGCAT CACTGGCAT TTTCTGCAAATAT GGTGAACTCCA CAGAGAGGG TGAAGATGGA GGCCAAGT TGAAGATGGA GGCCAAGGCAAGG	GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA 51 CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATCGAGA AAAGCCAGAA GAGACTCAGG CATCCTAATA TTTGAATTTC CCTCTTCCCC TCTCATCGGG ACCCATCAGG TATTCCACAG TATTCCACAG TATTCCACAG TATTCCACAG TATTCCACAG TATTCCACAG TATTCCACAG TATTCCACAG TATTCCACAG TCGGACCTCAT TCGGACTTGT CGGACTTGT CGGACTTGT CGGACTTGT CGGACTTGT CGCACGGCTC	3480 3540 3660 3660 3665 60 120 180 240 360 420 480 540 660 660 720 780 840 900 960
50 55 60 65	COTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding seq I GGAAGCAGGG TCAAGTTGGC ACGGTACTGG ACTTCCAAAA ACAAGTTGAC TGTGCACCAGGA TCATCAAGAG TCATCAAGAG TCATCAAGAG TCATCAAGAG TCATCAAGAG TCATCCACCAGG AGGACACTTGGCCCAGGAATATTGGCCAAGAT TGGTGACCCT TGGTGACCAT TGGTGACCAT TGGTGACCAT TAGTGGACCAT TAGTGGACCAT TCCTGGAGCAT TCCTGGAGCAT TCCTGGAGCAT TCCTGGAGCAT TCCTGGAGCAT TCCCTGGAGCAT TCCCTGGAGCAT TCCCTGAGGA TATGAGGTGGT GGGCCCGGCA TATCACAAAT ACCCTTTCTT	TCAGAAGGGG CTTGATAGGGG ATGATTCTTG ACCCTAATGC 175 DNA Sei did Accession uence: 234. 11 GGGGGCCTCT CAAATTGACA GCCCTGTTTC GCTCGGAGAGGTG TACTGCCATC GCTGGATCAGCA CTACTGTTC AGACCTAAAA TGACTAACA TGACTACCA TCTCAAGAAA CTATCTGTTC AGACCTAAC TTCTCAGACTT TGGCCAGCA AGATTTTAGT GCTGCACTAC CCAGGATTTG	GAACAGTCAG CTCTGATTTG CAATAAAAGT Quence n #: NM_001 .1130 21 GGTGCGGGTC AGAGGGAGAG CCCCTCCTCG CAGGGCCGGG ATCGGAGAGG ATCGGAGAG TCGGAGAGG TTCAGAGAGT TCAGAGAGT AGAGAGT TCAGAGAGT TCAGAGT TCAGAGT TCAGAGT TCAGAGT TCAGAGT TCAGAGCT AGAGCT TTACTT AAAGTT TAAAGT ACCAAGCCT AACCAAGCCT AACCAAGCCCT ACCAAGCCCT ACCAAGCCCT ACCAAGCCCAACAC ACCAAGCCAACAC ACCAAGCACAC ACCAACAC ACCAAGCACAC ACCAACAC ACCAAGCACAC ACCAACAC ACCAACAC ACCAACAC ACCAACAC ACCAACCACAC ACCAACCAC ACCAACCAC ACCAACCAC ACCAACCAC ACCAACCAC ACCAACCAC ACCAACCAC ACCAACCAC ACCAACCAC ACCAACCAC ACCAACCAC ACCAACCAC ACCAAC	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2 31 GGGAACTCGG GCCCCGAGA GCACTGACG GCACGTACGG GCACGTACGG GCACGTACGG GCACGTACGG TCTCTCTTAA AAAATAAACT CCTCTGCTCT TCCTCTGCTCT TCCTCTGGATTT TCCTCAGTATT TCCCTGATTA CTCCCTGGA	GATGGAACCT AGTGGAATAA CACTTAAGTG GGACTGCTAC 41 I TGGGAGGCGG TTCCATCCCG GCCAGGGTTCC TGGTGGCAC AGTTGTTAC CACTGGACACT TTTCTGGCAT CACAGAGGGG TGGTACTTAC CTGCAATAT TGGTACTCCC TGGCAATAT TGAAGATGGA GGCAAGCT TGAAGATGGA TTGAAGATGGA TGGAACTCTG CAAGCCAAGT TGAAGATGGA TGCAACTCAG TGAAGATGGA TGGACTCTGC TGCAAGCAT TGAAGATGGA TGCAACTCTAC TGCAAGCAAGT TGAAGATGGA TGCACTCTAC TGCAAGCAAGT TGAAGATCTTAC TGCACTCTAC TG	GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA 51 CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATGAGG AAAGCCAGAA AGGACTGAGG CATCCTAATA TTTGAATTTC CCTCTTCCCC TCTCTTCCCC ACCCATGAGG GCCATCAAGC ACCCATGAGG TATTCCACAG GGGACCCCAG TTCCCCAAGT CGGAGCTTGT GCGAGCTTGT GCGAGCTTGT CTGCATGTT CCCCAAGT CGGAGCTTGT CTGCATCTTTTT	3480 3540 3660 3660 3665 60 120 180 240 360 420 480 540 600 660 720 780 840 900 900 1020 1080
50 55 60 65 70	COTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding seq I GAAGCAGGG TCAAGTTGGC ACGGTTCCCAG ACTTCCACAG ACTTCCACAG TTGACCAGGA TCATCAGAGAC TATCGCAAAT ACCCTTTCTT	TCAGAAGGGG CTTGATAGGGG ATGATTCTTG ACCCTAATGC 175 DNA Seid Accession Lence: 234. 11 CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCGCTC GCTGGAAAAG GGGAGAGGTG TACTGCCATC GCTGGATGTC TCTCAAGAAA TGGACTAGAC TGGTACCGA TGGTACCGA TGGCACCAGAAATGTCAGATT GTGGCACCAGAAATGTCGCATCC TCTGAGATTT CTGAGATTTAGTTGCATCC TCTGAGATTTAGTTGCATCCAGAAAATGTCAGACCTAGAAAAATGTCAGAAAAAATGGACTAGAAAATGTCAGAGATTTAGTGCACTAGAAATGCCAGAGATTTAGCTGCACTAACCTAGAATTTAGTGCCAGGATTTAGCCAGGATTTAGCCAGGATTTAGCCAGGATTAGCCAGGATTAACTACCAGGATTAGCCAGGATTAACTACACAATGATCATAGATTAGTTGCACCAAGAATTAACTAGCCAGGATTACAACATTAACTAGATCAAATCAAATCATAGATCAAAATCAAAATCAAAAAAAA	GAACAGTCAG CTCTGATTTG CAATAAAAGT QUENCE n #: NM_001 .1130 21 GGTGCGGGTC AGAGGGAGGG CCCCTCCTGG CAGGGCGGGG ATCGGAGGTC ATTCAACAAGT TTCAACAGAG TTCATGGATTG GGTGCTGTTG CAGGGTGTTC CGTGAGATTC AGAGGTTTTG GGTCCTGAATC AGAGCTTTTG GCTCCTGAAA AGAGTTTTG GCTCCTGAAAA AGAGCTTTG GACCAGCTCT GACCAGCTCT GACCAAGCCAAG	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2 31	GATGGAACAT GATGGAATAA A1 I TGGAGGCG TCCATCCGG GCCAGGGCC TGCTGGCCC TGCTGGCCC TGCTGGCATTAC TACCTGGT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TGAGAGGGG TGGACTCTG CAGCCAAGT TGAACATGGA GCCCAAGGCA GCCCAAGCCA TGAACTCTG TGAACATGCA TGAACATGCA GCCCAAGCCA TGAACTCTG TGAACATGCA GCCCAAGCCA TCGACTCTGA GCTTGACCAG GCCCAGC GCCCAG GCCCAG GCCCAG GCCCAG GCCCAG GCCCAG GCCCAG GCCCAC GCCCACC GCCCAC GCCCACC GCCCAC GCCCACC GCCCACC GCCCAC GCCCACC GCCCCC GCCCC GCCCACC GCCCACC GCCCACC GCCC GCCCC GCCC GCCC GCCC GCCC GCCCC GCCC GGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA 51 CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATGGAGA AAAGCCAGAA ATTGAATTTC CCTCTTCCCC TCTCATCGGG GCCATCAATA TTTGAATTTC CCTCTTCACCGGCCTATCAAGG ACCCATGAGG TATTCCACAGG TATTCCCCAAGT TCCCCAAGT TCCCCAAGT TCCCCAAGT TCCCCAAGT TCCCCAAGT TCCCCCAAGT TCCCCCAGT TTCCCCAAGT TCCCCCAGT TCCCCCAGT TCCCCAAGT TCGGAGCTTGT GGGACCTCTT TGGAGCTTCTT TGGAGCTTTCTT TGCTTGGCCTTT	3480 3540 3660 3660 3665 60 120 180 240 300 420 480 540 600 720 780 960 91020 1020 1080 1140 1200	
50 55 60 65	COTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding seq I GGAAGCAGGG TCAACTTGGC ACGGTTCCAGA ACTACTGGC ACGTTCCACAGA ACTACTCAGAA ACTACTCAGAA TCATCAGAG TCATCAGAGA TCATCAGAGA TCATCAGGG TAGCAGGACT TGGTCCACGG TAGCAGGACT TGGTCCACCG TAGCAGGACT TGGTGACCT TGGTGACCT TGGTGACAT TCCCTGGGACA ATGAGGTGGT TACCCAGAA ATGAGGTCTT ACCCTTCTT AGCCAAAT ACCCTTTCTT AGCCAAAT ACCCTTTCTT GGGCAATTTGCCAGAAT ACCCTTTCTT	TCAGAAGGGG CTTGATAGGGG ATGATTCTTG ACCCTAATGC 175 DNA Sei did Accession uence: 234. 11 CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCTCGAAAAG GGGAGAGGTG TACTGCCATC CTCAAGAAA CTATCTGTTC AGACCTTAGC GTGGTACCGA CTGGAGCCTG GTGGTACCGA GTTCTGAGACT GTGGACTGG GCCCAGCA AGATTTTAGT GCTGCACTAC CCAGGATGTG GCCCTAATCT CCAGGATGTG GCCCTAATCT CACAGGATGTG GCCCTAATCT GACTCAGGTG GACTCAGGTG GCCCTAATCT CACAGGATGTG GCCCTAATCT CACAGGATGTG GCCCTAATCT CACAGGATGTG GCCCTAATCT CACAGGATGTG GCCCTAATCT CACAGGATGTG GCCCTAATCT CACAGGATGTG GCCCTAATCT CACAGGATGTG GCCCTAATCT CACAGGATGTG GCCCTAATCT CACAGGATGTG GCCCTAATCT CACAGGATGTG GCCCTAATCT CACAGGATGTG GACTCAGGT GACTCAGGTG GACTCAGGT GACT GAC	GARCAGTCAG CTCTGATTTG CAATAAAAGT quence n #: NM_001 .1130 21 GGTGCCGGTC AGAGGCAGGG CCCCTCCTCG CAGGCCCGGG ATCGGAGAGG TTCATGGAGAGG TTCATGGAGAGG TTCATGGATTC GAGAGATCT AGAGTGTTCC GAGAGATTTG GCTCCTGAAAC GGTCCATCT GTTACTTCTA AAAGTTGTAC ACCAAGCCAG ACCAAGCCAG CACCCCTCTCG CACCCTCTCC CGCCCTCTCACA	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2 31 GGGAACTCGG GCCCCCGGA GCACCTACCGG CCCCCCGGA GGAAATCCG CTCTGCTTAA AAAATAAACT TCCTCTGCTTATA AGGGCCTAGC TGCTTATTAA CAGTGCGGATTTCCCCCTGGG TTGCTGAGAT TCCCCTGGGTTGCCCCCTGGGTTGCCCCCTGGGTTGCCCCCTGGGTTGCCCCCTGGGTTGCCCCCTGGGTTGCCCCCTGGGTTGCCCCCTGGATACCCCCCTGGATACCCCCCTGGATTACCCCATGCTGCCCCTGGATACCCCCCTGGATTACCCCATGCTGCCCCTGGATTACCCCCATGCTTCCCCCTGGATTACCCCATGCTGCCCCTGCATACCCCCATGCTTCCCCCTGGATTACCCCATGCTTCCCCCTGGATTACCCCATGCTTCCCCCTGGATTACCCCATGCTTCCCCCTGGATTACCCCATGCTTCCCCCTGGATTACCCCATGCTTCCCCCTGGATCTCCCCCTGCATCCCCCCTGCATCCCCCCCTGCATCCCCCCCC	GATGGAACCT AGTGGAATAA CACTTAAGTG GGACTGCTAC 41	GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA 51 CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATGGAGA AAAGCCAGAA GAGACTGAGG CATCCTAATA TTTGAATTTC CCTCTTCCCC TCTCATCGGG GCCATCAAGC TACTCACAGG TATTCCACAG CGGGCCCTAT GGGACCTCCAG TCCCCAAGT CGGACTTGT CGGACTTGT CGCTTGCCT TAGCTTCTT TTCTAGCTTT TTCTAGCTTT TTCTAGCTTT TTCTAGCTTT TTCTAGCTTT TTCTAGCTTT TTCTAGCTTT TTCTAGCTTT TTCTAGCTTT	3480 3540 3660 3660 3665 60 120 180 240 300 420 480 660 660 6720 780 990 900 900 1080 1140 1260
50 55 60 65 70	COTGGGGAAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding seq I I GGAAGCAGGG TCAAGTTGGC GGGTTCCCAG ACTTCCAAAA ACAAGTTGAC TTGCACCAAGA TCATCAAGAT TCCACCAAGA TCATCAAGAT TCCACCACG TAGCAGACTTTGGCCCAG TCCTCACGACA TCCTCGACAG TCCTCCACCG TAGCAGACTTTGGCCCAGG TCCTCCACCG TAGCAGACTT TCGTGGACCAT TCCTTGAGACT TCCTTGAGACT TCCTTGAGACT TCCTTGAGACT TCGCCAGGC TATCGCAAAT ACCCTTTCTT GAGCCCCCAC GGCCTATTTG GAGCCCCCA	TCAGAAGGGG CTTGATAGGGG ATGATTCTTG ACCCTAATGC 175 DNA Seid Accession uence: 234. 11 GGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCGCTC GGTGGAAAAG GGGAGAGGTG TCTCAAGAAA TGACTAACGCATC TCTCAAGAAA TGACTTAAA TGGACTACGA TGCCATCA TTCTGAGATT GCCCAGGAT TCTGAGATT GCCCAGAT CCAGGATTAGCT AGACTTAAA TGGACTACGA AGATTTAGT CCCAGGATT CCAGGATT CCAGGATT CCAGGATT CCAGGATT CCAGGATT CCAGGATT CCAGGATT CCAGGATT CCTCAGGATT TCTCAGGATT CTCAGGATT TCTCAGGATT TCTCAGGATT TCTCAGGATT TCTCAGGATT TCTCAGGATT TCTCAGGATT TCTCAGGATT TCTCAGATT RCAGTCAG CTCTGATTTG CAATAAAAGT QUENCE n #: NM_001 .1130 21 GGTGCGGTC AGAGGCGGG ATCGAGGAGGG GTGGGCCTTA CAGGGCAGGG	TTTAGTTAAG CTCTTGCTCA TGCTCATTAT 798.2 31 GGGAACTCGG GTATACTGCG GCCCCGGGA CTGGCCCAGGA CTGGCCCAGGA CTGGCTTATA AGATCCCTCTGAA AGATAAACTC TCCTCTGCTTAA GAGTCCCTGTTATA GAGTCCCTGTTCCTTCAGGAC TCCTCCTGGAGAT TCCCCTGGATAT TCCCGATCTTTCCTCTGAGAT TCCCCTGGTTATAA CCTCTCCTGGAGAT TCCCCTGATTA TCCCCTGATTA TCCCCTGATTA TCCCCTGATTA TCCCCTGGAT AGCGGGATTCC TCCCCTGGAGAT TCCCCCTGGATA AGCGGGATTCC TCCCCTGGAGAT TCCCCTGGATATAA AGGGGGATTCC TCCCCTGGAGAT ACTCCCCTGATTAA AGGGGGGATTCC TCCCCTGGAGAT ACTCCCCTGGAGAT ACTCCCCTGGAGAT ACTCCCCTGGAGAT ACTCCCCTGGAGAT ACTCCCCTGGAGAT ACTCCCCTGGAGAT ACTCCCCTGGAAAAACCGGGGGATAC AACTCGCCTGAAT AACGGGGGGAAAAAACCGGGGGAAAAAAAAAA	GATGGAACCE AGTGGAATAA A1 TGGAGGCGG TTCCATCCCGG TCCATCCCGG TCCATCCCGG TCCATCGGAT CACCGGAT CACCGGAT CACCGGAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTCTGCCAT TTACTGCAATAT TTCACAGAGGG TCGTACTTAC CAGGCAAGCA TGGAATAT TGAAGATGGA GCCAAGTCAC AGCACTCACC AACACTCACC AACACTCACC AACACTCACC AACACTCACC AACACTCACC CACTGAATAAA	SGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA 51 CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATGGAGA AAAGCCAGAA GAGACTCAGAT ATTCCACAGG CCTCTTCCCC TCTCATCAGG TATTCCACAGG TATTCCACAGG TATTCCACAGG TCCTCATCAGG TCCTCATCAGG TCCTCATCAGG TCCTCATCAGG TCCTCATCAGG TCCTCATCAGG TCCTCATCAGG TCCCATGAGG TCCCCAAGT CGGACCCTAT GGGACCCCAG TCCCCAAGT TCGAGCTTCTT TCTAGTCTT CTAGTCT TCTAGTCT TCTAGTCT TCTT TCT	3480 3540 3660 3660 3665 60 120 180 240 300 360 420 480 560 720 780 840 900 1020 1020 1140 1200 1200 1320	
50 55 60 65 70	COTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding seq I GGAAGCAGGG TCAACTTGGC ACGGTTCCAGA ACTACTGGC ACGTTCCAGA ACTACTGAGA TTGTCAAGAT TGCACCAGA TCATCAGAGA TCATCAGAGA TCATCAGGG TAGCAGGACTT TGGTGCCCAG ACTTCAGCCAGA ACTACTCAGAGA TCATCAGGGCTT TGGTGCCAGG TAGCAGGACTT TGGTGCCCT CTGTGGACAT ACCCTTCTT GAGGCCTCCA GAGGCCCCGCA ATGAGGACTT TCCTTCAGACT TTCCTACAGAT ACCCTTTCTT GAGGCCCCAC ATTTCAGAATT TCCTCAAGAG TTTCAGTATT TCCTCAAGAGA TTTCAGTATT TCCTCAAGAGA	TCAGAAGGGG CTTGATAGGGG ATGATTCTTG ACCCTAATGC 175 DNA Sei did Accession uence: 234. 11 CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCTCGAAAAG GGGAGAGGTG TACTGCCATC CTCAAGAAA CTATCTGTTC AGACCTTAGC GTGGTACCGA CTGGAGCCTG GTTGGAGATTG GCCCAGCATGT GCTCCAGGATTTC GCTGCATGCT CTCAAGAAA CTATCTGTTC AGACCTTAAA CTATCTGTTC AGACCTTAAC CTCGAGCTTG GCTCCACAGCA GATTTTAGT CTCCAGGATTTC CCAGGATGTG GCCCTAATCT GACTCAGGTG CTCTGGGAAT AGATTCAGGTT GACTCAGGTG CTCTGGGAAT AGATTCAGTTG GCTCTGGTATA	GARCAGTCAG CTCTGATTTG CAATAAAAGT Quence n #: NM_001 .1130 21 GGTGCCGGTC AGAGGCAGGG CCCCTCCTCG CAGGCCCGGG ATCGGAGAGG TTCATGGAGAGG TTCATGGAGAGG TTCATGGATTC GAGAGATCT AGAGGTTTTG GCTCCTGAAA GGCTGCATCT GTTACTTCTA AAAGTTGTAC ACCAGCCAG ACCAGCCAG ACCAGCCAG ACCATCT CACCAGCTCT GTTACTTCTA AAAGTTGTAC ACCAGCCTAACA ACCAAGCCAG ACCATTCC ACCAGCTCT AAAATTAGTTGTAC ACAGGGGTGA AAAATATTT	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2 31 GGGAACTCGG GCCCCCGGA GCACCTACAGC CCACTGACC CTGACCTACA AGAATCCG CTCTCCTTAA AAAATAAACT TCCCCTGGG TTGCTGAGCAT TCCTCTGCTCT TCCTCCTGGG TTGCTGAGCAT TCCCCTGGA AGGGGCTACC TCCCCTGGA AGGGGCTATA AGGGGCTACC TTCCCCTGGA AGACTCTT TCCCCTGGA AGGGGCTTAC TCCCCTGGA AGGGGCTTAC TCCCCTGGA AGGGGGTTTC TACCCCATCT TCCAGTGTGG ACTTGCCTTA AAGGGGGGAA CCACCCT TAAAAAAGCC	GATGGAACCT AGTGGAATAA A1 I TGGGAGGCGG TTCCATCCGG CCCAGGGTCC CCTGGACACT TACTGGCATT TTCTGCCAT CACAGAGGGC TGGAATATA TGGCAATT TTCTGCAT CAGACACT TGAAATAT GGTAACTCGC CAGCCACT TGAAACATGA GCCAAGGCAC TGAACACCC CAGCCACC CCAGCCCC CCAGCCCC CCAGCCCC CCAGCCCC CCAGCCCC CCAGCCCC CCAGCCACC CCAGCCACC CCAGCCAAAT TTCCCCCCC CCAGCCACC CCAGCCAAAT TTCCCCCCC CCAGCCAAAAT TTCCCCCCC CCAGCCAAAA TTCCCCCCCCCC	GGGAAAGGCC AACCCATGG ATGATCCTTA AAAAAAAAA 51 CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATGGAGA AAAGCCAGAA GAGACTGAGG CATCCTAATA TTTGAATTTC CCTCTTCCCC TCTCATCGGG TCCCCAAGG TATTCCACAG GGGACCTCAGG TCCCCAAGT CGGACCTCAGG TCCCCAAGT TCCCCAAGT TCCCCAAGT TCCCCAAGT TTGGATTGTTTTTTTTTT	3480 3540 3660 3660 3665 60 120 180 240 360 420 480 540 660 720 780 960 1020 1080 11200 1260 1380
50 55 60 65 70	COTGAGAAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding seq I I GAAGCAGGG TCAAGTTGGC TCAAGTTCGCCAG TGTTCCCAGG TTGTCCCAGG TTGTCCCAGG TTGTCCCAGG TCATCAGAGA TCATCAAGAT TCCACCAAGA TCATCAAGAT TCCTCACCG TAGCAGACT TCGTGGACCAT TCGTGGACCAT TCGTGGACCAT TCGTGGACCAT TCGTGGACCAT TCCTGGACAT TCCTGAGAGA TTTCAGAGT TCTTCTTGAGTGT GGCCTACTGAGAGA TTTCAGTAAT TCCTTGAAGAG TCTTCAGAGAG TTTCAGAGAG TTTCAGAGAG TTTCAGAGAG TTTCAGAGAG TTTCAGAGAG TTTCAGAGAG TCTTCAGAGAG TCTTCCAGACAG TCTTCCAGAC TCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTC	TCAGAAGGGG CTTGATAGGGG ATGATTCTTG ACCCTAATGC 175 DNA Seid Accession uence: 234. 11 GGGGGCTCT CAAATTGACA GCCCTGTTTC GCCCCGGTC GGTGGAAAAG GGGAGAGGTG TCTCAAGAAA TGACTAACTGCATC TCTCAAGAAA TGACTTACA TGGCATC TCTCAAGATGTC TCTCAAGATGTC TCTCAAGATGTC TCTCAAGATGTC TCTCAAGATGTC TCTCAAGATGTC TCTCAAGATGTC TCTCAAGATGTC TCTCAAGATTAAGTCCAGTC TCTCAAGATTAAGTCCAGTC TCTCAAGATTAAGTCCAGTC TCTCAGATTAAGTCCACTAGTCT GACTCAGGTTG TCTCAGGATTAACTCAGGTTC TCTCTAGGATTAACTCAGATTCTAATCTCAGATTCTCAGATTAACTCCAGATTAACTCTCAGTTCTTTCT	GARCAGTCAG CTCTGATTTG CAATAAAAGT QUENCE n #: NM_001 .1130 21 GGTGGGGTC AGAGGGGGGG ATGGGGGTC AGAGGGAGAGG TTCATGGAT TTCATCACAG TTCATGGAT GCTCCTGA AGGCTTTG GCTCCTGAATC AGAGCTTTTG GCTCCTGAATC AGAGCTTTTG GCTCCTGAAA AGGCTTTTG GCCCTACTGAAA AGGCTTTTG GCCCTACTGAAA AAGTTTTG ACCAGGCTTA AAAGTTTTT CACAGGTTA AAAGTTTTC ACCAGGTTA AAAATTATTC ACCAGGTTA ACCAGGCTAAA ACCAGGCTAAA ACCAGGCTAAAAATAATTTT CCATAAATTAT	TTTAGTTAAG CTCTTGCTCA TGCTCATTAT 798.2 31	GATGGAACCE AGTGGAATAA A1 TGGAGGCGG TTCCATCCCGG GCCAGGGCCG TGGCTGCCAT CACTGGATTAC CTGGACACT CGAGCTTAC CTGGACACT CACTGGACT TACTGGCAT TTCTGCCAT TTCTGCCAT TTACAGAGGG TCGTACTTAC CAGAGATCTAC CAGACTAC CAGACTCTAC TGAACATCTAC CAGACTCAC TCCAGTGAAAA TTCCCCTTCC TCTTCGACT TCTTTCGACT TCTTTCGACT TCTTTCGACT TCTTTCGACT TCTTTCGACT TCTTTCGACT TCTTCTTCCACT TCTTTCGACT TCTTTCGACT TCTTTCGACT TCTTTCGACT TCTTTCGACT TCTTTCGACT TCTTTCGACT TCTTCGACT TCTTTCGACT TCTTCGACT TCTTCGACT TCTTCGACT TCTTCGACT TCTTTCGACT TCTTCGACT TCTTCGACT TCTTCCACT TCT	GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAAA	3480 3540 3660 3660 3665 60 120 180 240 300 360 420 480 560 720 780 840 900 1020 1020 1140 1200 1200 1320
50 55 60 65 70	COTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Seq ID NO: Nucleic Ac: Coding seq I GGAAGCAGGG TCAAGTTGAC ACGGTTCCAGG ACTTCCAGA ACTACTCAGAC TTGCACCAGGA TCATCAGAGA TCATCAGAGA TCATCAGAGA TCATCAGAGA TCATCAGAGA TCATCAGAGA TCATCAGAGA TCATCAGAGA TCATCAGAGA TCATCAGAGA TCATCAGAGA TTGCACCAGGA ATGAGGTGGT TGGGCCCCCA GGGCTATTTG GGCCCGGCA ATTGCAGATTT GGCCCGCCA ATTTGCAGATT TCAGGGATTT TGAGGCCCTC GGCCTATTTG GCCCAGCCAAA TTTCAGTATT TGCTGAAGAG CCTACCAATC CAAGCCTCCT CAAGCCTCCT	TCAGAAGGGG CTTGATAGGGG ATGATTCTTG ACCCTAATGC 175 DNA Sei did Accession usence: 234. 11 CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCTCCGATCTC GCTGGAAAAG CTACTGACAC TCTCAAGAAA CTATCTGTTC AGACCTTAGC GTGGTACCCA CTGGACTTT GCCCCCCTT	GAACAGTCAG CTCTGATTTG CAATAAAAGT Quence n #: NM_001 .1130 21 GGTGCCGGTC AGAGGAGAGG CCCCTCCTCG CAGGCCCGGG ATCGGAGAGG TTCATGGAGAGG TTCATGGAGAGG TTCATGGAGAGG TTCATGGATTC CAGAGGTCTC CCTCAGAATC CCTCAGAATC GGCCCTTCTC GGCCCTTCTC AAAGTTGTAC AAAGTTGTAC ACAGGGCTCA ACAGGGGTCA ACAGGGGTCA ACAGGGGTCA ACAGGGGTCA ACAGGGTCTC CGCCCTCCC ACAGGCTCTC CGCCCTCTCA ACAGGGTCA ACAGGGTCA ACAAGGATCT ACAAAATAATTT CCATATTAAA	TTTAGTTAAG CTCTTGCTCA TGCTCATTAT 798.2 31 GGGAACTCGG GTATACTCGG GCCCCGGGA CTGACCCGAC CCGCTTAATACTCGG CACCTACATACTCGG TTGCTCTTAA AAAATAAACTCG TTCCCTGGGT TTCCTGCTTATTAC AGGCCTACGG AGGCATCTT TCCCGGATCT TCCCTGGGT TCCTCGTGAGAT TCCCGGATCT TCCCGGATCT TCCCTGGATCT TCCGGATCT TCCGGATCT TCCGGATCT TCCGGATCT TCCGGGTTATA AAGGCGATCT TCCAGTGTGG AGCGGATTT TCCAGTTTAAAAAGCC TAAAAAAGCC TAAAAAAGCC TAAAAAAGCC TAAAAAAGCC TAAAAAAGCC TAAAAAAAGCC TAAAAAAAGCC TAAAAAAAGCC	GATGGAACAT AGTGGAATAA CACTTAAGTG GGACTGCTAC 41	GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA 51 CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATGGAGA AAAGCCAGAA ATGATCAGG CATCCTAATA TTTGAATTTC CCTCTTCCCC TCTCATCGGG TATTCCACAG TCCATCAGG TATTCCACAG TCCCATTGGCTTT GGGACCCCAG TTCCCCAGGTTCT TGGAACTCTT TGTATTTT TGTATTTT TGTATTTT TGTATGGTTT TGTAAAGGAAG TTTTGGCTTT TTTTAGTTTT TGAAAGGAAG TTTTAGTTTT TTTAGTTTT TTAGTTTT TTTAGTTTT TTTAGTTTT TTTAGTTTT TTTAGTTTT TTTAGTTTT TTTAGTTTT TTTAGTTTT TTTAGTTTT TTTTAGTTT TTTTAGTTT TTTTAGTTT TTTTAGTT TTTTT TTTTT TTTTT TTTTT TTTTT TTTTT TTTT	3480 3540 3660 3660 3665 60 120 180 240 360 480 660 660 6720 780 900 960 1020 1080 1140 1260 1320 1320 1340
50 55 60 65 70	COTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding seq I GGAAGCAGGG TCAACTTGGC ACGGTTCCAGA ACTACTCGG GGGTTCCAGA ACTACTGAG TTGTCAAGAT TGCACCAGA TCATCAGAGA TCATCAGAGA TCATCAGAGA TCATCAGGGCTCCTGTGGACAT TGGTGCCCAGG AGGGCTGGACAT TGGTGACAT TGCTGGACAT TCCCTGGGAGA ATGAGGTGGT GGGCCCGGCA ATGAGGAGTTTTGGAGATT TCCCTGGAGA TTTCAGTATT TGCTGAAGAG TTTTCAGTATT TGCTGAAGAG CGTACCAAC CCTTTCTTGAGAAGAC CTTACCAAGAG CCTACCAAGAG CTTTCTAGAGAG CCTTTCTTAGAGAAC CCTTTCTTAGAGAG CCTACCAACC CCTTTCTTAGAGAG CCTACCAACC CCTTTCTAGAAA CCACTACCAACC CCTTTCTTAGAAA CCCTTCTTTTTAGAAA CCCTTTCTTTTAGAGAAC CCTTTCTTAGAAA CCTTTCTTTTAGAAA CCCTTTCTTTTTAGAAA CCTTTCTTTTAGAAA CCCTTTCTTTTAGAAA CCTTTCTTTTTAGAAA CCCTTTTTTAGAAA CCCTTTCTTTTTAGAAA CCCTTTCTTTTTAGAAA CCCTTTCTTTTAGAAA CCCTTTCTTTTAGAAA CCCTTTCTTTTAGAAA CCCTTTCTTTTAGAAA CCCTTTCTTTTAGAAA CCCTTTCTTTTAGAAA CCCTTTCTTTTAGAAA CCCTTCTTTTTAGAAA CCCTTCTTTTTAGAAA CCCTTCTTTTTAGAAA CCCTTCTTTTTAGAAA CCCTTCTTTTTAGAAA CCCTTCTTTTTAGAAA CCCTTCTTTTTAGAAA CCCTTCTTTTAGAAA CCCTTCTTTTAGAAA CCCTTCTTTTAGAAA CCCTTCTTTTTAGAAA CCCTTCTTTTAGAAA CCCTTCTTTTAGAAA CCCTTCTTTTAGAAA CCCTTCTTTTAGAAA CCCTTCTTTTAGAAA CCCTTCTTTTAGAAA CCCTTCTTTTAGAAA CCCTTCTTTTTAGAAA CCCTTCTTTTAGAAA CCCTTCTTTTAGAAA CCCTTCTTTTAGAAA CCCTTCTTTTAGAAA CCCTTCTTTTAGAAA CCCTTCTTTTAGAAA CCCTTCTTTTAGAAA CCCTTCTTTTAGAAA CCCTTCTTTTAGAAA CCTTCTTTTAGAAA CCTTCTTTTAGAAA CCTTCTTTTTAGAAA CCTTCTTTTAGAAA CCTTCTTTTAGAAA CCTTCTTTTTAGAAA CCTTCTTTTTAGAAA CCTTCTTTTAGAAA CCTTCTTTTAGAAA CCTTCTTTTTAGAAA CCTTCTTTTAGAAA CCTTCTTTTTAGAAA CCTTCTTTTTAGAAA CCTTCTTTTTAGAAA CCTTCTTTTTAGAAA CCTTCTTTTTAGAAA CCTTCTTTTTAGAAA CCTTCTTTTTAGAAA CCTTCTTTTTAGAAA CCTTCTTTTTAGAAAA CCTTCTTTTTAGAAA CTTTTTTAGAAAA CCTTTCTTTTAGAA	TCAGAAGGGG CTTGATAGGGG ATGATTCTTG ACCCTAATGC 175 DNA Sei did Accession uence: 234. 11 CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCTCGAAATGGCAT GCTGGAAAAG CTACTGTTC GCTGGATGTC CTCAAGAAA CTACTGTTC AGACCTTAGC GTGGTACCGA CTGCAGCCTG GTGGTACCGA CTCAGAGAT GCTCCAGAGAT GCTCCACAGAA AGATTTTAGT CTCAGAGT CTCAGAGT CTCAGGTG CTCTCAGGT CTCAGGT CTCAGGT CTCTCAGGT CTCTCAGGT CTCTCAGGT CTCTCAGGT CTCTCAGGT CTCTCAGGT CTCTCAGGT CTCTCAGGT CTCTCGGAAT AGATCACT CTCTCAGT CTCTCAGT CTCTCAGATC CCAGTATAAAA CCAGTAAAAA CCAGTAAAAA	GARCAGTCAG CTCTGATTTG CAATAAAAGT Quence n #: NM_001 .1130 21 GGTGCCGGTC AGAGGCAGGA CCCCTCTCG CAGGCCCGGG ATCGGAGAGG TCAGGAGAG TCAGGAGAGG TCAGGAGTTTAGAGAGT GACAGCTTTG GCTCCTGAAA GGTTGCTCTG GACCAGTTTG GACCAGTTTG GACCAGTTTG GACCAGTTTG GACCAGTTTG AAAGTTGTAC ACCAGCCGAAA ACCAAGCCAG ACCATTCT AAAGTTGTAC ACCAGCTTTG TTACTTCTA AAAGTTGTAC ACCAGCCTAAC ACCAGCCTAAC ACCAGCCTAAC ACCAAGCCAG AACAAACCAT CGGCCTTTTTATAAA AAAAACCATT	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2 31 GGGAACTCGG GTATACTGCG GCCCCCGAGA TGATACTGCG GCCCCCGAGA AGAAATCAG GCTGACCTTAA AAAATAAACT TCCTCTGCTTAA AGAGTCCTTATTAA GAGTCCTTTATTAA AGAGTCCTTTATTAA TCCCATGTGCT TCCCCTGGG TTGCTGAGATT TCCCCTGGG TTGCTGAGATT TCCCATGTGTG ACTCCCTGGG ACTGCCTTA AAAGGCGGATTA TAACCCATCT TCCAGTGTGG TACCCATCT TCCAGTGTGG TCCTCCTGGG TTCCTCCTGGG TTCCTCCTGGG TTCCTCCTGGG TTGCTGAGATTA TCCCCATGTGTGG TCCCCTGGAGTTTC TCCCCTGGAGTTC TCCCCTGGAGTTTC TCCCTGGAGTTTC TCCCCTGGAGTTTC TCCCCTGGAGTTTC TCCCCTGGAGTTTC TCCCCTGGAGTTTC TCCCCTGGAGTTTC TCCCCTGGAGTTTC TCCCCTGGAGTTTC TCCCCTGGAGTTC TCCCCTGGAGTTTC TCCCCTGGAGTTTC TCCCCTGGAGTTTC TCCCCTGGAGTTTC TCCCTGGAGTTTC TCCCCTGGAGTTTC TCCCCTGGAGTTTC TCCCCTGGAGTTTC TCCCCTGGAGTTC TCCCCTGGAGTTC TCCCCTGGAGTTC TCCCCTGGAGTTC TCCCCTGGAGTTC TCCCCTGGAGTTC TCCCCTGGAGTTC TCCCCTGGAGTTC TCCCCTGGAGTTC TCCCCTGGAGTTC TCCCCTGGAGTTC TCCCCTGGAGTTC TCCCCTGGAGTTC TCCCCTGGAGTTC TCCCTGGAGTTC TCCCCTGGAGTTC TGGAACCT AGTGGAATAA A1 I TGGGAGGCGG TTCCATCCGG CCCGGGGCCG CCTGGCACACT CACTGAAATAT CGGACTTAC CACAGAGGGG TGCAAATAT CGCAAATAT TGCAACACT TGAAACATGA CGCAAGCCA CCTGGACCT CAAGCCAAGT TGAACACCA CCACTGAAATAT TGCAAATAT TCCCTCGA	GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA 51 CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATGGAGA AAAGCCAGAA GAGACTGAGG CATCCTAATA TTTGAATTTC CCTCTTCCCC TCTCATCGGG GCCATCAAGC TCTCATCAGG TTCCCCAAGT TCGGACCCCAG TTCCCCAAGT TCGGACTTGT TCGAGTTGTTATTTCTAGCTTT TTCAAAGGAAG TCTTAGTTATTTTTTTAGATTTGC ACCAGGATCC TAAGTTTGCTAAAGTTGGTTG ACCAGGATCC TAAGTTTGCTTAATTTTGC ACCAGGATCC TAAGTTTGCTTAATTTGC ACCAGGATCC TAAGTTTGCTTAATTTGC ACCAGGATCC TAAGTTGGTTG AATTCGGTTG	3480 3540 3660 3660 3665 60 120 180 240 360 480 660 660 6720 780 900 960 1020 1080 1140 1260 1320 1340 1560 1560 1560 1560	
50 55 60 65 70	COTGGGGAAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding seq I I GGAAGCAGGG TCAAGTTGGC GGGTTCCCAG ACTTCCACA ACTACCAAGA TCATCAAGAT TCCACCAAGA TCATCAAGAT TCCACCAAGA TCATCAAGAT TCCACCAAGA TCATCAAGAT TCCTCACCG TAGCAGACTTTGACCT TAGGAGACTT TCGTGAGCAT TCCTTGAGACA TCATCGAAGAT TCCTTGAGACA TTCCGACAG TATTCGCAAAT TCCCTGAGAG TATTCGAAGAT TCCTGAGAGA TTTCAGTATT TCCTGAAGAG CTTTCTATAGACT CAAGCCTCCA GGCTATTTG CAAGCACCAA TTTCAGTATT TCCTGAAGAG CTTACCAATC CAAGCCTCCA ATTTCAGTATT TCCTGAAGAG CTTACCAATC CAAGCCTCCA AAAAAAATAGA	TCAGAGGGG CTTGATAGGGG ATGATTCTTG ACCCTAATGC 175 DNA Seid Accession uence: 234. 11 GGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCGCTG GGGGAGAGGTG TACTGCATC GCTGGAAAAG TGTGCATC TCTCAAGAAA TGGACTAGCC GTGGTACCGA AGACTTAGA AGACTTAGA TGGCATGC TCTGAGGATT GCTGCATTAG GCTGCATTAGC TGGGATACCG TGCTACCAGTAG CCAGGATTTAG GCTGCACTAC GCTGCATTAC GCTGCACTAC GCTGCACTAC CCAGGATGTG CTCTGGGATT GGTTGGAATT GGTTGGAATT TCTGAATGCC GCTCAGTACC GCTCAGTACC GCTCAGTACC GCTCAGTACC GCTCAGTACC GCTCAGTACC GCTCAGTACC GCTCAGTACC GCTCCACAA CCAGGATGC GCTCCACAA CCAGGTAGC CCAGGATGC GCTCCCACAA CCAGGTAGC GCTCCCACAA CCAGGTAGC CCAGGTAGC CCAGGTAGC CCAGGTAGC GCTCCCACAA CCAGGTAGC CCAGGTACC CCAGGTAGC CCAGGTACC CCAGGTAGC CCAGGT CCAGGTAGC CCAGGT CC	GARCAGTCAG CTCTGATTTG CAATAAAAGT QUENCE n 8: MM_001 .1130 21 GGTGCGGGTC AGAGGGAGGG ATCGGGCTGG ATCGGGCTGG ATCGGGCTGG ATCGAGAGGT TCATGGAGAGG TCATGGAGAGG GGTGCGCCTTA ATCACACAG TTCATGGATG AGCCTACCA ACCAGCTCT GACAGCTGT GACAGCTGT AAAGTTGTAC AACCAACT AAAGTAGTTAT ACATAATTAT TGTTTATAAAA CAAAACCACT TTTATACCCTT	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2 31	GATGGAACAT GACTGCATCA 41 TGGGAGGCGG TTCCATCCCGG GCCAGGGCCG TGGCTGCATCCGGATTACT CACTGGATTACT CACTGGATTACT CACTGGATT TTCTGCCAT TTCTGCCAT TTCACAGGGG TCGTACTTAC CAGGCAACTACT CAGGCAACTACT CAGGCAACTACT CAGGCAACTCGACT CAGCCAAGCA TGAACACCACC CCCCTCCTTCTACACG ACACTCCCCTC TTCTACACG TTCTTCACAG TTCTTCACAG TTCTTCACAG TTCTTCACAG TTCTTCACAG TTCTTCACAG TTCTTCACAG TTCTTCACAG TTCTTCACAG TTCTTCACAG TTCTTCACAG TTCTTCACACT TTCTCACACT SGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAAA	3480 3540 3660 3660 3665 60 120 180 240 360 420 540 600 720 780 960 1020 1080 11200 1200 1200 1200 1200 1380 1440 1560 1560 1680	
50 55 60 65 70	COTGGGGAAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Seq ID NO: Coding seq I GGAAGCAGGG TCAAGTTGAC ACGGTTCCAGG ACTTCCACAGG ACTTCCAAGA TCATCCAGAGA TCATCAAGAG TCAAGCCTCCT TTTTGAGAAA AAAAAAAA	TCAGAAGGGG CTTGATAGGGG ATGATTCTTG ACCCTAATGC 175 DNA Sei did Accession usence: 234. 11 CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCTCGGATGTC GCTGGAAAAG CTATCTGTTC AGACCTTAGC GTGGACAGC GTGGTACCGA CTGAGCTTG GCTGGACATG CTGAGCTTG GCTGGATTTC GCTGGAATTTC GCTGGAATTTAGT GGACTGAGCT GCTGCACTA CCAGGATGTC CCAGGATGTC CCAGGATGTC CCAGGATGTC CCAGGATGTC GCTCCACTAC CCAGGATGTC GCCCACAA CCAATCAGT CTCTAGAATGCC GCTGCCACAA CCAATCAGT CCAATCAGT ACTCAGCCC ACCAATCAGT ACCAATCAGC ACCAATCAGC ACCAATCAGC ACCAATCAGC ACCAATCAGC ACCAATCAGC ACCAATCAGC ACCAATCAGC ACCAATCAGC ACCAATCAGC ACCAATCAGC ACCAATCAGC ACCAATCAGC ACCAATCAGC ACCAACAC ACCAATCAGC ACCAACAC ACCAACAC ACCAACAC ACCAACAC ACCAACAC ACCAACAC ACCAACAC ACCAACAC ACCAACAC ACCAACAC ACCAAC ACCAAC ACCAACAC ACCAAC	GAACAGTCAG CTCTGATTTG CAATAAAAGT Quence n #: NM_001 .1130 21 GGTGCCGGTC AGAGGAGAGG CCCCTCCTCG CAGGCCCGGG ATCGGAGAGG TTCATGGATTCC CAGGCCTCG CAGGCCTGG ATCGGAGAGG TTCATGGATTC CAGAGGTCT CCTAGAATC CACAGCCTGG AAAGTTTTA CACAAG CACCCTCTCG GCCCTCTCA AAAGTTGTAC CACAGGCTACCA ACAAGCCCAG CACCCTCTCC GCCCTCTCAAAATAATTT CCATAAATATTT CCATAAATATT TGTTTATAAACCACT TTATAACCCTT TTATAACCCTT TTATAACCCTT CGGGGGGGGGG	TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT 798.2 31 GGGAACTCGG GTATACTCGG GCACCGAGA CTGACCCGAC CCACTACAG CACCATACAG CACCTACAG AGAAATCAG CTCTCCTTCA AGAGTCCTGT TCCTCCTCGGT TTCCTCTGGATT TCCCGATATTA CTCCCTGGA AGCGCATTTCCAG AGCGCATTTCCAG AGCGCATTT TCCAGGATTT TCCAGGATTT TCCAGGATTT TCCAGGATTT TCCAGGATTT TCCAGGATTT TCAGGATTT TCAGGATTT TCAGGATTT TCAGAAATCAG GGGAGGATTC TAAAAAAGCC TATTTCAGT TAAAAAAGCC TATTTCAGT TAAAAAAGCC TATTTCAGT TAAAAAAGCC TATTTCAGT TCAGGAAATCA GGGAGGAGTC CAGGAAATCA CGGGAGGAGTC CCAGGAAATCA CGGGAGGAGTC CCAGGAAATCA CGGGAGGAGTC CCAGGAAATCA CGGGAGGAGTC CCAGAAATCA CGGGAGGAGTC CCAGAAAATCA CGGGAGGAGTC CCAGAAAAAATC CCAGAAAAAATC CAGGAAAAAATC CAGGAAAAAATC CAGGAAAAAAATC CAGAAAAAAATC CAGAAAAAAAAATC CAGAAAAAAAATC CAGAAAAAAATC CAGAAAAAAAAAA	GATGGAACAT AGTGGAATAA A1 I TGGGAGGCGG TTCCATCCGG GCCAGGCGCG AGTTGTTAC CTGCAGCAT CACTGGATT TTTCTGCAT CACTGGATT TTTCTGCAT CACTGGATT TTTCTGCAT CACTGGAT TGGTACTCTG CAGGCAGTCT CAGGCAATAT TGGTACTCGC CAGGCAAGT TGACCAGG TGGACTCTAC CAGGCAAGT TGACCAGG TGGACTCTAC CAGGCAAGT TGACCAGG TTGACCAG CTTTGCCAT TTCCTCACC TTCCTACCAG TTTTGGATT TTCCTCACC TTTCCTACCAG TTTTGGGAT TAGCGGGGC TATTTTAAAG TACCCCCTC TTCCTCACC TATTGCCCCC	GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA 51 CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATGGAGA AAAGCCAGAA GAGACTGAGG CATCCTAATA TTTGAATTTC CCTCTTCCCC TCTCATCGGG GCCATCAAGC TCTCATCAGG TTCCCCAAGT TCGGACCCCAG TTCCCCAAGT TCGGACTTGT TCGAGTTGTTATTTCTAGCTTT TTCAAAGGAAG TCTTAGTTATTTTTTTAGATTTGC ACCAGGATCC TAAGTTTGCTAAAGTTGGTTG ACCAGGATCC TAAGTTTGCTTAATTTTGC ACCAGGATCC TAAGTTTGCTTAATTTGC ACCAGGATCC TAAGTTTGCTTAATTTGC ACCAGGATCC TAAGTTGGTTG AATTCGGTTG	3480 3540 3660 3660 3665 60 120 180 240 360 420 540 600 720 780 960 1020 1080 11200 1200 1200 1200 1200 1380 1440 1560 1560 1680

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40	Seq ID NO:						
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5	GTGGCGTAGC C GGTCCCCTGC C CAGCAGCATG A CACCCTCTCC A AGCCTGGGTT C	CCCGCCAGCC A ACTGACAGAC A ACGTGCAGAC (CAGGCTGGG 1 CGCTGGGAC (CCCATGCGTC (GCACGTCCT C TACGTCGGG C CGGAGCCTG C	CCTCTCCAG C TTCCTGCTG G TGTGTGGGC G	CCCACAGGG GGCGGCCAG	2460 2520 2580 2640 2683
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45 50	CCAGGGTGGG GGCCATCAGC CTAAAGACAG ATGGTCCCAC ACACCTGCAG CAGAGGAGGA	CCCCGGGGGT CCCCATTTCT TGCCAAGTGC GCAGGAGCGC AGCCTGGGAC AGAGGAGGAG	CAGGAGCTCC GCTGCAAACC CTGCACCGTG TGTGGACCCC CACGTGGATG GGCGCCGGGG	GTGGCAGGCC AGAAGGGCCA TGGTCAGAGC GACCACAGCC GCTCTCTGGG GGCAGATCCT CCACCTTGTC	GCTGGGCATA CAGTGTTCCC GAGCCACTGG CAGCCCTGTC GGGCCAGCTG CAGGGGGGCCT	TTCTGAGATT TCCATGGGAC GCAGCCGGTG CTAGGCCTGG CGGCCCCTGA GCCTTCCCCG	120 180 240 300 360 420
	CCAGGGTGGG GGCCATCAGC CTAAAGACAG ATGGTCCCAC ACACCTGCAG CAGAGGAGGA GCATGGGCTC	CCCCGGGGGT CCCCATTTCT TGCCAAGTGC GCAGGAGCGC AGCCTGGGAC AGAGGAGGAG TGAGGAGTTG	CAGGAGCTCC GCTGCAAACC CTGCACCGTG TGTGGACCCC CACGTGGATG GGCGCCGGGG CGTCTGGCCT	GTGGCAGGCC AGAAGGGCCA TGGTCAGAGC GACCACAGCC GCTCTCTGGG GGCAGATCCT CCACCTTGTC CCTTCTATGA	GCTGGGCATA CAGTGTTCCC GAGCCACTGG CAGCCCTGTC GGGCCAGCTG CAGGGGGCCT CTGGCCGCTG	TTCTGAGATT TCCATGGGAC GCAGCCGGTG CTAGGCCTGG CGGCCCCTGA GCCTTCCCCG ACTGCTGAGG	120 180 240 300 360 420 480
50	CCAGGGTGGG GGCCATCAGC CTAAAGACAG ATGGTCCCAC ACACCTGCAG CAGAGGAGGA GCATGGGCTC TGCCACCCGA	CCCCGGGGT CCCATTTCT TGCCAAGTGC GCAGGAGCGC AGCTGGGAC AGAGGAGGAG TGAGGAGTTG GCTGCTGGCT	CAGGAGCTCC GCTGCAAACC CTGCACCGTG TGTGGACCCC CACGTGGATG GGCGCCGGGG CGTCTGGCCT GCTGCCGGCT	GTGGCAGGCC AGAAGGGCCA TGGTCAGAGC GACCACAGCC GCTCTCTGGG GGCAGATCCT CCACCTTGTC CCTTCTATGA TCTTCCACAC	GCTGGGCATA CAGTGTTCCC GAGCCACTGG CAGCCCTGTC GGGCCAGCTG CAGGGGGCCT CTGGCCGCTG AGGCCATCAG	TTCTGAGATT TCCATGGAC GCAGCCCGTG CTAGGCCTGG CGGCCCCTGA GCCTTCCCCG ACTGCTGAGG GACAAGGTGA	120 180 240 300 360 420
	CCAGGGTGGG GGCCATCAGC CTAAAGACAG ATGGTCCAC ACACCTGCAG CAGAGGAGGA GCATGGGCTC TGCACCCGG GGTGCTTCTT AGCATGCCAA	CCCCGGGGGT CCCCATTTCT TGCCAAGTGG GCAGGAGGGC AGCCTGGGAC AGAGGAGGTTG GCTGCTGGC CTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	CAGGAGCTCC GCTGCAAACC CTGCACCGTG TGTGGACCCC CACGTGGATG GGCGCCGGGG CGTCTGGCCT GCTGCCGGCT AGCTGCCGGCT AGCTGCAGA AGCTGTCAGT	GTGGCAGGCC AGAAGGGCCA TGGTCAGAGG GACCACAGCC GCTCTCTGGG GCAGATCCT CCACCTTGTC CCTTCTATGA TCTTCCACAC GCTGGAAGCG TCCTGCTCCG	GCTGGGCATA CAGTGTTCCC GAGCCACTGG CAGCCAGCTG CAGGGGGCCT CTGGCCGCTG AGGCCATCAG CCGGGACGAC GTCAAAAAGGA	TTCTGAGATT TCCATGGGAC GCAGCCGTG CTAGGCCTGG CGGCCCTGA GCCTTCCCCG ACTGCTGACG GACAAGGTGA CCCTGGACGG AGAGACTTTG	120 180 240 300 360 420 480 540 600 660
50	CCAGGGTGGG GGCATCAGC CTANAGACAG ATGGTCCCAC ACACTGCAG GCATGGGGGA GCATGGGGGTC TGCCACCCGA GGTGCTTCTT AGCATCCCAA TCCACAGTGT	CCCCGGGGGT CCCATTTCT TGCCAAGTGC GCAGGAGGCGC AGCCTGGGAC AGAGGAGGAG TGAGGAGTTG GCTGCTAGCG CTGCTATCGC GTGGTTCCCC GCAGGAGACT	CAGGAGCTCC GCTGCAAACC CTGCACCGTC TGTGGACCCC CACGTGGATG GGCCCCGGGG CGTCTGGCCT GCTGCCGGCT AGCTGTCAGA AGCTGTCAGT AGCTGTCAGT	GTGGCAGGCC AGAAGGGCCA TGGTCAGAGC GACCACAGCC GCTCTCTGGG GGCAGATCCT CCATCTTCTATGA TCTTCCACAC GCTGGAAGCG TCCTGGTCCG TCCTGGTCCG TCTGGTCCG TCTTGGCTCG	GCTGGGCATA CAGTGTTCCC GAGCCACTGC CAGCCAGCTG CAGCGGGGCCT CTGGCCGCTG AGGCCATCAG CGGGGACCAG CTCAAAAGGA CTGGGACCCG	TTCTGAGATT TCCATGGGAC GCAGCCCGTG CTAGGCCTGG CGGCCCTGA ACTGCTGAGG GACAAGGTGA CCCTGGACGG AGAGACTTTG TGGGAAGAAC	120 180 240 300 360 420 480 540 600 660 720
50	CCAGGTGGG GGCATCAGC CTANAGACAG ATGGTCCCAC ACACCTGCAG CAGAGGAGGA GCATGGGCTC TGCCACCCGA GGTGCTTCTT AGCATGCCAA TCCACAGTGT CCGAAGAGGC	CCCCGGGGGT CCCCATTTCT TGCCAAGTGC GCAGGAGCGC AGCCTGGGAC AGAGGAGGAG TGAGGAGTTG GCTGCTGGCT CTGCTATGGG GCAGGAGACC AGCCCCTGTG	CAGGAGCTCC GCTGCAAACC CTGCACCGTG TGTGGACCCC CACGTGGATG GGCCCCGGGG GGTCTGGCCT GCTCCGGCT GGCTTCAGA AGCTGTCAGA AGCTGTCAGG GCCCCTCCGGG GCCCCTCCGGG GCCCCTCCGG	GTGGCAGGCC AGAAGGGCCA AGAAGGGCCA GCACAGCC GCTCTCTGGG GGCAGATCCT CCACCTTGTC CCTTCTATGA TCTTCCACAC GCTGGAAGCG TCCTGCTCCT TGCTGCTGCT TGCTGGGCTC TCCTGGCTCT TCCCTGCCTCC	GCTGGGCATA CAGTGTTCCC GAGCCACTGC GAGCCACTGC GGGCCAGCTG CAGGGGGCCT CTGGCCACTCA AGGCCATCAG CGGGACGAC CTCAAAAGGA CTGGGACCCC TGGGTACCCCT	TTCTGAGATT TCCATGGGAC GCAGCCCTGG CGGCCCTGA GCCTTCCCCG ACTGCTGACGG GACAAGGTGA CCCTGGACGG AGAGACTTG TGGGAAGAAC GAGCTGCCCA	120 180 240 300 360 420 480 540 600 660
50 55	CCAGGOTGGG GGCATCAGC CTAAAGACAG ATGGTCCCAC ACACCTGCAG ACACCTGCAG GCAGGGGGGA GCATGGGCTC TGCCACCCGA GGTGCTTCTT AGCATGCCAA TCCACAGTGT CCGAAGACGC CACCCAGGAG AGGCCCAGAG	CCCGGGGT CCCATTICT TGCCAAGTGC GCAGGAGCGC AGCCTGGGAC AGAGGAGGAG TGAGGAGTTG GCTGCTATGGG TGAGTATGGC GCAGGAGACT AGACCCTGTG AGAGGTCCAG GGCGTGGTGGGGC GGCGTGGTGGGGGGGGGG	CAGGAGCTCC GCTGCARACC CTGCACCCTG TGTGGACCCC CACCTGGATG GGCCCCGGGG GGTCTGGCCT GCTCCAGCC GCCTCCAGC CACTCCAGC GCCTCCAGC GCCTCCAGC GCCCTCCAGC GCCCTTCGACT GTTCTGACCT GTTCTGACCT	GTGGCAGGCC AGAAGGGCCA TGGTCAGAGG GACCACAGCC GCTCTCTGGG GGCAGATCCT CCACCTTGTC CCTCTCAGAG GCTGCACAGGC TCTTCACACA GCTGCACAGGC TCCTGCTCCG TGCTGGCTCC TCCCTGGCTCC CCCAGGAGCC CCCCAGGAGCC CCCCAGGAGCG	GCTGGGCATA CAGTGTTCCC GGGCCAGCTG GGGCCAGCTG CAGGGGCCT CTGGCCGCTG AGGCCATCAG GGGGCATCAG GGGGCATCAG GGGGACGAC CTGGGACCAC CTGGGACCAC CTGGGACCAC CAGGGACCAC CAGGACCAC CAGGACCAC CAGGACCAC CAGGACCAC CAGGACCAC CAGGACCAC CAGGACT	TTCTGAGATT TCCATGGGAC GCAGCCGGTG CTAGGCCTGG GGGCCCCTGA GCCTTCCCCG ACTGCTGAGG GACAAGGTGA CCCTGGACGG AGAGACTTTG TGGGAAGAAC GAGCTGCCCA AGTCCAGCCC GAGGCGCAGC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50	CCAGGOTGGG GGCATCAGC CTANAGACAG ATGGTCCCAC ACACTIGCAG AGAGGAGGA GCATGGGGTC TGCCACCCGA GGTGCTTCTT AGCATGCCAA TCCACAGTGT CGGAAGACGC CACCCAGAG AGGCCCAGAG TGCGCCGAGAG TGCGCGCGGT	CCCCGGGGGT CCCCATTICT TGCCAAGTGC GCAGGAGCGC AGCCTGGGAC AGCCTGGAC TGAGGAGTTG CCTCCTGCTT CTGCTATTGGG GTGGTTCCCC GCAGGAGACT AGCCCTGTG AGAGCTCCAG GCCGTGGTG GCAGGAGACA	CAGGAGETEC GCTGCAAACC GCTGCACCC GCTGGACCC CACGTGGATG GGCCCGGGG GGTCTGGCCT GCTGCCAGA AGCTGTCAGC CACCTCCAGC TCTGAAAGTG GTTCTGAGA AGGACGTGCA AGGACGTGCA	GTGGCAGGCC AGAAGGGCCA TGGTCAGAGG GACCACAGCC GCTCTCTGGG GGCAGATCCT CCACCTTGTC CCTTCTATGA TCTTCCACAC GCTGGAAGCG TCTGGTCCCC TCCTGGCTC TCCCGGCTC TCCCGGCTC CCCAGGAGCC CCCCAGGAGCA AGGTGTGCCT	GCTGGGCATA CAGTGTTCCC CAGCCACTGG CAGCCACTGG CAGCCAGCTG CAGCGGCCT CAGCGGGCCT CAGCGCGCTG CAGCGGACCAC CTCAAAAAGA CTCGAACACC TGGGTACCCT AGGACGGGTC CAGCGATTGC CAGCGATTGC GGACCACC GGACCACC GGACCACC GGACCACC GGACCACC GGACCACC GGACCACC GGACCACC GGACCACC CAGCACCCC CAGCACCCC CAGCACCCCC CAGCACCCCC	TTCTGAGATT TCCATGGAC GCAGCCGTG CTASGCCTGG CGGCCCCTGA GCCTTCCCCG ACTGCTGACG GACAAGTGA GCACAGCG AGACACTTG GGGAAGAAC GAGCTGCCC GAGCGCAG GTGCCACCG GAGCCACC GTGCCACCG GTGTCCACCC GAGCCCACC GTGTCCACCC GTGTCCATCC	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960
50 55	CCAGGTGGG GGCATCAGC CTANAGACAG ATGGTCCCAC ACACTGCAG GCAGGAGGA GCATGGGCTC TGCCACCCGA AGCATGCAG GGTGCTTCTT AGCATGCCAA TCCACAGTGT CCGAAGACGC CACCCAGGAG AGGCCCAGAG TGCGCCGCT TCTTTGTCCC	CCCCGGGGT CCCCATTICT TGCCAAGTGC GCAGGAGCGC AGCCTGGGAC AGAGGAGCGA TGAGGAGTTG GCTGCTGGCT CTGCTATGGG GTGGTTCCCC GCAGGAGCAC AGAGGAGCAC AGAGGAGCAC GCAGGAGGAG GCAGGAGGAG GTGGTGCCAC GCAGGAGGAG GTGGTGCCAC GTGGCGCAC GTGGCGCAC GTGCGCCAC GTGCGCCAC GCCCATTTG GTGCGCCAC GTGCGCCAC GTGCGCCAC GTGCGCCAC GTGCGCCAC GTGCGCCAC GCCCATTTC	CAGGAGETICE GCTGCAAACE CTGCACCGTG TGTGGACCCC CACCTGGATG GGTGCGGGG GGTCTGGCCT GCTGCCGGGT CACCTGCAGA AGCTGTCAGT CACTCCCAGC GCTCCCAGC GCTCCCAGC GCTCCCAGC GCTCTGAGAAAGTG GTTCTGAACG ACGCGCACGTCCA ACGCGTCCA	GTGGAGGC AGAAGGCCA TGGTCAGAG GACACAGC GCCACACGC GCCACATCTGGG GCCAGATCCT CCACCTTGTC CCTTCTAGA TCTTCACAC GCTGAAGGC TCCTGCTCCG TGCTGGCTC TCCCAGGAGGC CCCAGGAGCC CCCAGGAGC CCCAGGAGC CCCAGGAGC CCCAGGAGC TGTGATTGCT TGATTGTTC TGATTGTT TGATTGTT TGATTGT TGATTT TGATTGT TGATTGT TGATTGT TGATTT TGATTT TGATTGT TGATTT TGATTT TGATTT TGATTT TGATTT TGATTT TGATTT TGAT	GCTGGGCATA CAGTGTTCCC GAGCCACTGG CAGCCCACTGG CAGCGCACTGG CAGGGGCCT CTGGCCGCTG AGGCCATCAG CGGGACCAC GTCAAAAGGA CTGGGACCCG TGGGACCGC CAGGGGGTTGGGACCGCCCC CCCCGGCCTG CGCCCCCCCCCC	TTCTGAGATT TCCATGGAC GCAGCCOGTG CTAGGCCTGG CGGCCCCTGA ACTGCTGACG ACTGCTGACG ACAGGTGA AGAGATTTG TGGGAAGAAC AGTCCACC GAGCTGCCCC GAGCGCAGC GAGCTGCCCC CAGCTGCACC CAGCTGCCC CAGCTGCCC CAGCTGCCC CAGCTGTCCACC CAGCTGTCCC CAGCTGTCC	120 180 240 300 360 420 480 540 660 720 780 840 900 1020
50 55	CCAGGOTGGG GGCATCAGC CTANAGACAG ATGGTCCCAC ACACCTGCAG CAGAGGAGGA GCATGGGGTC TGCCACCCGA GGTGCTTCTT AGCATGCAGA TCCACAGTGT CGGAAGACGC CACCCAGGAG AGGCCCAAGA TGCGCCGCAT TCTTTGTCCC CACTCTCCGCA ATGGCCGCGCT TCTTTGTCCC CACTCTCCCA	CCCCGGGGGT CCCCATTICT TGCCAAGTGC GCAGGAGCGC AGCCTGGGAC AGAGGAGGAG TGAGGAGTTG CCTGCTTT GCTGCTTGCTT GCTGCTTGCTA AGACGAGAGAG GCCCTGTG AGACGTCAG GCCCTGTG AGACGTCAG GCAGGAGAGA GTGCGCCCAC AGCCCCCCTG AGACGCCAGAGAGA AGCCCCCGTG AGAGGAGGAG AGCCCCCGTG AGAGGAGGAG AGAGGAGGAGAGAGAGAGAGAGAGA	CAGGAGETICE GCTGCANACE GCTGCACCCC GCTGGATCC CACGTGGATC GGCCCGGGG GGTCTGGCCT GCTGCCGGCT GCCTGCAGA AGCTGTCAGT CACTTCCAGC GCCCCTCCG TCTGAAAGTG GTTCTTGAGC TCGACCCGGG CGAGCCGGG CAGAGTGCACC CAGAGTGCACCCCCC CAGAGTGGGC CAGAGTGGGC CAGAGTGGGC CAGAGTGGGC CAGAGTGGGC CAGAGTGGAC CCGCACCCCG CAGAGTGGGC CAGAGTGGAC CCGCACCCCG CAGAGTGGAC CAGAGTGCAC CAGAGTGGAC CAGAGTGGAC CAGAGTGGAC CAGAGTGGAC CAGAGTGGAC CAGAGTGGAC CAGAGTGGAC CAGAGTGGAC CAGAGTGCAC CAGAGTGCAC CAGAGTGCAC CAGAGTGCAC CAGAGTGCAC CAGAGTGCAC CAGAGTGCAC CAGAGTGCAC CAGAGTGCAC CAGAGTGCAC CAGAGTGCAC CAGAGTGCAC CAGAGTGCAC CAGAGTGCAC CAGAGTGCAC CAGAGTGCAC CAGAGTGCAC CAGAGTCCAC CAGAGTCCAC CAGAGTGCAC CAGAGTGCAC CAGAGTGCAC CAGAGTGCAC CAGAGTGCAC CAGAGTGCAC CAGAGTGCAC CAGAGTCCA	GTGGCAGGCC AGAAGGGCCA TGGTCAGAGG GACCACAGCC GCTCTCTGGG GGCAGATCCT CCACCTTGTC CCTTCTATGA TCTTCCACAC GCTGGAAGCG TCTGATCCC TCCTGGCCTC TCCCGGCTC CCCAGGAGCC CCCAGGAGCC CCCAGGAGCC TCTGAGTGCT TCCTGCCTC TCCCGCCTC TCCCGCCTC TCCCGCCTC TCCCGCCTC TCCCGCCTC TCCCGCCCC TGCGCACTT TCCCTGCCCC TCCCAGGAGC TCCCAGGAGCC TCCCAGGAGCC TCCCAGGAGCC TCCCAGGAGCC TCCCAGGAGC	GCTGGGCATA CAGTGTTCCC CAGCCACTGG CAGCCACTGG CAGCCAGCTG CAGGGGGCT CTGGCGCGTG AGGCCATCAG CGGGACCAC CTGAAAAGGA CTGGATACCCT AGGAGGGTCCCAG GGACGGCT CAGGGACTGC CAGGGATTGC CAGGGATTGC CCCTGCCTG CCTTCCTAG CCTTCCTAG TCTCTCCTGC	TTCTGAGATT TCCATGGAGT TCCATGGAGC GCAGCCGTG CTASGCCTGG CGGCCCCTGA GCCTTCCCCG ACTGCTGAGG GACAAGGTGA GAGAAGATTG TGGGAAGAAC GAGCTGCCCA AGTCCAGCCG GAGCGCAGC GAGCGCAGC GAGCGCAGC GAGCGCAGC TGTCCATCC CAGCTGTGCC CAGCTGTGCC TTCTGGACTT	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080
50 55 60	CCAGGOTGGG GGCATCAGC CTANAGACAG ATGGTCCCAC ACACCTGCAG CAGAGGAGGA GCATGGGTTC TGCACCCGA GGTGCTTCTT AGCATGCAG CCACAGTGT CCGAAGAGAG CCACCAGGAG AGGCCCAGAG TCTGCAGCGGCT TCTTTGTGCC CCATTGCAG ATGCCCGCT TGTTTGTGCC TGTTTTTGGGC	COCCAGGGGT COCCATTICT TGCCAAGTGC GCAGGAGGGG GCAGGAGGAG AGAGGAGGAG AGAGGAGGAG AGAGGAGAGAG AGAGGAG	CAGGAGETICE CTGCAACCC CTGCACCGTG CTGCACCGTG CTGCACCGGG GGCTGCAGA GGCTGCAGA AGCTGTAGA AGCTGCAGA AGCTGCAGA AGCTGCAGA AGCTGCAGA AGCTGCAGA AGCGTGCAGA AGCGTGCAGA AGCGTGCAGA AGCGTGCAGA AGCGTGCAGA AGCGTGCAGA AGCGTGCAGA AGCGTGCAGA AGCGTGGCA CTGGAAGTGGGC CAGAGTGGGC CAGAGTGGGC CAGAGGGGT	GTEGCAGGCE AGAAGGCCA TGGTCAGAGG GACACAGGC GCCACATCTGGG GCCAGATCCT CCACCTTGTC CCTCTCAGAG GCTGAAGGC TCTTCAGAG TCTTCAGAG TCTTCAGAG TCCTGCTCG TCCTGGAGGC TCCAGGAGGC TCCAGGAGGC TCCAGGAGGC TCCAGGAGGC TCCAGGAGGC TCCAGGAGGC TGGAGGT TCCCTGGCTC TGGGAGCT TCGGCACCTT TCCGGCACCT TCGGCACCT TCGGGACCT TCGGGACCT TCGGCACCT TCGGGACCT TCCGGGCCCATC	GCTGGGCATA CAGTGTTCCC GAGCCACTGG CAGCCCTGTC GGGCCAGCTG CAGGGGCCT CTGGCCCCTG CAGGGGCCT CTGGCACCAC CAGGGACCAC CTCAAAAGGA TCGGACCCG CAGGGACCAC CAGGGACTACA GGACCGCCCC CCCCCGCCCCC CCCTGCCTAG CCCCCCCCCC	TTCTGAGATT TCCATGGAC GCAGCCGGTG CTAGGCCTGG GGCCCCTGA GCCTTCCCCG ACTGCTGACGG GACAAGTGA CCCTGGACGG AGGACATTG TGGGAAGAC AGGACTTG GAGGAGTG CAGGCGCG GAGCGCAGC GAGCGCAGC GAGCGCAGC GAGCTGCCC GAGCTGCCC GCAGGTGCC GAGCCTGACT CAGCCCTGAT CAGCCCTGAT CAGCCCTGAT CAGCCCTGAT	120 180 240 300 360 420 660 660 720 780 840 900 960 1020 1040 1140
50 55	CCAGGOTGGG GGCATCAGC CTAAAGACAG ATGGTCCCAC ACACCTGCAG ACACCTGCAG CAGAGGAGGA GCATGGGCTC TGCCACCAGA TCCACCAGAG TCCACCAGAG TCCACCAGAG TGCGCCACAGAG TCCGCACAGAG TCCGCGCGCT TCTTTGTGCC CACTTGCAG ATGGCCGCGCT TCTTTCTGCAG TTCCCCGACCA	CCCCGGGGGT CCCCATTICT TGCCAAGTGC GCAGGAGCGC AGCCTGGGAC AGAGGAGGAG TGAGGAGTGC CTGCTATGGG GCTGCTGGCT CTGCTATGGG GCAGGAGACT AGACCCTGTG AGAGGTCCAG GCAGGAGACT AGACCCCCGTC AGAGGTCCAG CTGCTGGCCAC CTGCTGGGCCAC AGCCCCCGTC AGAGGAGAC AGCCCCGTC AGGTGGGCGCAC CCCCCGTC CCCCGCCCACGC CCCCCACGC	CAGGAGETEC GCTGCANACC CTGCACCCTG GTGGACCC CACGTGGATG GGCCCCGGG GGCTGCAGA AGCTGCAGA AGCTGCAGA GCCCCTCCG TCTGAAGTG GTTCTGGCT GTGCTGCAGA AGCGTGCAGA AGGACGTGCA CCGAGCCGCG CCGAGAGGAGGA CCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	GTGGCAGGCC AGAAGGGCCA AGAAGGGCCA TGGTCAGAGG GACCACAGCC GCCCTCTGGG GCCAGATCCT CCACCTTGTC CCTCTCAGAG GTGCAGAGGG TCTTCACACA GCTGCACAGGG TCCTGCTCCG TCCTGGCTCC TCCCAGGAGCC CCCCAGGAGCC CCCCAGGAGCC TCTGGTGTCCAT TCCGTGCCT TCCGGCACT TCCGGGCTC TCCGGGCCT TCCGGGCCC TCGGGCCCT TCCGGGCCCT TCCGTGCCAG	GCTGGGCATA CAGTGTTCCC CAGCCCTGTC CAGCCCCTGTC CAGCGGGCCTC CAGCGGGCCTC CAGCGGGCCTC CAGCGGGCCTC CAGCGGGCCTC CAGCACACAC CAGCACACACACACACACACACACACA	TTCTGAGATT TCCATGGAC GCAGCCGGTG CTAGGCCTGA GCCTTCCCCG ACTGCTTGACGG GACAAGGTGA CCCTGGACGG AGACACTTTG TGGGAAGAAC GAGCTGCCCA AGTCCACCCC AGTCCACCCC TGTGCATCG CAGCTGCCCA CTTCCACCCC CAGCTGCCC CAGCTGCCC CAGCTGCCC TCTGGACTGC CAGCCTGCC TCTGGACTGC CAGCCTGCC CAGCTGCCC CAGCTGCCC TCTGGACTGC CAGCCTGACC CAGCCTGCT CAGCCCTGAT CAGCCCTGAT	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080
50 55 60	CCAGGOTGGG GGCATCAGC CTAAAGACAG ATGGTCCCAC ACACCTGCAG ACACCTGCAG CAGAGGAGGA GCATGGGCTC TGCCACCAGA TCCACCAGAG TCCACCAGAG TCCACCAGAG TGCGCCACAGAG TCCGCACAGAG TCCGCGCGCT TCTTTGTGCC CACTTGCAG ATGGCCGCGCT TCTTTCTGCAG TTCCCCGACCA	CCCCGGGGGT CCCCATTICT TGCCAAGTGC GCAGGAGCGC AGCCTGGGAC AGAGGAGGAG TGAGGAGTGC CTGCTATGGG GCTGCTGGCT CTGCTATGGG GCAGGAGACT AGACCCTGTG AGAGGTCCAG GCAGGAGACT AGACCCCCGTC AGAGGTCCAG CTGCTGGCCAC CTGCTGGGCCAC AGCCCCCGTC AGAGGAGAC AGCCCCGTC AGGTGGGCGCAC CCCCCGTC CCCCGCCCACGC CCCCCACGC	CAGGAGETEC GCTGCANACC CTGCACCCTG GTGGACCC CACGTGGATG GGCCCCGGG GGCTGCAGA AGCTGCAGA AGCTGCAGA GCCCCTCCG TCTGAAGTG GTTCTGGCT GTGCTGCAGA AGCGTGCAGA AGGACGTGCA CCGAGCCGCG CCGAGAGGAGGA CCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	GTGGCAGGCC AGAAGGGCCA AGAAGGGCCA TGGTCAGAGG GACCACAGCC GCCCTCTGGG GCCAGATCCT CCACCTTGTC CCTCTCAGAG GTGCAGAGGG TCTTCACACA GCTGCACAGGG TCCTGCTCCG TCCTGGCTCC TCCCAGGAGCC CCCCAGGAGCC CCCCAGGAGCC TCTGGTGTCCAT TCCGTGCCT TCCGGCACT TCCGGGCTC TCCGGGCCT TCCGGGCCC TCGGGCCCT TCCGGGCCCT TCCGTGCCAG	GCTGGGCATA CAGTGTTCCC CAGCCCTGTC CAGCCCCTGTC CAGCGGGCCTC CAGCGGGCCTC CAGCGGGCCTC CAGCGGGCCTC CAGCGGGCCTC CAGCACACAC CAGCACACACACACACACACACACACA	TTCTGAGATT TCCATGGAC GCAGCCGGTG CTAGGCCTGG GGCCCCTGA GCCTTCCCCG ACTGCTGACGG GACAAGTGA CCCTGGACGG AGGACATTG TGGGAAGAC AGGACTTG GAGGAGTG CAGGCGCG GAGCGCAGC GAGCGCAGC GAGCGCAGC GAGCTGCCC GAGCTGCCC GCAGGTGCC GAGCCTGACT CAGCCCTGAT CAGCCCTGAT CAGCCCTGAT CAGCCCTGAT	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080 1140 1260
50 55 60	CCAGGGTGGG GGCATCAGC CTAAAGACAG ATGGTCCCAC ACACCTGCAG ACACCTGCAG CAGAGGAGGA GCATGGGTTCTT AGCATCCCAA ATCCACAGTGT CCGAAGACGC CACCCAGGAG AGGCCCAGAG AGGCCCAGAG ATGCGCCACAGAG TCTTTTGTGCC CCATTTGCAC CCATTTGCAG ATGCCCGACA ATGCCCGACA CTGTACCTGT	CCCCGGGGGT CCCCATTICT TGCCAAGTGC GCAGGAGCGC AGCCTGGGAC AGAGGAGGAG TGAGGAGTCC CTGCTATGGG GTGCTCAGCT CTGCTATGGG GTGGTTCCCC GCAGGAGACT AGACCCCTGTG AGAGGTCCAG GCAGGAGACT AGCCCCTGTG AGAGGTCCAG GCAGGAGAGAC AGCCCCGTC AGGTGGGCA	CAGGAGETEC GCTGCANACC CTGCACCCTG GTGGACCC CACGTGGATG GGCCCCGGG GGCTGCAGA AGCTGCAGA AGCTGCAGA AGCTGCAGA GCTCCAGC GCCCCTCCG TCTGAAGTG GTTCTGGCC CGGACGTGCA CGGACGTGCA CGCACCCGCG CCAGAGTGCA CGCACCCGCG CAGAGTGGA CTGAATAGAA	GTGGCAGGCC AGAAGGGCCA AGAAGGGCCA TGGTCAGAGG GACCACAGCC GCCCTCTGGG GCCAGATCCT CCACCTTGTC CCTCTCAGAG GTGCAGAGGG TCTTCACACA GCTGCACAGGG TCCTGCTCCG TCCTGGCTCC TCCCAGGAGCC CCCCAGGAGCC CCCCAGGAGCC TCTGGTGTCCAT TCCGTGCCT TCCGGCACT TCCGGGCTC TCCGGGCCT TCCGGGCCC TCGGGCCCT TCCGGGCCCT TCCGTGCCAG	GCTGGGCATA CAGTGTTCCC CAGCCCTGTC CAGCCCCTGTC CAGCGGGCCTC CAGCGGGCCTC CAGCGGGCCTC CAGCGGGCCTC CAGCGGGCCTC CAGCACACAC CAGCACACACACACACACACACACACA	TTCTGAGATT TCCATGGAC GCAGCCGGTG CTAGGCCTGA GCCTTCCCCG ACTGCTTGACGG GACAAGGTGA CCCTGGACGG AGACACTTTG TGGGAAGAAC GAGCTGCCCA AGTCCACCCC AGTCCACCCC TGTGCATCG CAGCTGCCCA CTTCCACCCC CAGCTGCCC CAGCTGCCC CAGCTGCCC TCTGGACTGC CAGCCTGCC TCTGGACTGC CAGCCTGCC CAGCTGCCC CAGCTGCCC TCTGGACTGC CAGCCTGACC CAGCCTGCT CAGCCCTGAT CAGCCCTGAT	120 180 240 300 360 420 540 660 720 780 900 960 1020 1140 1200 1260 1320
50 55 60	CCAGGGTGGG GGCATCAGC GTAAAGACAG ATGGTCCCAC ACACCTGCAG CAGAGGAGGA GCATGGGTTC TGCCACCCGA GGTGCTTCTT AGCATGCCAA TCCACAGTGT CGGAAGACGC CACCCAGGAG AGGCCCAAGAG TGCGCGGCT TCTTTGTGCC CATTTCGAG ATGCCGCC TGTTCTGCAG ATGCCCGCC TGTTCTGCAG ATGCCCGCC TGTTCTGCAG ATGCCCGCC TGTTCTGCAG ATGCCCGCC TGTTCTGCAG CTGTTACCTGT CA Seq ID N0:	CCCCGGGGGT CCCCATTICT TGCCAAGTGC GCAGGAGCGC AGCCTGGGAC AGAGGAGGAG TGAGGAGTGC CTGCTATGGG GCTGCTGGCT CTGCTATGGG GCAGGAGACT AGACCCTGTG AGAGGTCCAG GCAGGAGACT AGACCCCCGTC AGAGGTCCAG CTGCTGGCCAC CTGCTGGGCCAC AGCCCCCGTC AGAGGAGAC AGCCCCGTC AGGTGGGCGCAC CCCCCGTC CCCCGTCC CCCCCGCCCACGCC CCCCCACGCCCACCC	CAGGAGETEC GCTGCANACC CTGCACCCTG GTGGACCC CACTGGATG GGCCCGGGG GGTCTGGCCT GCTGCCGGCT GCCCCCCGG GCCCCCCGGG GCCCCCCGG TCTGAAAGT GTTCTTGAGC AGGACGTGC CTGCTGTGTGC CGCAGACGGC CGGAGAGGA CTGCAGAAGAC CTGGAAAGAC CTGGAAAGAC CTGAAAGA	GTGGCAGGCC AGAAGGCCA TGGTCAGAGG GACACAGCC GCTCTCTGGG GGCAGATCCT CCACCTTGTC CCTTCTATGA TCTTCACAC GCTGGAAGCG TCCTGCTCCG TCCTGCTCC TCCCTGCCTC TCCCTGCCTC TCCTGCCTC GGTGTCCATC ATAAAGTGCC	GCTGGGCATA CAGTGTTCCC CAGCCCTGTC CAGCCCCTGTC CAGCGGGCCTC CAGCGGGCCTC CAGCGGGCCTC CAGCGGGCCTC CAGCGGGCCTC CAGCACACAC CAGCACACACACACACACACACACACA	TTCTGAGATT TCCATGGAC GCAGCCGGTG CTAGGCCTGA GCCTTCCCCG ACTGCTTGACGG GACAAGGTGA CCCTGGACGG AGACACTTTG TGGGAAGAAC GAGCTGCCCA AGTCCACCCC AGTCCACCCC TGTGCATCG CAGCTGCCCA CTTCCACCCC CAGCTGCCC CAGCTGCCC CAGCTGCCC TCTGGACTGC CAGCCTGCC TCTGGACTGC CAGCCTGCC CAGCTGCCC CAGCTGCCC TCTGGACTGC CAGCCTGACC CAGCCTGCT CAGCCCTGAT CAGCCCTGAT	120 180 240 300 360 420 540 660 720 780 900 960 1020 1140 1200 1260 1320
50 55 60 65	CCAGGGTGGG GGCATCAGC CTAAAGACAG ATGGTCCCAC ACACCTGCAG CAGAGGAGGA GCATGGGTTCTT AGCATGCCAA ATGCATGCCAA ATGCATGCAA ATGCAGCAGAGAGCCACCAGGAG TGCGCCAGAGAGCCCAGAGA TGCGCCGCATTCTTTGTGCC CCATCTGCAG ATGGCCGCCC TCTTCTGGCC TCTCCCGACCA CTGTACCTGT CA Seq ID No: Nucleic Ac Coding seq	COCCAGGGGT CCCCATTICT TGCCAAGTGC GCAGGAGCGC AGCCTGGGAC AGAGGAGGGA TGAGGAGTCAG GCTGCTATGGG TCTGCTATGGG TCTGCTATGGG TGGTTCCCC GCAGGAGACT AGACCCCTGTG AGAGGTCCAG GCAGGAGACT AGCCCCCGTC AGAGGTCCAG TGGCACCAGGG TTGGATGGCT TGGATGCT 182 DNA Se tid Accessic	CAGGAGETEC GCTGCANACC CTGCACCCTG GTGGACCC CACTGGATG GGCCCCGGG GGCTTGCAGA AGCTTCAGT TCACTCCCAGC GCCCCTCCG TCTGAAGTG GTTCTGAGT CGTACTGGACT CGCACCCGGC AGGACGTGCA CTGGAAGTG CCCACCCGG CCAGAGTGCA CTGGAAGTG CCCACCGGC CAGAGTGGA CTGGAAGAGA CTGGAAGAGA CTGGAAGAGA CTGGAAGAGA CTGGAAGAGA CTGAATAGAA	GTGGCAGGCC AGAAGGGCCA AGAAGGGCCA TGGTCAGAGG GACCACAGC GCTCTCTGGG GCCAGATCCT CCACCTTGTC CCTCTCAGA GCTGGAAGGG TCCTCACAG GCTGGAAGGG TCCTGCTCCG CCCCAGGAGCC CCCCAGGAGCC CCCCAGGAGCC TCCCTGCTCCT CCCAGGAGCC TCCCAGGAGCC TCCCAGGAGCC TCCCAGGAGCC TCCCAGGAGCC TCCCAGGAGCC TCCCAGGAGCC TCCAGGAGCC TCCAGGAGCC TGCGCACCT TCCGCACCT CCGTGCCC TCCGCTGCCT TCCGCCCC TCCTGCT	GCTGGGCATA CAGTGTTCCC GAGCCACTGG CAGCCCTGTC CAGGGGGCCT CTGGCGCCTG CAGGGGACAC CTCAAAAGGA CTCAAAAGGA CTCAAAAGGA CTCAGGACCC TGGGTACCCT AGGACGGGTC CAGGGATGTG GACCGCCGC CCCCCGGCCTG CCTTCCTAG TCTTCCCTAG TTTCCCTGG TTTCCCTGG	TTCTGAGATT TCCATGGAC GCAGCCGGTG CTASGCCTGG GGCCCCTGA GCCTTCCCCG ACTGCTGACGG ACGCCTGACGG AGACACTTG TGGGAAGAC GAGCTGCCCA AGTCCACCCC AGTCCACCCC TTCTCACCC CAGCTGGCC GCCAGGTGCC TTCTGGACTG CAGCCTGTCC CAGCCTGACC TTCTGACTG CAGCCTGACC TTCTGCACTG CAGCCTGACC TTCTGCACTG CAGCCCTGAT CAGCCCTGAT CAGCCCTGAT CAGCCCTGAT CAGCCCTGAT CAGCCCTGAT CAGCCCTGAT AGGTACCCAG	120 180 240 300 360 420 540 660 720 780 900 960 1020 1140 1200 1260 1320
50 55 60 65	CCAGGGTGGG GGCATCAGC CTAAAGACAG ATGGTCCCAC ACACCTGCAG CAGAGGAGGA GCATGGGTTCTT AGCATGCTAG TCCACAGTGT CGGAAGAGGG CACCAGGA TGCGCCAGAG TGCGCCCAGAG TGCGCCCAGAG TCTTTTGTGCC CCATCTGCAG ATGGCCGCCT TCTTTGTGCC TCTTACCTGT CAGAGCACA CTGTACCTGT CA Seq ID NO: Nucleic Ac	COCCAGGGGT CCCCATTICT TGCCAAGTGC GCAGGAGGGC GCAGGAGGAGAGAGAGAGAGAGAGAG	CAGGAGETICE GCTGCANACE CTGCACCOTG TGTGGACCCC CACGTGGATG GGCCCGGG GGCTGCAGA AGCTGTCAGCT TCTGAAGTG GCCCCCTCG TCTGAAGTG CTCCCAGC AGGACGTGCA AGGTGGGCT TCTGAAGTG CTGCAGCTGGA CTGGAGTGGGC TGCAGAGGGC TGGAGAGGG CTGGAATAGAA CTGGATAGAA CTGGATAGAA CTGGATAGAA CTGGATAGAA CTGAATAGAA CTGAATAGAA CTGAATAGAA CTGAATAGAA CTGAATAGAA CTGAATAGAA	GTGGCAGGCC AGAAGGCCA TGGTCAGAGG GACACAGCC GCTCTCTGGG GGCAGATCCT CCACCTTGTC CCTTCTATGA TCTTCACAC GCTGGAAGCG TCCTGCTCCG TCCTGCTCC TCCCTGCCTC TCCCTGCCTC TCCTGCCTC GGTGTCCATC ATAAAGTGCC	GCTGGGCATA CAGTGTTCCC CAGCCCTGTC CAGCCCCTGTC CAGCGGGCCTC CAGCGGGCCTC CAGCGGGCCTC CAGCGGGCCTC CAGCGGGCCTC CAGCACACAC CAGCACACACACACACACACACACACA	TTCTGAGATT TCCATGGAC GCAGCCGGTG CTAGGCCTGA GCCTTCCCCG ACTGCTTGACGG GACAAGGTGA CCCTGGACGG AGACACTTTG TGGGAAGAAC GAGCTGCCCA AGTCCACCCC AGTCCACCCC TGTGCATCG CAGCTGCCCA CTTCCACCCC CAGCTGCCC CAGCTGCCC CAGCTGCCC TCTGGACTGC CAGCCTGCC TCTGGACTGC CAGCCTGCC CAGCTGCCC CAGCTGCCC TCTGGACTGC CAGCCTGACC CAGCCTGCT CAGCCCTGAT CAGCCCTGAT	120 180 240 300 360 420 540 660 720 780 900 960 1020 1140 1200 1260 1320
50 55 60 65 70	CCAGGGTGGG GGCATCAGC CTAAAGACAG ATGGTCCCAC ACACTGGAG CAGAGGAGGA GCATGGGTTC TGCACCCGA GGTGCTTCTT AGCATGCCAA TCCACAGTGT CCGAACACGC CACCCAGGA AGGCCCAGAG AGGCCCAGAG ATGGCCCCACCA TCTTTGTGCC CCATTTTGTGCC CATTTTCGAG ATGGCCGCCA TCTTTTTGCAC TCCCGACCA CTGTACCTGT CA Seq ID NO: Nucleic Ac Coding seq 1	COCCAGGGGT COCCAGTTCT TGCCAAGTGC GCAGGAGCGC AGCCTGGGAC AGAGGAGGGA TGAGGAGTGG GCTGCTGGCT CTGCTATGGG GTGTTCCCC GCAGGAGCT AGACCAGGAGCT AGACCCCTCTG AGAGGTCCAG GCAGGAGCT AGCCCCTCTG AGAGGTCCAG CCAGCCGTC AGCTGCCCAGGG TTGGATGCT 182 DNA Se cid Accessic quence: 174. 11	CAGGAGETICE GCTGCAAACC CTGCACCGGG GGCCCGGGG GGTCTGGCCT GGCCCGGGT GGCCCCCGGG TCTGAAGTG GTCCCAGC AGGACGTGCA CTGCAGAAGTG GTCCTGAAGTG GTCCTGAAGTG GCCACAGA AGATCTGAG CTGAAAGTG CTGAATAGAA CQUENCE J1 J1 J2 J2 J3 J6 AGGGTGTCTC CTGAAAGTC CTGAAAGTG CTGAATAGAA CQUENCE J1 J6 J6 J6 J6 J6 J6 J6 J6 J6 J6 J6 J6 J6	GTGGCAGGCC AGAAGGGCCA AGAAGGGCCA TGGTCAGAGG GACCACAGCC GCTCTCTGGG GGCAGATCCT CCACCTTGTC CCACCTTGTC CCTTCACACA GCTGGAAGGG TCCTTGCTCCCG TGCTGGCCT CCCCAGGAGCC TCCTGGCCCC CCCAGGAGCC TCCTGGCCCC TCCCTGCCCC GGTGTCCACT TCCCTGCCCC GGTGTCCATC TCCCTGCCCC GGTGTCCATC ATAAAGTGGG 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GCTGGGCATA CAGTGTTCCC CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCAGCTG CAGCGGCCT CTGGGCGCTG CAGCGGCCC CTGGGCACTACA CGGGACCAC CTGAAAAGGACCA CTCAAAAGGACCA CCCCCCCCCC	TTCTGAGATT TCCATGGAC GCAGCCGGTG CTASGCCTGG GGCCCCTGA GCCTTCCCCG ACTGCTGACGG ACGCCTGACGG AGACAGTGA CCCTGGACAG AGACATTG CAGCCAGC AGTCCACCC AGTCCACCC CAGCTGCCC CAGCTGCCC TCTCGACTG CAGCCCTGAT CAGCCCTGAT CAGCCCTGAT AGGTACCCAG 51	120 180 240 300 420 480 540 660 720 780 840 900 960 1020 1020 1140 1200 1320 1322
50 55 60 65	CCAGGGTGGG GGCATCAGC CTAAAGACAG ATGGTCCCAC ACACTGCAG CAGAGGAGGA GCATGGGTTC AGCATGCAT AGCATGCAG CCACAGTGT CGGAAGAGGC CACCAGGAG TGGGCCCAGAG TGGGCCCAGAG TGGGCCCAGAG TGGGCCCAGAG TCTTTTTTTTTT	COCCOGGGGT CCCCCATTICT TGCCAAGTGC GCAGGAGGGG GCAGGAGGAGAGAGAGAGAGAGAGAG	CAGGAGETICE GCTGCAAACC CTGCACCGTG TGTGGACCCC CACGTGGATG GGCCCGGG GGCTGCAGA AGCTGCAGA AGCTGCAGA TCTGAAAGT GTTCTGAGC TCTGAAAGT GCCACCCGGG CAGAGCTGGA TCTGAAAGT CCAGAGAGCTGGA TGGAGAAGA CTGAATAGAA CQUENCE IN 8: NM_022 .1016 21	GTGGCAGGCC AGAAGGGCCA TGGTCAGAGG GACCACAGGC GCTCTCTGGG GGCAGATCCT CCACCTTGTC CCTCTCTAGAG CTGGAAGGC TCTGCTCGG TGCTGGGCT TCCCAGGAGGC CCCAGGAGGC CCCAGGAGGC CCCAGGAGGC TGCTGCTCG TGCTGGCAGGT TGCTGGCAGGT TGCTGGCAGGT TGCTGGCAGGT TGCTGGCAGGT TGCTGGCAGGT TGCTGGCAGGGCC TGGGCAGGGCC TGGCAGGCC GGCAGGCC TGGCAGGCC TGGCAGCC TGGCAGGCC TGGCAGGCC TGGCAGGCC TGGCAGGCC TGGCAGGCC TGGCAGGCC TGGCAGCC TGGCAGGCC TGGCAGGCC TGGCAGGCC TGGCAGGCC TGGCAGGCC TGGCAGGCC TGGCAGGCC TGGCA	GCTGGGCATA CAGGGTCTCC GAGCCACTGG CAGCCCTGTC CAGGGGCCAGCTG CAGGGGCCACCACCACCACCACCACCACCACCACCACCAC	TTCTGAGATT TCCATGGGAC GCAGCCGGTG CTAGGCCTGG GCGCCCCTGA GCCTTCCCCG ACTICTCACGG GACAAGTGA CCCTGGACGG GAGAGACATTG TGGGAAGAC GAGCTGCCCG GAGCGCAGC GAGCGCAGC GAGCGCAGC GAGCGCAGC GAGCGCAGC GAGCGCAGC GAGCGCAGC GAGCGCAGC GAGCGCAGC GAGCGCAGC CTCTCGACATG GAGCCCTGAT GATGGCTTAA AGGTACCCAG 51	120 180 240 300 360 420 480 540 660 720 840 900 1020 1020 1140 1200 1320 1322
50 55 60 65 70	CCAGGGTGGG GGCATCAGC CTAAAGACAG ATGGTCCCAC ACACCTGCAG CAGAGGAGGA GCATGGGTTCTT AGCATGCCAA ATGCATGCCAA ATGCATGCAA ATGCATGCAA ATGCACCAGGAG TGCGCCAGAGAGCA TGCGCCAGAGAGCA CTATTCTGGG TTCTTTGGGC TCCCCGACCA CTGTACCTGT CA Seq ID No: Nucleic AC Coding seq 1 1 1 1 CCCTGGGATA CCAGGGTGCA CCAGGGTGCA	COCCOGGGGT COCCOGGGGT COCCOGTTTCC TGCCAAGTGC GCAGGAGGGC AGAGGAGGGA AGAGGAGGGA GCTGCTGGGCT CTGCTATGGG GTGGTTCCCC GCAGGAGGTCCAG AGACCTGGGAGACT AGCCCCTGTG AGAGGTCCAG GGCGTGGTGGGC AGCCCCGTC AGGTGGGCT AGCCCCCGTC AGGTGGGCT CTGCTAGGA CCGCCCAGGG TTGGATGCTT 11 ACTCCCCTCCC CCCCGGGGGT CCCCCGGGGGT CCCCCATTCCT	CAGGAGETEC GCTGCANACC CTGCACCCTG GTGGACCCC CACTGGATG GGCCCGGGG GGCTGCAGA AGCTGCAGA AGCTGCAGA GCCCCTCGG TCTGAAGTG GTCCCAGC GCCCCTCGG TCTGAAGTG CTGCAGA AGCTGCAC CTGGACTGCA CTGGACTGCA CTGGACTGCA CTGGACTGCA CTGGACTGCA CTGGACTGCA CTGGACTGCA CTGGACTGCA CTGGACTGCA CTGGACTGCA CTGAATAGAA CQuence on 8: NM_022 .1016 21	GTGGCAGGCC AGAAGGGCCA AGAAGGGCCA TGGTCAGAGG GACCACAGGC GCTCTCTGGG GCCAGATCCT CCACCTTGTC CCTCTCATGA CTCTCAGAG CTCTCAGAG CTCTCAGAG CTCTCAGAGGC TCCTGCTCCG CCCAGGAGGC CCCAGGAGGC CCCAGGAGGC TCCGCTCCT TCCTGCTCCG TCCGAGAGGC TCAGAGGCC TCAGAGGGC TCAGAGGGC TCAGAGGGC TCAGAGGGC TCAGAGGGC TCAGAGGGC TCAGAGGGC TCAGAGGGCC TCAGAGGGC TCAGAGGGCC TCAGAGGGCC TCAGAGGGCC TCAGAGGGCC TCAGAGGGCC TCAGAGGGCC TCAGAGGGCC TCAGAGGGCC TCAGAGGGCC TCAGAGGGCC TCGTGCAGGGCC TCGTGCTAGAGGCC TCGTGCAGGGCC TCGTGCAGGGCC TCGTGCAGGGCC TCGTGCAGGGCC TCGTCAGAGGCC CGTCAGAGC TCGTCAGAGGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC TCGTCAGAGCC	GCTGGGCATA CAGTGTTCCC CAGGGGCCACCTGG CAGCCCGCTG CAGGGGCCACCC CAGGGGCCACCC CAGGGGCCACCC CAGGGGCCACCC CAGGGACCAC CAGGGACCAC CAGGACCAC CAGGACCAC CAGGACCAC CAGGACCAC CCCCCGGCCTG CCTCTCCCTGC CCTCTCCTAC CAGGACTGAC CAGCACTCAC CAGGACTGAC CAGGACTGAC CAGGACTGAC CAGGCCTCCCCCCCCCC	TTCTGAGATT TCCATGGAC GCAGCCGTG CTAGGCCTGA GCCTTCCCCG ACTICTTCACCG GACACCTGACGG GACAAGTGA CCCTGGACGG GAGAGACATTG TGGGAAGAC GAGCTGCCCA GAGCCGCCC GCAGGTGCC TTCTGACTG CAGCCCTGACCG CAGCCTGCC GCAGGTGCC TTCTGACTG CAGCCCTGAT CATCCCTGACCA 51 CCTGCTGTCC TTCTGAGATT TCCATGGATT TCCATGGATT TCCATGGATT TCCATGGATT	120 180 240 300 420 480 540 660 720 780 840 900 960 1020 1020 1140 1200 1320 1322
50 55 60 65 70	CCAGGGTGGG GGCATCAGC CTAAAGACAG ATGGTCCCAC ACACTGCAG ACACTGCAG GCATGGGTT GGCACCCGA GGTGCTTCTT AGCATGCTGC CCACAGGGT TCCTACAGGTGT CGGAAGAGGC CACCAGGAG AGGCCCAGAG AGGCCCAGAG ATGGCCGCC TCTTTGTGCC CCATCTGCAG ATGGCCGCC TCTTACCTGT CA Seq ID NO: Nucleic Ac Coding seq 1 CCCTGGGATA CCAGGGTGGG GGCATCAGC CTAAAGACAG CTAAAGACAG CTAAAGACAG ATGGTCCCAC	COCCOGGGGT CCCCATTICT TGCCAAGTGC GCAGGAGGGC GCAGGAGGAGGAG AGAGGAGGAG AGAGGAGGAG CTGCTATGGG GTGCTGGGT CTGCTATGGG GCAGGAGAGAC AGCCCCTGTG AGAGGAGAGAC AGCCCCGTGC AGCCCCAGGG TTGGATGGCT CTGCTAGGA CCGCCCAGGG TTGGATGGCT 182 DNA Se cid Accessic quence: 174. 11 1 A CTCCCCTCCC CCCCCTCC CCCCATTCC CCCCCCC CCCCATTCC CCCCCCC CCCCC CCCCC CCCCC CCCCC CCCC CCCC	CAGGAGETICE GCTGCAAACC CTGCACCGTG TGTGGACCCC GCTCGCACGGG GGTCTGGCT GCTGCAGGA AGCTGTCAGCT CACTTCGAG TCTGAAAGTG CTCCAGC AGGACTGCAC TCGAAAGTG CTGCAGAAGA CTGAATAGAA CTGAACTCCC CTGCAACCGC CTGCAACCC CTGCACCGTC CTGCACCGTC CTGCACCGTC CTGCACCGTC CTGCACCGTC CTGCACCGTC CTGCACCGTC CTGCACCGTC CTGCACCGTC CTGCACCGTC CTGCACCGTC CTGCACCGTC CTGCACCGTC CTGCACCGTC CTGCACCGTC CTGCACCGTC CTGCACCGTC CTGTGCACCGTC CTGCACCGTC TGCACCGTC CTGCACCGTC CTGCACCGTC CTGCACCTC CTGCA	GTGGCAGGCC AGAAGGCCAA TGGTCAGAGG GACCACAGGC GCTCTCTGGG GGCAGATCCT CCACCTTGTC CCTCTCTAGAG TCTTCCACAC GCTGGAAGGC TCCTGCTCG TGCTGGGCAGCT TCCCAGGAGGC CCCAGGAGCC CCCAGGAGCC TGGCAGGCT TGCCTGCTCG TGCTGGCACCT TGCCAGGAGCC TGGCACCTT TCCCAGGAGCC TGGCACCTT TCCCAGGAGCC TGGCACCTT TCCCTGCCCC TGGCACCTT TCCCTGCCCC TGGCACCTT TCCCTGCCCC TGGCACCTT TCCCTGCCCC TGGCACCTT TCCCTGCCCC TGGCACCTT TCCCTGCCCC TGGCACCTT TCCCTGCCCC TGGCACCTT TCCCTGCCCC TGGCACCTT TCCCTGCCCC TGGCACCTT TCCCTGCCCC TGGCACCT TCCCTGCCCC TGGCACGCC TGGTCAGGCC TGGCACGCC TGGTCAGAGCCC TGGTCAGAGCCC TGGTCAGAGCCC TGGTCAGAGCCC TGGTCAGAGCCC TGGTCAGAGCCC TGGTCAGAGCCC TGGTCAGAGCCC TGGTCAGAGCCC TGGCCAGGCC TGGTCAGAGCCC TGGTCAGAGCCC TGGTCAGAGCCC TGGTCAGAGCCC TGGCCAGGCC TGGTCAGAGCC TGGTCAGAGCCC TGGTCAGAGCCC TGGTCAGAGCCC TGGTCAGAGCCC TGGTCAGAGCC TGGTCAGAGCCC TGGTCAGAGCCC TGGTCAGAGCCC TGGTCAGAGCCC TGGTCAGAGCC TGGTCAGAGCCC TGGTCAGAGCCC TGGTCAGAGCCC TGGTCAGAGCCC TGGTCAGAGCC TGGTCAGAGCCC TGGTCAGAGCCC TGGTCAGAGCCC TGGTCAGAGCCC TGGTCAGAGCC TGGTCAGAGCC TGGTCAGAGCC TGGTCAGAGCC TGGTCAGAGCC TGGTCAGAGCC TGGCAGAGCC TGGTCAGAGCC GGTCAGAGCC TGGTCAGAGCC TGGTCAGAGCC TGGTCAGAGCC TGGTCAGAGC TGGTCAGAGCC TGGTCAGAGCC TGGTCAGAGCC TGGTCAGAGC TGGTCAGAGC TGGTCAGAGC TGGTCAGAGC TGGTCAGAGC TGGTCAGAGC TGGTCAGAGC TGGTCAGAGC TGCC TGGTCAGAGC TGGTCAGAGC TGGTCAGAGC TGGTCAGAGC TGGTCAGAGC TGGTCAGAGC TGCTCAGAGC TGCTCAGAGC TGCC TGC	GCTGGGCATA CAGGCTCTCC CAGGCACCCCTGC CAGGCACCACCCCCCCCCC	TTCTGAGATT TCCATGGAC GCAGCCGGTG CTAGGCCTGG GCGCCCCTGA GCCTTCCCCG ACTICTCACGG GACAGCTGGACGG GACAGCTGCCG GAGAGACACTTG GAGAGACACTTGGGAAGAC GAGCTGCCCG GAGCGCAGC GTGTCCATCG GCAGCTGCC GCAGGTGCC TTCTGAGCTG ATGGCTTAA AGGTACCCAG 51 CCCTGCTGTCC TTCTGAGATT CTCCATGGC TTCTGAGCTG TTCTGAGCCCGGC TCTTAGCCCTGG TTTTGAGCCCTG	120 180 240 300 360 420 480 540 660 720 1020 1020 1140 1200 1320 1322
50 55 60 65 70	CCAGGGTGGG GGCATCAGC CTAAAGACAG ATGGTCCCAC ACACCTGCAG CAGAGGAGGA GCATGGGTTCTT AGCATCCCAA ATGCATCCCAA ATGCATCCCAA ATGCATCCAA ATGCATCCAA ATGCATCCAA ATGCATCCAA ATGCATCCAA ATGCATCCAA ATGCATCAA ATGCATCAA ATGCATCAA ATGCATCAA ATGCATCAA CACATGTT CCAAAGACAC CTATACTGTC CA Seq ID No: Nucleic AC COding seq 1	COCCOGGGGT COCCOGGGGT TGCCAAGTGC GCAGGAGGGC AGAGGAGGGA AGAGGAGGGA AGAGGAGGGA TGAGGAGTTCCC GCAGGAGGTCCC GCAGGAGGTCCAGGCT AGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CAGGAGCTCC GCTGCAACCC CACGTGGATCC CACGTGGATCC CACGTGGATCC CACGTGGATC GGCCCCGGG GGCCTGCAGA AGCTGCAGA AGCTGCAGA AGCTGCAGA AGCTGCAGC CCACGTGGATC CTGCAGAAGTG CCACGCGGC CAGAAGTGGGC CAGAAGTGGGC CAGAAGTGGGC CAGAGTGGAC CTGGAAGTG	GTGGCAGGCC AGAAGGGCCA TGGTCAGAGG GACCACAGGC GCTCTCTGGG GCCAGATCCT CCACCTTGTC CCTCTCAGAG TCTTCAGAG TCTTCAGAG TCTGCAGAGG TCCTGCTCCG CCCAGGAGGC CCCCAGGAGGC CCCCAGGAGGC TCCTGCTCCG CCCAGGAGGC TCCTGCTCCG CCCAGGAGGC TCCTGCTGCT CCAGAGGGC TCCTGCTGCT CTGAGTGGC TGCGCACCTT TCCTGCCCC GGTGTCCAT ATAAAGTGGG AGAAGGGCCC AGAAGGGCCC TGCTAGAGG TCTGCTAGAGG TCTGCTAGAGG TCTGCTAGAGG TCTGCTAGAGGGC TGTGCAGGCC TGGTGCAGGCC GGTGCAGGCC TGGTGCAGGCC TGGTGCAGGCC TGGTGCAGGCC TGGTGCAGGCC TGGTGCAGGCC TGGTGCAGGCC TGGTGCAGGCC TGGTGCAGGCC TGGTGCAGGCC TGGTGCAGCC TGGTGCAGCC TGGTGCAGGCC TGGTGCAGGCC TGGTGCAGGCC TGGTGCAGGCC TGGTGCAGGCC TGGTGCAGGCC TGGTGCAGGCC TGGTGCAGGCC TGGTGCAGGCC TGGTGCAGGCC TGGTGCAGGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGTGCAGCC TGGTGCAGGCC TGGTGCAGGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGTGGCAGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGTGGGCAGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGCAGGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGTGGGCAGCC TGGTGGCAGGCC TGGTGGCAGGCC TGGGCAGGCC TGGGCAGGCC TGGGCAGCC TGGGCAGGCC TGGGCAGGCC TGGGCAGGCC TGGGCAGGCC TGGGCAGGCC TGGGCAGGCC TGGCAGGCC TG	GCTGGGCATA CAGTGTTCCC GAGCCACTGG GAGCCACTGG GAGCCACTGG GAGCCACTGG GAGCCACTGG CAGGGGGCCT CTGGCGCGCTG GGGCACGAC CTGAAAAGGA CTGGAACCG CCCCCGCCTG CCTGTCCTAG CCTGCTCCTAG TCTCTCCTAG TCTCTCCTAG TTTCCCTGG TTTCCCTGG TTTCCCTGG TTTCCCTGG TTTCCCTGG TTTCCCTGG TTTCCCTGG TTTCCCTGG TTTCCCTGG TTTCCCTGG TTTCCCTGG TTTCCCTGG TTTCCCTGG TTTCCCTGG TTTCCCTGG CCGCCCTTTC CAGCCATTCC CAGCCATTCC CAGCCACTCC CAGCCCCTGT CCGCCCCTGT CCGCCCCTGT CCGCCCCCTGT CCGCCCCTGT CCCCCCCTGT CCCCCCCC	TTCTGAGATT TCCATGGAC GCAGCCGGG CCTGAGCGGGCCCTGA GCCTTCCCCG ACTICTCAGGG GCACAGGTGA CCCTGGACGG AGACACTTG GAGCAGGC AGACACTTG GAGCAGCC GAGCAGCCAG GTGCCAGCG CAGCTGCCC CCCGCTGACGG AGACACTT CCACCGC CAGCTGCC CAGCTGCC CAGCTGCC CAGCTGCC CAGCTGCC CAGCTGCC CAGCTGCC CAGCTGCC CAGCTGCC CAGCCCTGAT CAGCCCTGAT TCCATGGGAC TTCTGAGATT TCCATGGGAC GCAGCCGGG CTTAGGGAC GCAGCCGGG CTAGGCCTGG CCTAGGCCTGG CCTGCTGCC CTCGCGCTGC CCCGCCCGGC CCCGCCCG	120 180 240 300 360 420 480 540 660 720 780 840 1020 1140 1260 1320 1322
50 55 60 65 70	CCAGGGTGGG GGCATCAGC CTAAAGACAG ATGGTCCCAC ACACTGGAG CAGAGGAGGA GCATGGGTTC TGCACCCGA GGTGCTTCTT AGCATGCCAAA TCCACAGTGT CCGAACACGC CACCCAGAG AGGCCCAGAG ATGGCCCAAA ATGGCCCACA CTGTACCTGT CA Seq ID NO: Nucleic Ac Coding seq 1	CCCCGGGGGT CCCCCATTICT TGCCAAGTGC GCAGGAGCGC AGCCTGGGAC AGAGGAGGAG AGAGGAGGAG TGAGGAGTTG GCTGCTGCT GCTGCTTTG GCTGCTTTG AGAGGAGACT AGCCCCTCTG AGAGGTCCAG GCAGGAGACT AGCCCCTGTG AGAGGTCCAG AGCCCCGTG AGCCCCATTCC TTGGATGCT TTGCATGCT 11	CAGGAGETICE GCTGCAAACC CTGCACCGGG GGCCCGGGG GGTCTGGCT GGCGCCGGG GGCCCCGGG GGCCCCGGG GGCCCCCGG GGCCCCCGG GGCCCCCGG GGCCCCCGG GGCCTCCAGA AGCTTCAGC GCCCCCTCG GTCTGAAGTG GTTCTTGAG GCAGAGCTGCA CTGAATAGAA CQUENCE TGGAAAGCA TGGAAAGCA TGGAAAGCA TGGAAAGCA TGGAAAGCA TGGAAAGCA TGGAAAGCA TGGAAAGCA TGGAAAGCA TGGAAAGCA TGGAACGCCC TGGAACCCCCC CTGATGAACCC CTGATGAACCA CTGATGAACCA CTGAATAGAA CQUENCE TGGAACCCC CTGACCGCCC CTGCACCCCC CTGCACCCGTC CTGCACCCGTC CTGCACCGTC CTGCACCGTGCAAACC CTGCACCCGTC CTGCACCGTC CTGCACCGTC CTGCACCGTC CTGCACCGTGCAAACC CTGCACCGTC CTGCACCGTGCAACC CTGCACCGTGCAACC CTGCACCGTGCAACC CTGCACCGTGCAACC CTGCACCGTGCAACC CTGCACCGTGCAACC CTGCACCGTGCAACC CTGCACCGTGCACC CTGCACCGTGCACC CTGCACCGTGCACC CGCGCCGGCCGCC	GTEGCAGGCE AGAAGGCCA TGGTCAGAG GACCACAGCC GCTCTCTGGG GCCAGATCCT CCACCTTGTC CCTCTCTAGAA TCTTCCACAC GCTGGAGCG TCCTGCTGGGCT TCCCCAGAGCG CCCAGGAGCC CCACAGGAGCC CCACAGGAGCC CCACAGGAGCC GGTGTCCATC ATAAAGTGGCT ATAAAGTGGG CTGGCTGCT ATAAAGTGGG CTGGCAGGCC CTGGCTGCT ATAAAGTGGG CTGGCAGGCC CTGGTCCATC GGCCTTGCT CTGGCAGGCC CTGGTCCATC GGCCTTGCT CTGGCAGGCC CTGGTCCATC GGCCTTGCT CTGGCAGGCC CTGGTCCATC GGCCTTGCT CTGGCAGGCC CTGGTCCATC CGGCCTTGCT CTGGCAGGCC CTGGTCAAGC CCACCTTGCT CTGGCAGGCC CTGGTCCAGGC CTGGTCCAGC CGGCCTTGCT CTGGCAGGCC CGCCTTGCT CGGCCAGGCC CGCCTTGCT CGGCCAGGCC CGCCTTGCT CGGCCACCTGCT CGGCCACGCC CGCCCTGCT CGCCCC CGCCCTGCT CGCCCC CGCCCC CGCCCCC CGCCCC CGCCCC CGCCCCC CGCCCC CGCCCCC CGCCCCC CGCCCCC CGCCCCCC	GCTGGGCATA CAGTGTTCCC GAGCCACTGG CAGCCACTGG CAGCCAGCTG CAGCGGCCT CTGGGCGCTG CAGCGGCCT CTGGGCACTGC CAGCGACTAC CAGCACTAC CAGCACTAC CAGCACTAC CAGCACTAC CAGCACTAC CAGCACTGCC CAGCACTGCC CAGCACTGCC CAGCACTGCC CAGCACTGCC CAGCACTGCC CAGCACTGCC CAGCACTGCC CAGCACTGCC CAGCACTGCC CAGCACTGCC CAGCACTGCC CAGCCACTGCC CAGCCCTGCC CAGCCCTGCC CAGCCCTGCC CAGCCCTGCC CAGCCCTAC CAGCCCTAC CAGCCCACTCC CAGCCCACTCC CAGCCCACTCC CAGCCCACTCC CAGCCCACTCC CAGCCCACTCC CAGCCCACCC CAGCCCACCC CAGCCCACCC CAGCCCACCC CAGCCCCACCC GCCCCACCC CAGCCCCCC CAGCCCCCC CAGCCCCACCC CAGCCCCACCC CAGCCCCCC CAGCCCCCC CAGCCCCCC CAGCCCCCC CAGCCCCCC CAGCCCCCC CAGCCCCCC CAGCCCCCC CAGCCCCCC CAGCCCCCC CAGCCCCCC CAGCCCCCC CAGCCCCCCC CAGCCCCCCC CAGCCCCCCC CAGCCCCCCC CAGCCCCCCC CAGCCCCCCC CAGCCCCCCC CAGCCCCCCC CAGCCCCCCCC	TTCTGAGATT TCCATGGAC GCAGCCGGTG CTASGCCTGG GGCCCCTGA GCCTTCCCCG ACTGCTGACGG ACGCCTTGACGG AGACATTG CGGAACAAC GAGCTGCCCA AGTCCACCC AGTCCACCC AGTCCACCC AGTCCACCC AGTCCACCC AGTCCACCC CCAGCGTGCC TCTGGACTG CCAGCTGTCC TCTGGACTG CCAGCTGTCC TTCTGGACTG CAGCCCTGAT CAGCCCTGAT 51 CCTGCTGTCC TTCTGAGTTC CTTCGAGTGC CTTCTGAGTGC CTTCTGGCCTTGG CCGCCCCTGA CCGCCCCTGA CCGCCCCTGG CCGCCCCTGA CCGCCCCTGA CCGCCCCTGA CCGCCCCTGA CCGCCCCCTGA CCGCCCCTCTA	120 180 240 300 360 420 480 540 660 720 1020 1020 1140 1200 1320 1322
50 55 60 65 70	CCAGGGTGGG GGCATCAGC CTAAAGACAG ATGGTCCCAC ACACCTGCAG CAGAGGAGGA GCATGGGTTCTT AGCATCCCAA ATGGTCCCAA ATGCATCCAAA ATGCATCCAAA ATGCATCCAAA ATGCATCCAAA ATGCATCCAAA ATGCACCAAGAG TCCGAAGAGCC CCATCTGCAG ATGCGCGCCT TCTTTGTGCC CAATTGCAC CCATCTGCAG ATGCCCGACCA CTGTACCTGT CA Seq ID NO: Nucleic AC CCATGGGATA CCAGGGTGGG GGCCATCAGC ATGGTCCCAA ATGGTCCCAA ATGGTCCCAA ATGGTCCCAA ATGGTCCCAA ATGGTCCCAA ATGGTCCCAA ATGGTCCCAC CTAAAGACAC ATGGTCCCAC CAGAGGAGGG GCATGGGC CAGAGGAGGG GCATGGGC CAGAGGAGGG GCATGGGC CAGAGGAGGG GCATGGGC CAGAGGAGGG GCATGGGC CAGAGGAGGG GCATGGGC CAGAGGAGGG GCATGGGC CAGAGGAGGG GCATGGGC CAGAGGAGGG GCATGGGC CAGACCCCG CTCACCCCCT ACCCTCCACCCCC ATGGCCACCCCC ATGGCCACCCCC ATGGCCACCCCC ATGGCCACCCCC ATGGCCACCCCC ATGGCCACCCCC ATGGCCACCCCC ATGGCCACCCCC ATGGCCACCCCC ATGCCCCCCC ATGGCCACCCCC ATGGCCACCCCC ATGGCCACCCCC ATGGCCACCCCC ATGGCCACCCCC ATGGCCACCCCCC ATGGCCACCCCC ATGGCCACCCCC ATGGCCACCCCC ATGGCCCACCCCC ATGGCCACCCCC ATGGCCACCCCC ATGGCCACCCCC ATGGCCACCCCC ATGGCCACCCCC ATGGCCACCCCC ATGGCCACCCCC ATGGCCACCCCC ATGCCCCCCCC ATGCCCACCCCCCCCCC	COCCOGGGGT COCCOGGGGT TGCCAAGTGC GCAGGAGCGC AGAGGAGGGA AGAGGAGGAG GTGAGGAGTTCCC GCAGGAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	CAGGAGETEC GCTGCANACC CTGCACCCTG GTGGACCC CACGTGGATG GGCCCCGGG GGCTGCAGA AGCTGCAGA AGCTGCAGA GCCCCTCGG TCGGAGT CACTCCCAGC GCCCCTCGG TCGAAGTG CGCACCGGG CCAGATGGGC CAGGAGTGGA CTGAATAGA GUENCE AGGGTGTCT CAGGAGTGCA CTGAATAGA CTGAATAGAA CTGAATAGAA CTGAATAGAA CTGAATGGG CCCCCCC CCCCCCGG CCCCCCCC CCCCCCCCC	GTGGCAGGCC AGAAGGGCCA TGGTCAGAGG GACCACAGGC GCTCTCTGGG GCCAGATCCT CCACCTTGTC CCTCTCAGAG TCTTCAGAG TCTTCAGAG TCTGCAGAG CCCAGGAGGC TCCTGGCAGGC CCCAGGAGGC CCCAGGAGGC TCCTGGCAGGC TCCTGGCAGGC TCCTGGCAGGC TCCTGGCAGGC TCCTGGCAGGC TCCTGGCAGGC TCGGAAGGGC TCGGAAGGGC TCGGAAGGGC TCGGAGGGC TCGGAGGGC TCGGAGGGC TCGGAGGGC TCGGAGGGC TCGGAGGGC TCGGAGGGC TCGGAAGGGCC TCGGAGGGC TCGGAGGGC TCGGAGGGC TCGGAGGGC TGGGAGGGC TGGGCAGGCC TGGGCAGCC TGGGCAGGCC TGGGCAGGCC TGGGCAGGCC TGGGCAGGCC TGGGCAGGCC TGGGCAGGCC TGGGCAGGCC TGGGCAGGCC TGGGCAGGCC TGGGCAGGCC TGGGCAGGCC TGGGCAGGCC TGGGCAGGCC TGGGCAGGCC TGGGCAGGCC TGGGCAGGCC TGGGCAGGCC TGG	GCTGGGCATA CAGTGTTCCC GAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGC CAGCGGGCCT CTGGCCACTGC CAGCGGGCCACTGC CAGCGGACACC TGGACCACC TGGGACCAC TGGACCACC TGGGACCAC TGGGACCAC TGGGACCAC TGGGACCAC TGGGACCAC TGGCACTGC CCCCCCCCC CCCCCCCC CCCCCCCC TGGCTACCC TGGCCTTCC TAGCCTCCTAC TTTCCCTGG TTTTCCCTGG TTTTCCCTGG TTTTCCCTGG CAGCACTTCC CAGCCACTTC CAGCCACTTC CAGCCACTCC CAGCGCCCTC CAGGGGGCCC CAGGGGGCCC CAGGGGGCCC CAGGGGGCCC CAGGGGGCCC CAGGGGGCCC CAGGGGGCCC CAGGGGCCCC CAGGGGGCCC CAGGGGCCCTCC CAGGGGGCCC CAGGGGCCCTCC CAGGGGCCCCC CAGGGGCCCCC CAGGGGCCCCC CAGGGGCCCCC CAGGGGCCCCC CAGGGGCCCCCC CAGGGGCCCCCC CAGGGGCCCCCC CAGGGGCCCCCC CAGGGCCCCCC CAGGGCCCCCC CAGGGCCCCCC CAGGGCCCCCC CAGGGCCCCCC CAGGGCCCCCC CAGGCCCCCCC CAGCCCCCCC CAGCCCCCCCC	TTCTGAGATT TCCATGGAC GCAGCCGGTG CTAGGCCTGA GCCTTCCCCG ACTICTTCACGG GCACACGTG GCCTTCCCCG ACTICTGACGG GACAAGTGA CCCTGGACGG GAGAGACATTG GAGCAGCG GAGCAGCAGC GCAGCTGCCC GCCAGGTGC CTTCTGACTG CAGCCTGAT CAGCCCTGAT CAGCCCTGAT CAGCCCTGAT CAGCCCTGAT CCTTCTCCC TTCTGACTG CCTGCTGTCC TTCTGAGATG CCTGCTGTCC TTCTGAGATG CCTGCTGCC TTCTGAGATG CCTGCTGCC TTCTGAGATG CCTGCTGTCC TTCTGAGATG CCTGCTGTCC TTCTGAGATG CCTGCTGTCC TTCTGAGATG TCCATGGGAC GCAGCCCGGT CCTGCTGCC TTCCCGG CTAGGCCTGG CCTGCTTCCCG CTAGGCCTGG CCTGCTTCCCG CCTGCTGCCG CCGCCCTGA GCCTTCCCGG ACTGCTGCGG CGCCCCTGA GCCTTCCCGG ACTGCTGCGGG CACAGGGTGA	120 180 240 300 420 480 540 600 660 720 780 840 1020 1080 1140 1200 1320 1322
50 55 60 65 70	CCAGGGTGGG GGCATCAGC CTAAAGACAG ATGGTCCCAC ACACTGGAG ATGGTCCCAC ACACTGGAG GCATGGGGTC TGCACCCGA GGTGCTTCTT AGCATGCCAA ACACCAGGAG AGGCCCAGAG AGGCCCAGAG AGGCCCAGAG ATGGCCCAC CCATTTCGAG ATGGCCGACA CTGTACCTGT CA Seq ID NO: Nucleic Ac Coding seq 1	CCCCGGGGGT CCCCCATTICT TGCCAAGTGC GCAGGAGCGC AGCCTGGGAC AGAGGAGGAG AGAGGAGGAG TGAGGAGTTG GCTGCTGCT GCTGCTTTG AGAGGAGCT AGCCCTCTG AGAGGTCCAG GCAGGAGCT AGCCCCTGT AGAGGTCCAG AGCCCCGTG AGCCCCCTG AGTGGCCCAC AGCCCCGTG AGCCCCAGGG TTGGATGCT 182 DNA Se sid Accessic quence: 174. 11	CAGGAGETICE GCTGCAAACC CTGCACCGGG GGCCCGGGG GGCCCGGGG GGCCCGGGG GGCCCCCGGG GGCCCCCGGG TCTGAAGTG GTCTCTGAAGTG GTCTCTGAAGTG GCCCCCTCG CTGAAAGTG GTCTCTGAAGTG CGCACCGGG CAGATCAGA CTGATTAGAC CTGATTGAGC CAGAGCGTGCA CTGATTGAGC CTGATTGAGC CTGATTGAGC CTGATTGAGC CTGATTGAGC CTGATTGAGC CTGATTGAGC CTGATTGAGC CTGATTGAGC CTGATTGAGC CTGATTGAGC CTGATTGAGC CTGATTGAGC CTGATTGAGC CTGATTGAGC CTGATTGAGC CTGATTGAGC CTGATTGAGC CTGATTGAGC CTGACCGTGAAAC CTGACCGTGAAACC CTGACCGTGAAACC CTGACCGTGAAACC CTGACCGTGAACC TGACCGTGACC CTGACCGTGACC CTGACCGTGACC CTGCACGTGACC CTGCACCGTCGACG CGCTCGCCGCG GCTCTGCCGCG CGCTCCCGCGGG GGCCTGCCGCGGG GGCCTGCCGCGGG GGCCTGCCGCGGG GGCCTGCCGCGGG GGCCTGCCGCGCGGG GGCCTGCCGCGGG GGCCTGCCGCGGG GGCCTGCCGCGGG GGCCTGCCGCGGG GGCCTGCCGCGGG GGCCTGCCGCGCGGC GGCCTGCCGCGCGGG GGCCTGCCGCGCGGG GGCCTGCCGCGCGGC GGCCCGCGCGGGG GGCCTGCCGCGCGCG	GTEGCAGGCE AGAAGGCCA TGGTCAGAG GACCACAGCE GCTCTCTGGG GCCAGATCCT CCACCTTGTC CCTCTCTAGAA TCTTCCACAC GCTGGAGCG TCCTCTCGG TCCTGGGCT TCCCAGAGGC CCCAGGAGCC CCACAGAGCC GGTGTCCATC AGAGGCCATGTC ATAAAGTGGC 1161.2 31 31 31 31 31 31 31 31 31 3	GCTGGGCATA CAGTGTTCCC GAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCACTCAC CAGCACTCAC CAGCACTCAC CAGCACTGAC CAGCACTGAC CAGCACTGAC CAGCACTGAC CAGCACTGAC CAGCACTGAC CAGCACTGAC CAGCACTGAC CAGCACTGAC CAGCACTGAC CAGCACTGAC CAGCACTGAC CAGCACTGAC CAGCCACTCAC CAGCCCACTCAC CAGCCCACTCAC CAGCCCACTCAC CAGCCCACTCAC CAGCCCACCAC CAGCCCCACCAC CAGCCCCACCAC CAGCCCCACCAC CAGCCCCCCCC	TTCTGAGATT TCCATGGAC GCAGCCGTG CTGAGCCTGA GCCTTCCCCG ACTICTCACG GCCTTCACGG GCCACTGACGG GCCACGCCGCAC TGGGAAGAC GAGCACTTG GAGAGACATTG GAGCAGCG GAGCCGCG GCCCCTGA 51 CCTGCTGCCG CTTCCACG CTTCCACG CAGCCCTGA 51 CCTGCTGCCG CTTCCACG CTTCCCCG CTCCCCCG CTCCCCTGACG CTCCCCTGACG CTCCCCTGACG CTCCCCTGACG CTCCCCTGACG CTCCCCTGACG CTCCCCTGACG CTCCCCTGACG CTCCCCTGACG CTCCCCTGACG CTCCCCCTGACG CTCCCCCTGACG CTCCCCCTGACG CTCCCCTGACG CTCCCCCTGACG CTCCCCCTGACG CTCCCCCTGACG CTCCCCCTGACG CTCCCCCTGACG CTCCCCCTGACG CTCCCCCCTGACG CTCCCCCTGACG CTCCCCCTGACG CTCCCCCTGACG CTCCCCCTGACG CTCCCCCTGACG CTCCCCCTGACG CTCCCCCCTGACC CTCCCCCCCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 1020 1080 1140 1260 1320 1322

	TCCACAGTGT	GCAGGAGACT	CACTCCCAGC	TGCTGGGCTC	CTGGGACCCG	TGGGAAGAAC	720
	CGGAAGACGC						780
	CACCCAGGAG CGCAGCTGCG						840 900
5	CCATCGTCTT						960
. •	TGTGCCCCAT						1020
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20	AAGCTGCGCA	AGTOCTOCOL	CCTCAAGAAG	CTCAACOGGT	ATTCCGACGG	GCTGCTGAGG	240
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•	GGCCCAGCCC	CTGTTTACTO	GITCITGCA	ATGGGAGCT	AGCAGCCTCT	GGACAGCCAG	2640
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, ,						G GAGGCGGTGG	3240
	TAGAGAGAGA	TAAAAGGTG	G AGTTTCTCT	G TICTITGGT	T CAGGGATTT	TTAATTTTAATT	3300
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75						C CAACTAGCTG	3420 3480
, ,						T AGGGACGGGG C ACCTGCCTTG	3540
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80						G ACAGCATCCC T GGGAACTTGC	3720 3780
50						A GACCCCGAGG	3840
						A GCCCTTCCCT	3900
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	GGTTAAACG	S TGCCCATCC	T GCCATCCTC	A AACGACAGA	G GAGCTTTTC	T GGAATTTCAA	4020

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	ACCATTOCTC TTAGTCCCAA GCTAGGCTTA AACCTGGAAT CTACAAGCCA AAAGTCCCTC	4080
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	TTCCTTGCGC CTCAGCCCTC AGTTCCTTCA TTTCCACCAG GCCGTGCCTT GTTTGAGTTT	4200 4260
5	TTCCTCCCAG TGAGACTGCC CCACGGAGAC AGAGGAAAGG GCTGGCTCCC CCTCCCCAGG CTGGAGACCC CCCCCAACTC CAGGAAAGAG CAGTCAGAGT CCAGTGCTCT GCCTCAGACG	4320
,	TTGCCTGAGA AGAAGTGGCT GCCACACCCA GGGGAAGGCC CTGAGGCGGA GGCTGTGCTC	4380
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Seq ID NO: 198 DNA Sequence

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65	HCKVVKGTFT RSPKKHGYIK MFEIPAGARH LLIQEVDATS HHLAVKNLET GKPILNEEND	780 840
	LNVDDNNVLE EDSVVYEWAL KKWSPCSKPC GGGSQFTKYG CRRRLDHKMV HRGFCAALSK	900
	PKAIRRACNP QECSQPVWVT GEWEPCSQTC GRTGMQVRSV RCIQPLHDNT TRSVHARHCN	960 1020
70	RTCRLGPCPR NISDPSKKSY VVQMLSRPDP DSPIRKISSK GHCQGDKSIF CRMEVLSRYC	1080
		1140 1200
	ENRKKENLIGK F	1211
75	Seq ID NO: 206 Protein sequence	
	Protein Accession #: NP_076927	
80	MGENDPPAVE APFSFRSLEG LDDLKISPVA PDADAVAAQI LSLLPLKFFP IIVIGIIALI LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLQVF	60 120
00	TAASWKTMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGGFREEFV SIDHLLPDDK	180
	VTALMHSVYV REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH LCGGSVITPL WIITAAHCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR	240 300
	LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCWT SGWGATEDGG DASPVLWHAA	360

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	VPLISNKICH HRDVYGGIIS PSMLCAGYLT GGVDSCQGDS GGPLVCQERR LWKLVGATSF	420
	GIGCAEVNKP GVYTRVTSPL DWIHEQMERD LKT	
5	Seq ID NO: 207 Protein Sequence	
)	Protein Accession #: CAC03433.2 1 11 21 31 41 51	
	MLSSTDFTPA SWELVVRVDH PREEQQKDVT LRVSGDLHVG GVMLKLVEQI NISQDWSDFA	60 120
10	LWWEQKHCWL LKTHWTLDKY GVQADAKLLP TPQHKMLRLR LPNLKMVRLR VSFSAVVFKA VSDICKILNI RRSEELSLLK PSGDYFKKKK KKDKNNKEPI IEDILNLESS PTASGSSVSP	180
	GLYSKIMIPI YDPINGIPAS SIMIWPSDSP LIEQNCSILA FSQPPQSPEA LADMYQPRSL	240
	VDKAKLNAGN LDSSRSLMEQ GIQEDEQLLL RFKYYSFFDL NPKYDAVRIN QLYEQARWAI	300 360
	LLEEIDCTEE EMLIPAALQY HISKLSLSAE TQDFAGESEV DEIEAALSNL EVTLEGGKAD SLLEDITDIP KLADNIKLPR PKKLLPKAFK QYWPIFKDTS IAYPKNKELE QGEPLEKLNL	420
15	RGCEVVPDVN VAGRKFGIKL LIPVADGNNE MYLRCDHENQ YAQWMAACML ASKGKTMADS	480
	SYQPEVLNIL SFLRMKNRNS ASQVASSLEN MDMNPECFVS PRCAKKHKSK QLAARILEAH QNVAQMPLVE AKLRFIQAWQ SLPEFGLTYY LVRFKGSKKD DILGVSYNRL IKIDAATGIP	540 600
	VITURETINIK QWIVINGETRQ VVIEFDQNVP TAFTCLSADC KIVHEYIGGY IFLSTRSKOQ	660
20	NETLDEDLPH KLTGGQD	677
20	Seq ID NO: 208 Protein Sequence	
	Protein Accession #: NP_114433.1	
	1 11 21 31 41 51	
25	MASRSMRLLL LLSCLAKTGV LGDIIMRPSC APGWFYHKSN CYGYFRKLRN WSDAELECQS	60
	YGNGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQQWQWIDG AMYLYRSWSG	120
	KSMGGNKHCA EMSSNNNFLT WSSNECNKRQ HFLCKYRP	158
	Seq ID NO: 209 Protein Sequence	
30	Protein Accession #: XP_051860.2	
	1 11 21 31 41 51	
	MGAAGRQDFL FKAMLTISWL TLTCFPGATS TVAAGCPDQS PELQPWNPGH DQDHHVHIGQ	60
35	GKTLLLTSSA TVYSIHISEG GKLVIKDHDE PIVLRTRHIL IDNGGELHAG SALCPFQGNF	120 180
33	TIILYGRADE GIQPDPYYGL KYIGVGKGGA LELHCQKKLS WTFLNKTLHP GGMAEGGYFF ERSWGHRGVI VHVIDPKSGT VIHSDRFDTY RSKKESERLV QYLNAVPDGR ILSVAVNDEG	240
	SRNLDDMARK AMTKLGSKHF LHLGPRHPWS FLTVKGNPSS SVEDHIEYHG HRGSAAARVF	300
	KLFQTEHGEY FNVSLSSEWV QDVEWTEWPD HDKVSQTKGG EKISDLWKAH PGKICNRPID IQATTMDGVN LSTEVVYKKG QDYRFACYDR GRACRSYRVR FLCGKPVRPK LTVTIDTNVN	360 420
40	STILNLEDNY QSWKPGDTLV IASTDYSMYQ AEEFQVLPCR SCAPNQVKVA GKPMYLHIGE	480
	EIDGVDMRAE VGLLSRNIIV MGEMEDKCYP YRNHICNFFD FDTFGGHIKF ALGFKAAHLE	540 600
	GTELKHMGOQ LVGQYPIHFH LAGDVDERGG YDPPTYIRDL SIHHTFSRCV TVHGSNGLLI KDVVGYNSLG HCPPTEDGPE ERNTFDHCLG LLVKSGTLLP SDRDSKMCKM ITEDSYPGYI	660
	PKPRODCNAV STPWMANPNN NLINCAAAGS EETGFWFIFH HVPTGPSVGM YSPGYSEHIP	720
45	LGKFYNNRAH SNYRAGMIID NGVKTTEASA KDKRPPLSII SARYSPHODA DPLKPREPAI IRHFIAYKNO DHGAWLRGGD VWLDSCRFAD NGIGLTLASG GTFPYDDGSK QEIKNSLFVG	780 840
	ESGNVGTEMM DNRIWGPGGL DHSGRTLPIG QNFPIRGIQL YDGPINIQNC TFRKFVALEG	900
	RHTSALAFRL NNAWQSCPHN NVTGIAFEDV PITSRVFFGE PGPWFNQLDM DGDKTSVFHD	960
50	VDGSVSEYPG SYLTKNDNWL VRHPDCINVP DWRGAICSGC YAQMYIQAYK TSNLRMKIIK NDFPSHPLYL EGALTRSTHY QQYQPVVTLQ KGYTIHWDQT APAELAIWLI NFNKGDWIRV	1020 1080
-	GLCYPRGTTF SILSDVHNRL LKQTSKTGVF VRTLQMDKVE QSYPGRSHYY WDEDSGLLFL	1140
	KLKAQNEREK FAFCSMKGCE RIKIKALIPK NAGVSDCTAT AYPKPTERAV VDVPMPKKLF	1200 1260
	GSQLKTKDHP LEVKMESSKQ HFFHLWNDFA YIEVDGKKYP SSEDGIQVVV IDGNQGRVVS HTSFRNSILQ GIPWQLFNYV ATIPDNSIVL MASKGRYVSR GPWTRVLEKL GADRGLKLKE	1320
55	QMAFVGFKGS FRPIWVTLDT EDHKAKIFQV VPIPVVKKKK L	1361
	Seq ID NO: 210 Protein Sequence	
	Protein Accession #: NP_036244.1	
60	1 11 21 31 41 51	
00	MSQVKSSYSY DAPSDFINES SLDDEGDTQN IDSWFEEKAN LENKLIGKNG TGGLEQGKTP	60
	LRKANLQQAI VTPLKPVDNT YYKEAEKENL VEQSIPSNAC SSLEVEAAIS RKTPAQPQRR	120
	SLRLSAQKDL EQKEKHHVKM KAKRCATPVI IDEILPSKKM KVSNNKKKPE EEGSAHQDTA EKNASSPEKA KGRHTVPCMP PAKQKFLKST EEQELEKSMK MQQEVVEMRK KNEEFKKLAL	180 240
65	AGIGQPVKKS VSQVTKSVDF HFRTDERIKQ HPKNQEEYKE VNFTSELRKH PSSPARVTKG	300
	CTIVKPFNLS QGKKRTPDET VSTYVPLAQQ VEDFHKRTPN RYHLRSKKDD INLLPSKSSV	360 420
	TKICRDPOTP VLOTKHRARA VTCKSTAELE AEELEKLOOY KFKARELDPR ILEGGPILPK KPPVKPPTEP IGFDLEIEKR IQERESKKKT EDEHFEFHSR PCPTKILEDV VGVPEKKVLP	480
70	ITVPKSPAPA LKNRIRMPTK EDEEEDEPVV IKAQPVPHYG VPFKPQIPEA RTVEICPFSF	540
70	DSRDKERQLQ KEKKIKELQK GEVPKFKALP LPHFDTINLP EKKVKNVTQI EPFCLETDRR GALKAOTWKH QLEEELROOK EAACFKARPN TVISQEPFVP KKEKKSVAEG LSGSLVQEPF	600 660
	QLATEKRAKE RQELEKRMAE VEAQKAQQLE EARLQEEEQK KEELARLRRE LVHKANPIRK	
	YQGLEIKSSD QPLTVPVSPK FSTRFHC	747
75	Seg ID NO: 211 Protein Sequence	
. •	Protein Accession #: NP_065169.1	
	1 11 21 31 41 51	
	MSRRKQAKPQ HINSEEDQGE QQPQQQTPEF ADAAPAAPAA GELGAPVNHP GNDEVASEDE	60
80⋅	ATVKRLRREE THYCEKCCAE FFSISEFLEH KKNCTKNPPV LIMNDSEGPV PSEDFSGAVL	120
	SHQPTSPGSK DCHRENGGSS EDMKEKPDAE SVVYLKTETA LPPTPQDISY LAKGKVANTN VTLQALRGTK VAVNQRSADA LPAPVPGANS IPMVLEQILC LQQQLQQIQ LTEQIRIQVN	
	MWASHALHSS GAGADTLKTL GSHMSQQVSA AVALLSQKAG SQGLSLDALK QAKLPHANIP	300
	SATSSLSPGL APPTLKPDGT RVLPNVMSRL PSALLPQAPG SVLFQSPFST VALDTSKKGK	
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	GKPPNISAVD V	KPKDEAALY	KHKCKYCSKV	FGTDSSLQIH	LRSHTGERPF '	VCSVCGHRFT	420
	TKGNLKVHPH R TSVGLPQNLS S						480 540
2	TPEPGSETLK L						600
5	RAFSTKGNLK T	HLGVHRTNT	SIKTOHSCPI	COKKETNAVM	LOQHIRMHMG	GQIPNTPLPE	660
	NPCDPTGSEP M TLGFAMMASL D	TVGENGSTG DAPGKVGPAP	AICHDDVIES FNLOPOGSRE	IDVEEVSSQE NGSVESDGLT	NDSSSLMGDO	PLPSIKSASP EYOSRSPDIL	720 780
	ETTSPQALSP A	unsqaes i ks	KSPDAGSKAE	SSENSRTEME	GRSSLPSTPI	rapptyvkve	840
10	VPGTPVGPST L	SPGHTPLLA	AQPRRQAKQH	GCTRCGKNFS	SASALQIHER	THTGEKPFVC	900
10	NICGRAFTIK C	NLKVHYMTH YTSMLNGGI.	GANNNSARRG AVKTNEISVI	OSCGVPTLPV	SLGATSVVNN	ATVSKHDGSO	960 1020
	SGISADVEKP S					-	1053
	Seq ID NO: 2	112 Drakaia	Comience				
15	Protein Acce						
	1 1	11	21	31	41	51	
	MGWDLTVIONL	AGNEFOVSI.S	SSMSVSELKA	(OITOKIGVHA	FOORLAVEPS	GVALODRVPL	60
••	ASQGLGPGST V	VLLVVDKCDE	PLSILVRNNK	GRSSTYEVRL	TOTVAHLKQQ	VSGLEGVQDD	120
20	LFWLTPEGKP I	LEDQLPLGEY	GLKPLSTVFM	nlrlrgggte	PGGRS		165
	Seg ID NO: 2	213 Proteir	sequence				
	Protein Acc	ession #: E	os sequence				
25	1 :	11 	21 1	31	41 	51 	
	MIILIYLPLL						60
	ERWDAYCYNP						120 180
	DLEDDPGCLA						240
30	QIKYVAMDPV .						
	Seg ID NO:	214 Protei	n sequence				
	Protein Acc	ession #: 1	NP_009046.1				
35	1	11	21	31 1	41	51 I	
55	MITLIYLPLL	LWEDTQGWGF	KDGIFHNSIW	LERAAGVYHR	EARSGKYKLT	YAEAKAVCEP	60
						IDYGIRLNRS	120 180
						QRIHLSFLDF SDASVTAGGF	240
40	QIKYVAMDPV						
	Seq ID NO:	215 Protei	n Semience				
	Protein Acc	ession #:	NP_006389.1		-0.0		
45	1	11	21 	31 1	41	51 	
						LLGSKILKPR	60
			VKPSDEELPL DGKMMADYGI			SVAQVKAMIE	120 165
	Algaritoini	TATCHGRADE	DOMENDIGI	KNOWDOL LINE	10100		-00
50	Seq ID NO:						
	Procein Acc	ession #:	NP_002349.1 21	31	41	51	
	Ī.	1	1	I	1	1	
55						KDDSAPREKS	60 120
-						GPOFITNSEE	180
	VRLRSFTTTI	HKVNSMVAY	IPVND				205
	Seq ID NO:	217 Protei	n sequence				
60	Protein Acc		NP_001889.1		41	51	
	i	11	1	31	ì	î	
						AISEYNKATK	60 120
65		RSLVKSRCQI		RTICTESQU	N LUTCAPHEUI	PELQKKQLCSP	120
					<u></u>		
			in sequence NP_009162.:	1	~		
70	1	11	21	31	41	51	
70	MUKI'KUBSEB	KCBERERIO	SCENERIO	N DENOUSCH	6 KK6DAtitem	 GYAVGLGNVW	60
	RFPYLTYSNG	GGAFLIPYA	I MLALAGLPL	P FLECSLGQF	a slgpvsvwr:	I LPLFQGVGIT	120
						V THENVSTVNK	180 240
75	PCFFFWFIA PLOFIT I OWN K	GAALFKGIK	S SCKVVYFTA	L FPYVVLLIL	L VRGATLEGA	N ETGVIVWYLA S KGISYYIGAQ	300
	SNFTKLKEAE	VWKDAATQI	P YSLSVAWGG	L VALSSYNKF	K NNCPSDAIV	V CLTNCLTSVF	360
						I LEFFMLLTLG G 1YWVHLIDHF	420 480
00	CAGWGILIAA	ILELVGIIW	I YGGNRFIED	T EMMIGAKRW	I FWLWWRACH	P VITPILLIAI	540
80			D WGVALGWCM D MVDPKKEAD			G NIFQRLISCC	600
			in sequence NP_006389.				
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	1	11	21	31	41	51 	
	MADNASCICU	HVRSEEWDLM	TEDANDADA	KKI KEHVRSK	TKVPVODOVL	LLGSKILKPR	60
_	RSLSSYGIDK	EKTIHLTLKV	VKPSDEELPL	FLVESGDEAK	RHLLQVRRSS	SVAQVKAMIE	120
5	TKTGI I PETQ	IVTCNGKRLE	DGKMMADYGI	RKGNLLFLAS	YCIGG		
		220 Proteir ession #: >					
	1	.ession w: 7	21	31	41	51	
10	1	1	1	Ī	1	1	
	MKANYSAEER	FLLLGPSDWP	SLQPVLFALV	LLCYLLTLTG	NSALVLLAVR	DPRLHTPMYY	60
	FLCHLALVDA	GFTTSVVPPL	LANLEGPALW	LPRSHCTAQL	CASLALGSAE	CVLLAVMALD	120 180
	PALLKLACCE	YAGLVSPRLC DGDTTENQMF	AARVUILLE	FAVILASYGA	VARAVCOMRE	SGGRRRAVGT	240
15	CGSHLTAVCL	PYGSAIYTYL	QPAQRYNQAR	GKFVSLFYTV	VTPALNPLIY	TLRNKKVKGA	300
	ARRLLRSLGR						
	Sea ID NO:	221 Protein	Seguence				
20		cession #: 1					
	1	11	21	31	41	51	
	1	<u> </u>			PODY CEN CHO	OM CCCEERS	60
	MOSSIEKTER	RTRARRENLQ	NLENKOPVES	TSAKSCSPSP	VSPOVOPOAA	DTISDSVAVP	120
25	ASLLGMRRGL	NSRLEATAAS	SVKTRMOKLA	EQRRRWDNDD	MIDDIPESSE	FSPMPSEEKA	180
	ASPPKPLLSN	ASATPVGRRG	RLANLAATIC	SWEDDVNHSP	AKQNSVQEQP	GTACLSKFSS	240
		SSVKQEATFC					300 360
						EICLQSQSKD LFKQDTSSST	420
30	THLACOLKOE	ROKELACLEG	RFDKGNIWSA	EKGGNSKSKQ	LETKQETHCQ	STPLKKHOGV	480
	SKTOSLPVTE	KVTENQIPAK	NSSTEPKGPT	ECEMTKSSPL	KITLFLEEDK	SLKVTSDPKV	540
	EOKIEVIRE	EMSVDDDDIN	SSKVINDLFS	DVLEEGELDH	EKSQEEMDQA	LAESSEEQED	600 660
	ALN I SSMSLI	, APLAGIVGVV	SPESLVSTPR	DELKDISKSU	SKLDEKNNAF	TRVPRAESGD PCQVNIKQKM	720
35	OELNNEINMO	OTVIYOASOA	LNCCVDEERG	KGSLEEAEAE	RLLLIATGKE	TLLIDELNKL	780
	KNEGPQRKNI	ASPOSEFMPS	KGSVTLSEIR	LPLKADFVCS	TVQKPDAANY	YYLIILKAGA	840
	ENMVATPLAS	TSNSLNGDAL	TETTTETLQU	VSNDFEINIE	VYSLVQKKDE	SGLDKKKKTS	900 960
						SVGNTKFVLD GNCISYWTYP	1020
40						TLVSQCRDTL	1080
		TKEERDLWMO					1124
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45	1	11	21	31	41	51	
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	MAENSVLTS	T TGRTSLADS:	FIFDSKVTEIS	KENLLIGST:	S YVEEEMPQII	TRVILVQEAG	60 120
	KAREPLKAP	C EDIAPECADA	. VCTSMMNI.VI	CPTGFRKKE	E LVRLVTLVH	YKADCRVIGP H MGGVIRKDFN	180
50	SKVTHLVAN	C TOGEKFRYA	SLGTPIMKP	WIYKAWERR	N EQDFYAAVD	FRNEFKVPPF	240
	QDCIFSPLG	F SDEEKTNME	E MTEMQGGKY	PLGDERCTH	L VVEENIVKO	L PFEPSKKLYV	300
	VKQEWFWGS	I QMDARAGETI	4 YLYEKANTP	E LKKSVSMLS	L NTPNSNRKR	R RLKETLAQLS K SSTPVPSKQS	360 420
	ADMOVAKET.	P KKKPSAEHS: V OTESNYVNI	L SIGSLLDIS	N IPESSINIG	P ILAPEEIKT	I FGSIPDIFDV	480
55	HTKIKDDLE	D LIVNWDBSK	S IGDIFLKYS	K DLVKTYPPF	V NFFEMSKET	I IKCEKQKPRF	540
						K STLEKAIGSL	600
	KEVMTHINE	D KRKTEAQKQ	I FDVVYEVDG	C PANLLSSHR	S LVQRVETIS	L GEHPCDRGEQ	660 720
	NAFALLUDE	D TECHNICALS	I GIFKSPHGQ F OMTSDELPK	E NWLKMLCRH	V ANTICKADA	V LDIRETEDCH E NLIYTADPES	780
60						S VEGRSPSSND	840
	KHVMSRLSS	T SSLAGIPSP	S LVSLPSFFE	R RSHTLSRST	T HLI		883
	Sea ID NO	: 223 Prote	in Semience				
		ccession #:					
65	1	11	21	31	41	51	
		.		_	n vocament	O MILVSEVNILIR	60
		V LYTIGTGSY				E EFVLRVMTQL	120
	TLALKECH	R SDGGHTVLH	R DLKPANVFL	D CKONVKLGE	F GLARILNHI	T SFAKTFVGTP	180
70	YYMSPEQM	IR MSYNEKSDI	W SLGCLLYEL	C ALMPPETAR	S QKELAGKIF	E GKFRRIPYRY	240
	SDELNEI I	TR MLNLKDYHF	P SVEEILENE	L IADLVADEQ	R RNLERRGRO	L GEPEKSQDSS	300
	PVLSELKL	LE IQLQERERA	L KAREERLEC	K EQELCVRES	L AEUKLAKA	en lliknyslike KC kolkkrihaa	360 420
		OI EKNYQLKSI		O VENTURSEL	Deventandi		445
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80		YN SSWIPGSH:	IV SPSLLLNLI	IN GOLLPLOIA	G PLNSWIPP	S GILQQQQQQAQ	
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						IP FYAQFGYIPQ AG VFMPSTSPKP	
		AV DQTITPEL			Attitudo	Tringioeke	271

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5	ī	1	ī	ī	i	ī	
•	RGKEHRSRMV	OT ELEPEDEN	TVUTVMVIII	LIGELGATES	ADT.TRODIMS	ACNOMBITIM	60
			PFSG1LQQQQ				
							120
			PPQTQPGPSH				180
10	QPQQTVPRSP						240
10	MSTGEEIPYL	QKEAINFRHD	SAGVFMPSTS	PKPSTTNVFT	SAVDQTITPE	LPEEKDKTDS	300
	LREP						304
	Seq ID NO:	226 Protein	Sequence				
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	MATTUDOGCO	NCI KEKAADI	CDKAEAWGIV	LETTIATACINI	TOUR PMI TID	I VOIGIODEN	60
			LTPAPIIGLD				
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20			PSLVQDVIAI				180
20			GSPTGWKRHG				240
			VSPEFWLLTK				300
	SQEELTQGFE	ETGDTLYAPY	STHFQLQNQP	PQKEFSIPRA	HAWPSPYKDY	EVKKEGS	357
	Seq ID NO:	227 Protein	Seguence				
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	MPKIVIMOUT	ADEBEODARA.	QQEYMTKVLE	CLOOKONGT	FCDTCTCVT	CI.I CTTI NUD	60
30			FPDRALSSWG				120
30			REQUCIHPEV				180
	KSLEQELASP	ILDIEDLVKS	GSKHRVCPYY	LSRNLKQQAD	I I FMPYNYLL	Daksrrahni	240
	DLKGTVVIFD	EAHNVEKMCE	ESASPOLTPH	DLASGLDVID	QVLEEQTKAA	QQGEPHPEPS	300
	ADSPSPGLNM	ELEDIAKLKM	ILLRLEGAID	AVELPGDDSG	VTKPGSYIFE	LFAEAOITFO	360
			GVFTNTAGLQ				420
35	YKVHIHPDAG	HERTAGESDA	WSTTAARKRG	KVI.SYWCESP	CHSMHET.VRO	GVPCLILTEG	480
			ENPHI I DKHO				
							540
			PSYPVMEKSL				600
			AVCRGKASEG				660
40			EWYRQQASRA				720
40	RAQLPSWVRP	HVRVYDNFGH	VIRDVAQFFR	VAERTHPAPA	PRATAPSVRG	EDAVSEAKSP	780
	GPFFSTRKAK	SLDLHVPSLK	ORSSGSPAAG	DPESSLCVEY	ECEPVPAROR	PRGLLAALEH	840
			LLSEKRPAEE				900
			DYKGSDDFAA				
							960
45			EHSI PRRQRA				1020
43			SQPQWGSGVP				1080
	AALTAYKQDD	DLDKVLAVLA	ALTTAKPEDF	PLLHRFSMFV	RPHHKQRFSQ	TCTDLTGRPY	1140
	PGMEPPGPQE	ERLAVPPVLT	HRAPQPGPSR	SEKTGKTQSK	ISSFLRQRPA	GTVGAGGEDA	1200
			HGRDIAGQQA				1260
						PVAAVPGVGA	1320
50						DVWPVSTAPL	1380
		PLLQRPLRGA		ACK ARTIGIDE	- Daire Englis	DINEVSINE	1400
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						CLLCTTLAWR	60
	ehlrogisar	KIAERAQGEL	FPDRALSSWG	NAAAAAGDPI	ACYTDIPKII	YASRTHSQLT	120
	QVINELRNTS	YRPKVCVLGS	REQUCIHPEV	KKQESNHLOI	HLCRKKVASR	SCHFYNNVEE	180
60	KSLEOELASP	ILDIEDLVKS	GSKHRVCPYV	LSRNL KOOAD	I I FMPYNYI.I.	DAKSRRAHNI	240
	DLKGTVVIFD	EAHNVEKMCE	ESASFOLTPH	DLASGLOVED	OVLEFOTRAL	QQGEPHPEFS	300
						LFAEAQITFQ	360
	I VOCTIMORY	AT TAUMORY	CALININGPO	VMOTIGIAL	SYDYSEGSPG	SPAGLGALQS	420
65						GVRSLILTSG	480
Q.	TLAPVSSFAL	EMQI PPPVCL	FNAHIIDKHÖ	IWVGVVPRGP	DGAQLSSAFD	RRPSEECLSS	540
	LGKALGNIAR	VVPYGLLIFF	PSYPVMEKSL	EFWRARDLAR	KMEALKPLFV	EPRSKGSPSE	600
	TISAYYARVA	APGSTGATFL	AVCRGKASEG	LDFSDTNGRG	VIVTGLPYPP	RMDPRVVLKM	660
	QFLDEMKGOG	GAGGQFLSGO	EWYROOASRA	VNOAIGRVIR	HRODYGAVFI	CDHRFAFADA	720
	RAQLPSWVRP	HVRVYDNFGH	VIROVAOFFR	VAERTMPAPA	PRATAPSVRC	EDAVSEAKSP	780
70	GPFFSTRKAM	SLDLHVDGL	ORSSCODARG	DDECC! CHO	EUEDADADAD	PRGLLAALEH	840
-						AQTDRAKLEN	
	UNUNCOI CO	MDATETONIO	POSCACAFE	PROGRAKIAL	VORPEERVAG	AUTOKAKLIM	900
	AUCLIAUAVAV	DALATIVALO	DIRGSDDFAA	LAACLGPLFA	PDPKKHNLLQ	GFYQFVRPHH	960
	KQQFEEVCIQ	LIGROCGYRP	LHSIPRRORA	QPVLDPTGRT	APDPKLTVST	AAAQQLDPQE	1020
75	HLNOGRPHLS	PRPPPTGDPG	SQPQWGSGVP	RACKQCQHAV	SAYLADARRA	LGSAGCSQLL	1080
75	AALTAYKQDD	DEDKALYATT	ALTTAKPEDF	PLLHRFSMFV	RPHHKQRFSQ	TCTDLTGRPY	1140
	PGMEPPGPQE	ERLAVPPVLT	HRAPOPGPSR	SEKTGKTOSK	ISSFLRORPA	GTVGAGGEDA	1200
	GPSQSSGPPH		4				1219
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	Sea to No-	229 Protei	n Semence				
80							
			NP_056462.1				
	1	11	21	31	41	51	
	1	1	1	1	1	1	
	MPAPAPRATA	PSVRGEDAVS	EAKSPGPFPS	TRKAKSLDLH	VPSLKQRSSC	SPAAGDPESS	60
-	LCVEYEQEPV	PARQRPRGLL	AALEHSEQRA	GSPGEEQAHS	CSTLSLLSEK	RPAEEPRGGR	120
					-	140	

	GPLPAEDPKK PTGRTAPDPK	EPVAGAQTOR HNLLQGPYQF LTVSTAAAQQ	LDPQEHLNQG VRPHHKQQFE	EVCIQLTGRG RPHLSPRPPP	CGYRPEHS1P TGDPGSQPQW	RRQRAQPVLD GSGVPRAGKQ	180 240 300
5	FSMFVRPHHK KTQSKISSPL	DARRALGSAG QRFSQTCTDL RQRPAGTVGA GCGAEDVVPP	TGRPYPGMEP GGEDAGPSQS	PGPQEERLAV SGPPHGPAAS	PPVLTHRAPQ EWGEPHGRDI	PGPSRSEKTG AGQQATGAPG	360 420 480 540 545
10	Protein Acc	230 Protein cession #: N 11	P_003814.1 21 	31 	41 	51 	
15	PCRRDSPTTC AHAGFCLEHA LNVPGSSSHD	LLCLVLALPA GPCPPRHYTQ SCPPGAGVIA TLCTSCTGPP AALQLKLRRR	PWNYLERCRY PGTPSQNTQC LSTRVPGAEE	CNVLCGEREE QPCPPGTFSA CERAVIDFVA	EARACHATHN SSSSSEQCOP PQDISIKRLQ	RACRCRTGPF HRNCTALGLA RLLQALEAPE	60 120 180 240 300
20	Protein Acc	231 Protein cession #: P 11	P_116563.1 21 	31 	41	51 	
25	PCRRDSPTTC AHAGFCLEHA LNVPGSSSHD	CLCLVLALPA GPCPPRHYTQ SCPPGAGVIA TLCTSCTGFP AALQLKLRRR	FWNYLERCRY PGTPSQNTQC LSTRVPGAEE	CNVLCGEREE QPCPPGTPSA CERAVIDPVA	EARACHATHN SSSSSEQCQP FQDISIKRLQ	RACRCRTGFF HRNCTALGLA RLLQALEAPE	60 120 180 240 300
30		232 Protein cession #: 1		31	41 [51 	
35	MASSRCPAPR GLSRWAVLWL APGSADSTRL GSETRRLSLP	GCRCLPGASL GACGVLRATV LHWGSHPTAF LVLVVLSSLG	AWLGTVLLLL GSKSENAGAQ VVSYAAALPA EMAIPFFTGR	ADWVLLRTAL GWLAALKPLA AALWHKLGSL LTDWILQDGS	PRIFSLLVPT AALGLALPGL WVPGGQGGSG ADTFTRNLTL	ALFRELISWG NPVRRLLGCL MSILTIASAV	60 120 180 240 300
40	ENLSLFLWYL AKSSQVAIEA LLKVGILYIG YLDRTPRCPP	VRGLCLLGIM LSAMPTVRSF GQLVTSGAVS SGLLTPLHLE	LWGSVSLTMV ANEEGEAQKF SGNLVTFVLY GLVQFQDVSF	TLITLPLLFL REKLQEIKTL QMQFTQAVEV AYPNRPDVLV	LPKKVGKWYQ NQKEAVAYAV LLSIYPRVQK LQGLTFTLRF	DTSTLSDSLS LLEVQVRESL NSWTTSISGM AVGSSEKIFE GEVTALVGPN	360 420 480 540 600
45	YGLTQKPTME PCVLILDDAT	EITAAAVKSG	AHSFISGLPQ VEQLLYESPE	GYDTEVDEAG	SQLSGGGRQA	FGRSLQENIA VALARALIRK HILFLEGGAI	660 720 780 808
50	Protein Ac	233 Protei cession #: 11	NP_002414.1 21 	31 	41	51 	
55	EMOKFFGLP1 PHITVDRLVS APGTGLGGD/	TGMLNSRVIE KALNMWGKEI	IMQKPRCGVI PLHFRKVVMO GSSLGINFL	DVAEYSLFPN TADIMIGFAF	SPKWTSKVVI GAHGDSYPFI	(NANSLEAKLK YRIVSYTRDL) GPGNTLAHAF A VMYPTYGNGD	60 120 180 240 267
60		: 234 Protei cession #: 11 !		31 	41 	51 	
65	GPHGLRRTLI NRFRHSALSI NFSGHHCSA: ETNETSFEAG	N ALALLTSLAU D ADIFHLANLT S NFSVVYTRYC G IRVQIHSQEI	A FLYQAAGLAI F GLPPKDRDGI G KCYTFNADPI E PPYIHQLGF	R GYLTRPHLVÆ H RAAGLRYPE R SSLPSRAGG G VSPGFQTFV	A MDPAAPAPV P DMVDILNRT M GSGLEIMLD S CQEQRLTYL	I LHGLGRACGP A GFPAVTLCNI G HQLADMLKSC I QQEEYLPIWR P QPWGNCRAES Y IECADHTLDS	60 120 180 240 300 360
70	LGGGPEGPC EALTSEAME	F CPTPCNLTR Q RAAYGLSAL	Y GKEISMVRI L GDLGGQMGL	P NRGSARYLA F IGASILTLL	R KYNRNETYI E ILDYIYEVS	R ENFLVLDVFF W DRLKRVWRRP P GGLFEDFAC	420 480 539
75	Protein A	: 235 Prote ccession #: 11 	BAC03567	31 	41 pccl-snppy	51 P PRSGSLALGD	60
80	PSSDPACSQ PDPVLSEEV TPYDLVRMS DQTLTLEDL AAKSCGDNI EGVLDMFSI	S GPMEAEEDS V EGIAAGIEA S MQLAPQELA V GPQMFMDCS F QKALSQTPM K RFRARAQLV	L PEQPEDSAQ A LWDLTQGTN R WRDQEEKRG P QALPIASED P APEMPKTRE S GHSCRLVQA	L QQEKPSLYI G RYKTKYRSL L NIIEQQQKE T TGQHDHHFL L SPTEPQDRV L PTVIRSAGC	G VRGTVVRSM L FNLRDPRNL P CRLPASKMT D PNCHICKDM P PSGLHVPAA I PSNIVWDLL	P PROSESSED PROS	120 180 240 300 360 420
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	GLEVTHSSLL GTPPPGGAWQ QHPYSVAPAG	QSQGRGSIAP HGFGRGQHFH	RGISAWQRPP RDSCPHQALL	RGRGRLWPEP RHLESLATMS	ENWQHPGRGQ	WPPEPGLRQS	540 600 660
5	RLSSALAAPE	PPGPARDSSL	GPTDEAGSEC	PFPRKA			696
	Seq ID NO: Protein Acc	ession #: N	P_005282		.,	<i>5</i> 1	
	1	11 	21 	31 	41 	51 	
10	SGNHWPFGEI AFLWVVVAVA	ILALVGNTLA ACRLTGPLPY MAPLLVSPQT	SGSDSSQSMN LWLFIRDHKS LNMYASIYFL VQTNHTVVCL AVRMIAIVLA	GTPANVPLMH TCI SADRFLA QLYREKASHH	LAVADLSCVL IVHPVKSLKL ALVSLAVAFT	VLPTRLVYHF RRPLYAHLAC FPPITTVTCY	60 120 180 240 300
15	RILALANRIT LSAKSEL	SCLTSLNGAL	DPIMYFFVAE	KFRHALCNLL	CGKRLKGPPP	SFEGKTNESS	360 367
20	Protein Acc	237 Protein cession #: 1		31	41	51	
20	1	ī	ī	1	1	1	
	MRKTRLNGLL	WMLFVSELRA	ATKLTEEKYE	PERECUTATION IN THE PROPERTY OF THE PROPERTY O	CDYTLEKFAS	SQKAWQIIRD YQCVIYQPPK	60 120
25	EPHMLFDRIR	LVVTKGFSGT	PGSNENSTQN VPVPNIVILL	VYKIPPTTTK	ALCPLYTSPR	TVTQAPPKST	180 234
		238 Proteintesion #: 1	NP_00345B		0.		
30	1	11	21 	31	41 	51	
	MEGISIYTSD	NYTEEMGSGD	YDSMKEPCFR	EENANFNKIP	LPTIYSIIFL	TGIVGNGLVI	60
	LVMGYQKKLR YSSVLILAFI	SLORYLAIVH	ATNSQRPRKL	LAEKVVYVGV	WIPALLLTIP	AVHVIYTVNL DFIFANVSEA	120 180
35	DDRYICORFY	PNDLWVVVFQ	POHIMVGLIL	PGIVILSCYC	IIISKLSHSK	GHQKRKALKT AFFHCCLNPI	240 300
33			SRGSSLKILS				352
		239 Protei	n Sequence NP_036338.1				
40	1	11	21	31	41	51	
	 	I W ADCUAC	. entraccessor	 CUTL DOUVE	 AVTSMCWNRO	 SCSLFTCQNG	60
	IVWTNGTHVT	YRKDTRYKLI	GDLSRRDVSL	TIENTAVSDS	GVYCCRVEHR	GWFNDMKITV	120
45						TTVPTTMTVS ETHPTTLQGA	180 240
-1,5	IRREPTSSPL	YSYTTDGNDT	VTESSDGLWN	NNQTQLFLEH	SLLTANTTKO	IYAGVCISVL	300
	VLLALLGVII	AKKYFFKKEV	QQLSVSFSSI	. QIKALQNAVE	KEVQAEDNIY	IENSLYATD	359
50		240 Protei					
50	Protein Ac	cession #:	NP_004923.1	31	41	51	
	i	1	1	1	Ĩ	1	
	MRTYRYFLLL	, FWVGQPYPTI	L STPLSKRTSC	FPAKKRALEI	. SGNSKNELNI . FIINENTGD	SKRSWMWNQF QATKRLDREE	60 120
55	KPVYILRAQA	INRRTGRPV	E PESEPIIKI	I DINDNEPIF	revytatvei	MSDVGTFVVQ	180
						E QYQVVIQAKD KASDADVGEN	240 300
	AEIEYSITO	G EGLDMFDVI	r DOETQEGII:	r vkklldfeki	K KVYTLKVEA:	S NPYVEPRFLY	360
60	LGPFKDSAT\ VDRHTDMDRI	/ RIVVEDVDE:	P PVPSKLAYII I PTSKLLDRE	L QIREDAQIN T LLWHNITVI	TTIGSVTAQDI A TEINNPKOS	P DAARNPVKYS S RVPLYIKVLD	420 480
	VNDNAPEFAI	e fyetfycek	A KADQLIQTU	H AVDKDDPYS	G HQFSFSLAP	E AASGSNFTIO	540
	DNKONTAGII	L TRKNGYNRH 3 LSTGALVAI	E MSTYLLPVV L LCIVILLVT	I SDNDYPVQS: V VLFAALRRO	S TGTVTVRVC R KKEPLIISK	A CDHHGNMQSC E DIRDNIVSYN	600 660
65	DEGGGEEDT	AFDIGTLRN	P EAIEDNKLR	R DIVPEALFL	P RRTPTARDN	T DVRDFINQRL	720
O)	YGGVDSDKD:		Y EGTGSVADS	L SSLESVITO	A DQDYDYLSD	W GPRFKKLADM	780 790
			in Sequence				
70	Protein A	ccession #:	BAB14227.1 21	31	41	51	
-	Ī	1	1	1) 	A AVENCONY	60
	VPVSPTPPY	D PVEGVLWIT Q RGHLPTGGH	V LLFFWVTKR L AVCHFPCLL	A LEVPTGPEV Q EAQPHLQTQ	V FLQVRCTLL	K VAGMSPWAPQ V YCTDLPPTSI	120
75	LITFHNEAR	S TLLRTIRSV	L NRTPTHLIR	E IILVDDFSN	D PDDCKQLIK	L PKVKCLRNNE	180 240
13	FTY I ESASE	k GADIAQGTT L RGGFDWSLH	L TELDSHCEV F QWEQLSPEO	N ROWLOPLLH K ARRLOPTEP	RTPIIAGGL	C PVIDIINLDT F VIDKAWFDYL	300
	GKYDMDMDI	W GGENFEISF	R VWMCGGSLE	I VPCSRVGHV	P RKKHPYVFF	D GNANTYIKNT	360
	KRTAEVWMD ESSIOKGNI	E YKQYYYAAR R QRQKCLESC	IP FALERPFGN R ONNOETPNI	IV ESRLDLRKN K LSPCAKVKG	E DAKSQVWAF	E NIYPELSIPK T YTQQILQEEL	420 480
80	CLSV1TLFP	G APVVLVLCK	ON CODROOWTH	T GSHIEHIAS	H LCLDTDMFC	D GTENGKEIVV	540
		SSVMDWH O					557
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Seq ID NO: 242 Protein Sequence Protein Accession #: AAH10659

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	1		1	Ī	1	1	
	MRRLTRRLVL I	PVFGVLWITV I	LLFFWVTKRK	LEVPTGPEVQ	TPKPSDADWD	DLWDQFDERR PPTSIIITFH	60 120
5	NEARSTLLRT	IRSVLNRTPT I	HLIREIILVD	DPSNDPDDCK	OFIKT BKAKC	Lrnnerqglv	180
	RSRIRGADIA (QGTTLTFLDS !	HCEVNRDWLQ	PLLHRVKEDY	TRVVCPVIDI	INLOTFTYIE	240
	SASELRGGFD DMDIWGGENF	WSLHFQWEQL	SPEQKARRLD	PTEPIRTPII	AGGLEVIDKA	WPDYLGKYDM VIKNTKRTAE	300 360
	AMMDEAKOAA .	YAARPFALER	PFGNVESRLD	LRINLRCOSF	KWYLENIYPE	LSIPKESSIQ	420
10	KGNIRQRQKC	LESQRQNNQE	TPNLKLSPCA	KVKGEDAKSQ	IQQTYTAWV	LQEELCLSVI	480
	TLFPGAPVVL SLMSQHWDMV		QWTKTGSHIE	HIASHLCLDT	DMFGDGTENG	KETAANACES	540 552
	SPHEGUNDAY	33					
15		243 Protein					
13		ession #: A 11	AH10659.1	31	41	51	
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	MRRLTRRLVL	PVFGVLWITV DDPYKLYAFN	LLFFWVTKRK	LEVPTGPEVQ	TPKPSDADWD	DLWDQFDERR RELILVDDFS	60 120
20	NDPDDCKQLI	KLPKVKCLRN	NEROGLVRSR	IRGADIAQGT	TLTFLDSHCE	VNRDWLQPLL	180
	HRVKEDYTRV	VCPVIDIINL	DTFTYIESAS	ELRGGFDWSL	HFQWEQLSPE	QKARRLDPTE	240 300
						EIVPCSRVGH NVESRLDLRK	360
25	NLRCOSFKWY	LENIYPELSI	PKESSIQKGN	IRQRQKCLES	QRQNNQETPN	LKLSPCAKVK	420
25		FTYTQQ1LQE GDGTENGKEI			KNGDDRQQWT	KTGSHIEHIA	480 519
	SHICLDIDAF	GLOTENGREI	VVIIICESSEI	Serrange			
		244 Protein					
30	Protein Acc	ession #: N 11	1P_078848.1 21	31	41	51	
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	MNGKVWSGPG	FGALTSPRAH	SDFLDSKCEV	NRDWLQPLLH KARRINDTER	RVKEDYTRVV	CPVIDIINLD CPVIDKAWFDY	60 120
	LGKYDMDMDI	WGGENFEISF	RVWMCGGSLE	IVPCSRVGHV	FRKKHPYVFP	DGNANTYIKN	180
35						ENITEDITOR	240 300
	KESSIQKGNI LCLSVITLFP	GAPVVLVLCK	NGDDROOWTK	TGSHIEHIAS	HLCLDTDMFG	TYTQQILQEE DGTENGKEIV	360
	VNPCESSLMS						378
40	Sea ID NO.	245 Protei	n Semience				
	Protein Ac	cession #:	NP_001209.1				
	1	11	21	31	41	51 I	
	I MPRRSLHAAA	VLLLVILKEQ	PSSPAPVNGS	KWTYFGPDGI	NSWSKKYPSO	GGLLQSPIDL	60
45						SRYSATQLHL	120 180
	HWGNPNDPHG PSYDKIPSHL	OHVKYKGOEA	FVPGFNIEE	LPERTAEYY	YRGSLTTPP	AVLIEMGSFN NPTVLWTVFR	240
	NPVQISQEQL	LALETALYCT	HMDDPSPREA	INNFRQVQK	F DERLVYTSFS	QVQVCTAAGL	300
50	SLGIILSLAL	AGILGICIVV	VVSIWLFRR	K SIKKGDNKG	/ IYKPATKME	г ЕАНА	354
	Seq ID NO:	246 Protei	n Sequence				
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55						GGLLOSPIDL	60
						O SRYSATQLHL L AVLIEMGSFN	120 180
	PSYDKIFSHI	QHVKYKGQEA	FVPGFNIEE	L LPERTAEYY	R YRGSLTTPP	C NPTVLWTVFR	240
60		, LALETALYCT VSIWLFRRKS				S QGIILSLALA	300 343
00	GILGICIVV	VOINDERRR	, IKWIDIKWA	. IRPAINEL			
		247 Protei					
	Protein AC	cession #:	NP_006623.	31	41	51	
65	ı	1	. !	1	. 1	1	60
	MQVDETLIP	R KGPSLCSAR! GLSKAPKSL	Y GIALVLHFC	N PTTIAQNVI P AIWEKWGPP	O ERSRLCSIS	S TSPQSQLNDS SGMLLGCFTA	120
	ILIGGFISE	r LGWPFVFYI	F GGVGCVCCL	L WEVVIYDDE	P SYPWISTSE	K EYIISSLKQQ	180
70	VGSSKQPLP:	I KAMLRSLPI	W SICLGOFSH	Q WLVSTMVVY	I PTYISSVYH	V NIRDNGLLSA P YLNSGYITAT	240 300
70	ALLTLSCGL	S TLCQSCIYI	N VLDIAPRYS	S FLMGASRGE	S SIAPVIVP	V SGFLLSQDPE	360
		L FAVNLLGLL					401
	Sea ID NO	: 248 Prote	in Sequence				
75		ccession #:					
	1	11	21	31	41	51	
	 MPTTVDDVL	 E HGGEFHFFQ	K QMFFLLALI	S ATFAPIYV	I VFLGFTPDI	IR CRSPGVAELS	60
0Λ	LRCGWSPAE	E LNYTVPGPG	P AGEASPRO	R RYEVDWNQ	ST FDCVDPLAS	L DINRSRLPLG	120
80	PCRDGWVYE	T PGSSIVTEF A GVIMATEDT	N LVCANSWMI	D LFQSSVNV	F FIGSMSIG	(I ADRFGRKLCL /G RRYRRTVGIF	180 240
	YQVAYTVGL	L VLAGVAYAL	P HWRWLQFT	A LPNFFFLL	YY WCIPESPRE	IL ISQNKNAEAM	300
	RIIKHIAKK	N GKSLPASLQ	R LRLEEETGI	KK LNPSFLDL	VR TPQIRKHT	4I LMYNWFTSSV	360
	LYQGLIMHM	C PECONIATE	r ribalveri	PA AFMIILTI	JR IGRKIPWAJ	AS NMVAGAACLA	420

	SVFIPGDLON LKIIISCLGR MGITMAYEIV CLVNAELYPT FIRNLGVHIC SSMCDIGGII TPFLVYRLTH IMLELPLMVF GVLGLVAGGL VLLLPETKGK ALPETIEEAE NMORPRKNKE KMIYLQVQKL DIPLN	480 540 555
5	Seq ID No: 249 Protein Sequence Protein Accession 8: Eos sequence 1 11 21 31 41 51 1	
10	MOPAIQVMFG EDLPLSPRSP LTPRHGPGLA NVCQYDEWIA VRHEATLLPM GEDLSIMLSG LLGIKVKAEK LLEELONGVL LCQLIDVLQM MVKTCNSEES GNFPMRKVPC KUDAASGSFF ARDNTANFLH MCRDIGVDET YLFESDGLVL HKDPRQVYLC LLEIGRIVSR YGVEPPVLVK LEKEIELEET LLHTSGPEDS ISIPKSCCRH EELHEAVKHI AEDPPCSCSH RFSIEYLSEG RYRLGDKILF IRMLHGKHVM VRVGGGMDTL GGFLLKYDPC RILQFATLEQ KILAPQKGVS	60 120 180 240 300
15	NESVPDSPAR TPOPPERGIPL SAVIMFOKON SKPSVPVSIP KSKEKOGRPP GALVPASSLK GGNLGSMSVR SKLPNSPAAS SHPKLKSSKG ITKKPOAPSN NASSLASLM PYGKNTSSPA LPRTAPCISE SPRKCISSPN TPKAKVIPAQ NSADLPESTL LPNKCSGKTQ PKYLKHNHIS SRDNAVSHLA AHSNSSSKCP KLPKANIFVR PKPSFQSSAK MTKTSSKTIA TGLGTQSOPS DGAPQAKPVP AQKLKSALNL NQPVSVSSVS PVKATQKSKD KNIVSATKKQ PONKSAFOKT	360 420 480 540 600
20	GPSSLKSPGR TPLSIVSLPQ SSTKTQTAPK SAQTVAKSQH STKGPPRSGK TPASIRKPPS SVKDADSGDK KPTAKKKEDD DHYFVMTGSK KPRK	660 694
25	Seq ID NO: 250 Protein Sequence Protein Accession #: NP_001035.1 1 11 21 31 41 51	60 120 180
30	COFNREGAG VMKICPILKE VGFTVILISL YVGFTXNVII AMALHYLFSS PTTELPMINC NNSMNSPNCS DAHPGDSSGD SSGLNDTFGT TPAAEYFERG VLHLHQSHGI DDLGPPRWQL TACLVLVIU LYFSLMKGVK TSGKVVMITA TMPYVVLTAL LLRGVTLPGA IDGIRAYLSV DFYRLCEASV WIDAATQVCP SLGVGFGVLI AFSSYNKFTN NCYRDAIVTT SINSLTSFSS GFVVFSFLGY MAQKHSVPIG DVAKDGPGLI FIIYPEAIAT LPLSSAMAVV FFIHLITLGI DSAMGGMESV ITGLIDEFGL LHRHRELFTL FIVLATFILS LFCVTNGGIY VFTLLDHFAA	240 300 360 420 480
35	CTSLIFOCUL EAIGVANFYG VGOFSDDIQO MTGORPSLYW RLCMKLUSPC FLLFVVVVSI VTFRPPHYGA YIFPDWANAL GWVIATSSMA MVPIYAAYKF CSLPGSFREK LAYAIAPEKD RELVDRGEVR QFTLRHWLKV	540 600 620
40	Seq ID NO: 251 Protein Sequence Protein Accession #: NP_071356.1 1 11 21 31 41 51	60 120
45	LAGPRAGVSK RHLRGDQITW IGGNEEGCEA ISFLESLIDR LVLYCGSRLG KYYVKERSKA MVACYPGNGT GYVRHVDNPN GDGRCITCIY YLNKNWDAKL HGGILRIFFE GKSFIADVEP IFDRLLFFWS DRRNPHEVQP SYATRYAMTV WYFDAEERAE AKKKFRNLTR KTESALTED	180 239
50	Seq ID NO: 252 Protein Sequence Protein Accession 8: NP_647475.1 1 11 21 31 41 51	60 120 180
55	HKVAQQORHL EKQHLRIGHL QSQFGLLDHK HLDHEVAKPA RRKRLPEMAQ PVDPAHAVSR LHRLPRDCQE LFQVCERQSG LFEIQPGGSP PFLVXCOMTS DGGWTVIQRR HDGSVDFMSR WEAYKAGFGD PHGEFWLGLE KVHSITGDRN SKLAVQLRDW DGNAELLQFS VHLGGEDTAY SLQXIAPVAG QLGATTVPPS GLSVPFSTWD QDHDLRRDKN CAKSLSGGWW FGTCSHSNLN GQYFRSIPQQ RQKLKKGIFW KTWRGRYYPL QATTMLIQPW AAEAAS	240 300 360 406
60	Seq ID NO: 253 Protein Sequence Protein Accession #: NP_001207.1 1 11 21 31 41 51	
65	MAPLCPSPML PLLIPAPAPG LTVQLLLSLL LLMPVHPQRL PRMQEDSPLG GGSSGEDDPL GEEDLPSEED SPREEDPPGE EDLPGEEDLP GEEDLPEVRP KSEEEGSLKL EDLPTVEAFG DPQEPQNNAH RDKEGDDQSH WRYGGDPPWP RVSPACAGRP QSPVDIRPQL AAFCPALRPL ELLGFQLPPL PELRLRNNGH SVQLTLPPGL EMALGPGREY RALQLHLHWG AAGRPGSEHT VEGHRPPAEI HVVHLSTAFA RVDEALGRPG GLAVLAAFLE EGPENSAYE QLLSRLEETA EBGSETQVPG LDISALLPSD FSRYFQYEGS LTTPPCAQGV IWTVFNQTVM LSAKQLHTLS DTLWGPGDSR LQLNFRATQP LWGRVIEASF PAGVDSSPRA AEPVQLMSCL AAGDILALVF	60 120 180 240 300 360 420
70	GLLFAVTSVA FLVQMRRQHR RGTKGGVSYR PAEVAETGA	459
75	Seq ID NO: 254 Protein Sequence Protein Accession #: NP_003030.1 1 11 21 31 41 51	120
80	GLENLLANVD GWPILLGLTG VPAALQLLLL PFFPESPRYL LIQKKDEAAA KKALQTLRGW DSVDREVAEI RQEDEAEKAA GFISVLKLFR MRSLRWOLLS IIVLMGGQQL SGVWAIYYYD DQIYLSAGUP EEHVQYYTAG TGAWVAVNTF CAVFVVELLG RELLLLEGFS ICLIACCYLT AALALQDTVS WMPYISIVCV ISYVIGHALG PSPIPALLIT EIFLQSSRPS AFWYGGSVHW LSMFTYGLIF PFIQEGLGPY SPIVFAVICL LITIYIFLIV PETKAKTFIE INQIFTKMNI VSEVYPEKEE LKELPPVTSE Q	240 300 360 420

	Seq ID NO: 2						
_	Protein Acce			31	41	51	
5	MPEEGSGCSV I	 RRRPYGCVLR	 AALVPLVAGL) Vicivvcior	PAQAQQQLPL DGIYMVHIOV	 ESLGWDVAEL TLAICSSTTA	60 120
10	SRHHPTTLAV (GICSPASRSI					160 193
10	Seq ID NO: :	ession #: N	P_060562.2	31	41	51	
15	MLPTSFVEQK	 KKAGVFEQIT	 KTHGTIIGIT	 SGIVLVLLII	 SILVQVKQPR MRRSSTASRC	KKVMACKTAF THORHOGSOA	60 120
	SSVKQSRTNL PCEIYVRGRE	SSMELPLRND	FAQPQPMKTP	NSTFKKSSYT	FRQGHECPEQ	ALEDRVMEEI	180 201
20	Seq ID NO: Protein Acc			9 31	41	51	
	1 ,	1	1	1	Ĭ.	1	
25		SSPEGTLADT	EAGYVAQLSE	IKMYISILEE	AVSSAKSEIM QICQIRGETE		60 120 152
30		ession #: 1	IP_003256.1	••	4.	51	
30	1	11	21	31 	41	1	
	MROTLPCIYE	WGGLLPFGML	CASSTTKCTV	SHEVADOSHL	KLTQVPDDLP	TNITVLNLTH	60 120
	FCTNLTELHL	MSNSIQKIKN	NPFVKQKNLI	TLDLSHNGLS	LKVLNLQHNE STKLGTQVQL	enlqellish	180
35	NKIQALKSEE	LDIFANSSLK	KLELSSNQIK	EFSPGCFHAI	GRLFGLFLNN	VQLGPSLTEK	240
	LCLELANTSI EYFPLEYNNI	RNLSLSNSQL	LFNVRYLNLK	RSFTKOSISL	LSYNNLNVVG ASLPKIDDFS	FOWLKCLEHL	300 360
	NMEDND I PG I	KSNMFTGLIN	LKYLSLSNSP	TSLRTLTNET	FVSLAHSPLH	ILNUTKNKIS	420
40					I Y LSYNKYLQ INDDMLEGLE		480 540
	NLARLWKHAN	PGGPIYFLKG	LSHLHILNLE	SNGFDEI PVE	VFKDLFELKI	IDLGLNNLNT	600
	LPASVFNNQV	SLKSLNLQKN	LITSVEKKVF	GPAFRNLTEL	DMRFNPFDCT PFELFFMINT	CESIAWFVNW	660 720
					IKAYKDKDWV		780
45	DQSLKFCLEE	RDFEAGVFEL	EAIVNSIKRS	RKIIFVITHH	LLKDPLCKRP	KVHHAVQQAI	840
	eqnldsiilv NSVH	FLEEIPDYKL	NHALCLRRGM	FKSHCILNWE	• VQKERIGAFR	HKIQVAIGSK	900 904
50		259 Protei					
50	Protein Ac	cession #: 1	NP_000570.1 21	31	41	51	
	î	1	1	1	1	İ	
	MDYQVSSPIY	DINYYTSEPC	OKINVKQIAA	RLLPPLYSLV	FIFGFVGNML CQLLTGLYFI	VILILINCKR	60 120
55	LLTIDRYLAV	VHAVFALKAR	TVTFGVVTSV	ITWVVAVFAS	LPGIIFTRSC	KEGLHYTCSS	180
						HRAVRLIFTI	240 300
					RSTGEQEIS	CINPIIYAFV GL	352
60	Protein Ac	260 Protei cession #:	Eos sequend		41	51	
	1	11 }	21 	31 j	ĩ	1	
65	PQGPPGPPGI	PGARGELGLE	GAPGIDGEK	PKGOKGDPG	PGPAGLKGE	GEMGLSGLPG	60
03	GERGPSGLPG		PGTKGEKGRI	GEPGLDGFP		DGAKGEKGAS RGEKGERGVP	120 180 216
70		261 Proteices	NP_004852.				
	1	11	21 	31	41 	51 1	
	MLPPQKKPWE					A SCSPPALEPE	60
75						N GRNDFDYPTF F ESSFHYFGPV	120 180
13						P SSPQVQEHIL	240
	EVERRFHLVI	LOEYFDESLY	LIKDLLCHE	L EDVLYFKLN	A RRDSPVPRL	S GELYGRATAW	300
						H AVDAAAIQDE V TKLWKFIRDF	360 420
80	LRW						423
		262 Prote					
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	MASVLSRRLG I	 KRSLLGARVI.	GPSASEGPSA	(APPSEPLLEG	AAPOPFTTSD	DTPCQEQPKE	60
	VLKAPSTSGL (QQVAFQPGQK	VYVWYGGQEC	TGLVEQHSWM	EGOVIVWLLE -	ÖKTÖACCKAE	120
-	EVWLAELQGP (CPQAPPLEPG	AQALAYRPVS	RNIDVPKRKS	AMMEDMEVAD	AMVLTSLSCS	180 240
5	PVVQSPPGTE / YLGDAFGSPQ	ANFSASRAAC	DPWKESGDIS	DSGSSTTSGH	WSGSSGVSTP KCI MONCGKV	SPPHPQASPK LBSTVGIKRH	300
	VKALHLGDTV	DSDOFKREED	FYYTEVOLKE	ESAAAAAAA	AGTPVPGTPT	SEPAPTPSMT	360
	GLPLSALPPP :	LHKAQSSGPE	HPGPESSLPS	GALSKSAPGS	FWHIQADHAY	QALPSFQ1PV	420
10	SPHIYTSVSW				KSHLIVTSPP	RAQSGARKAR	480 513
10	GEAKKCRKVY	GIEHRDQWCT	ACRWICKACOR	FLD			343
	Seq ID NO:	263 Protein	Sequence				
	Protein Acc						
15	1	11	21	31	41	51 1	
IJ	 MRENYETLVS	VCTAFLLPLS	APLSPSEPGR	AVGGGSHADE	GOEPAGCGDP	OGGOPRHSLH	60
	LTALVOLVKE	IPEFLFGEVK	GAMDSPESES	RGASLDGERA	SPEAAAAREP	CPLRGLLSCL	120
	PDGPTSQPHL	ATTPTDSSCS	SGPTGDGVQG	SPLPIKTADK	PWPTRKEGPG	ALGGEPSPPT	180 240
20	HSPSRRKSHR	GOERGTSEAG	ISPGNSPLQG	PINCPKEIPA	PGPRHPETSP EAQDRHPSPS	GVGNRRLOEN	300
20	PGAWKRGSGG	PGYLLTPPPH	PDLGAGGLLS	VIONENSWYQS	PPGPASCOPG	ROPLSPSATG	360
	DTRGVPOPSW	GPEAQAASAS	SSPLEALEAC	LKGIPPNGSS	PSQLPPTSCS	QNPQPGDSRS	420
	OKPELOPHRS	HSEEATREPV	LPLGLQSCVR	DGPSRPLAPR	GTPTSPSSSS CSSAADRGPR	DAEDDNWTAD	480 540
25	KEGLRAFACE	SARLGOGRGE	APTRSLHLVS	POVFTSSCVP	ACHORGEKOP	GATRPGVWRW	600
	LPEGSAPKPS	PLHCLESALR	GILPVRPLRF	ACVGGPSPSP	SPGSSSSPSG	SEGEDPRPEP	660
	ELWKPLPQER	DRLPSCKPPV	PLSPCPGGTP	AGSSGGSPGE	DPRRTEPRYC	SGLGAGTAQD	720 780
	PCPVSQLEKR	PRVSEASRGL	CELGHGRPRVA	AKTHERLLPU	GPPELPSESP LAGLAQEVAT	MRTOVNRLGR	840
30	RPOGPGPMGO	ASWMWTLPRG	PRWAHGPGHR	HLPYWRQKGP	TRPKPKILRG	QGESCRAGDL	900
	QGLSRGTARR	ARPLPPDAPP	AEPPGLHCSS	SQQLLSSTPS	CHAAPPAHPL	LAHTGGHQSP	960
		LQGASPPAAS	ADADVPTSGV	APDGIPERPK	EPSSLLGGVQ	RALQEELWGG	1020 1030
	EHRDPRWGAH						
35	Seq ID NO:	264 Protei	n Sequence				
		cession #:		•-	41	51	
	1	11	21 i	31 !	11	i .	
	PAGCGDPQGG	QPRHSLHLTA	LVQLVKEIPE	PLFGEVKGAN	DSPESESRGA	SLDGERASPE	60
40	AAAREPCPLR	GLLSCLPDGR	TSQPHLATTI	TDSSCSSGP1	GDGVQGSPLP	IKTADKPWPT	120
	RKEGPGALGG	EPSPPTHSPS	RRKSHRGQE	R GTSEAGISPO	NSPLQGLING	LKEILVPGPR CLKELPEAQD	180 240
	RHPSPSGVGN	RRLOENPGA	KRGSGGPGY	LTPPPHPDLO	AGGLLSVKME	NSWVQSPPGP	300
4.5	ASCQPGRQPL	SPSATGDTRO	VPQPSWGPE	A QAASASSSPI	. EALEACLKGI	PPNGSSPSQL	360
45	PPTSCSQNPQ	PGDSRSQKPE	LOPHRSHSE	E ATREPVLPLO	LOSCVRDGPS	RPLAPRGTPT	420 480
	ADDCODDAFO	DLDFGSPVG	APKPSPLHC	L ESALEGILE	RPLRFACVGC	LRPAWPCSSA PSPSPSPGSS	540
	SSFSGSEGED	PRPEPDLWK	LPQERDRLP	S CKPPVPLSP	PGGTPAGSSC	GSPGEDPRRT	600
50	EPRYCSGLGA	GEPGVS					616
30	Sea ID NO.	265 Protes	in Sequence				
			AAH29071.1				
	1	11	21	31	41	51	
55	PTROPTOCRI	POCUMENT N	E NGNI NOGGG	D SATEWACIL	I PRTPRHKOP	LLMVRASRRS	60
33	GKTSAVLKAG	ROSVSGRKN	S TSKDLVTLG	A SSLREERGH	P LHPRHRKAVI	I LRTRGRTRGW	120
	VOTLARMSRE	R TRGPVERAA	A AAAAAAGGD	A GHAPFPPPP.	A ADGARAPRS	P GQVTPRGLRL	180
			L GFRESDSAK	P ASLRLLQHT	P SARRNYRIA	S ARLMRSNYPP	240 256
60	PLSSAALRG	Grikki					
	Seq ID NO:	266 Prote	in Sequence	0			
	Protein A	ccession #:	NP_002095.	1	41	51	
	1	11	21 1	31 i	1	1	
65	MTKFSSFSL	P PLIVGAYMT	H VCFNMEIIG	G KEVSPHSRP	F MASIQYGGH	H VCGGVLIDPQ	60
	WYLTAAHCO	Y RFTKGQSPT	V VLGAHSLSK	N EASKQTLEI	K KFIPFSRVT	S DPQSNDIMLV	120
	KLQTAAKLN	K HVKMLHIRS	K TSLRSGTKO	K VTGWGATDE	C KGVFHAIVS	E VTVTVLSRKL G GHECGVATKP	180 240
	GIYTLLTKK	Y QTWIKSNLV	P PHTN	ic Robboolba			264
70							
			in Sequence				
	rrotein A	ccession #:	NP_443179.	31	41	51	
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75	MOVNTLFET	S QVPDWSDPE	O VQVQETVRI	T ISCSOMPA	S EPAGEESPE	T GTTTISFSNL	60 120
	GGVHKENAS	L AQHSEVKPO	T CGPQQEEK	OT ALTICADO	E PROBERVO	S EANDETMSPG M ECFEASDQGT	
	CFDTIDSLV	G TPVDNYSPO	E ICSVDTEL	AE GQNKVSDLO	S SNDKTLEVE	P QTQVSETSVS	240
00	TCKSSKDGN	S VMSPLFIST	F TLNISHTA	SE GATGENLAI	CV EKSTYPLAS	T VHAGQEQPSP	300
80	SNSGGLDET	O LLSSENNPI	LV QFKEGGDK	SP SPSAADTT	AT PASYSSIVS	SP PWEKPTTLTA S QFPSQVQVDH	360 420
						D KSQTVDRADF	
	RSYEENFOE	R GSETKQGV	QQ QSLSQQGS	LS APDFQQSLI	PT TSAAQEERN	L VPTAPSPASS	540
	REGAGORSG	W GTRVSVVA	ET AGEEDSQA	LS NVPSLSDII	LL EESKEYRPO	N WEAGNKLKII	600

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5 10	TLEASASEIW PPRQLTNSES KASDGGLIIP DKWMAVPDSL KADAVVPELA PSEIAALAHS PEDAESALAD SRESKGEEP TISVHWRSLS SRGFSQPRLL ESSVDPVDEK ELSVTDSLSA ASETGGKENV NNVSQDQEEK QLØMDHTAFF KKPLTCPKIL ESSVDPIDEI SVIEYTRAGK PEPSETTPQC AREGOGSNDG NNCHEAEIGS AILØVPCLOG TILSERRISR SQCSMKQEA EQIQPEEAKT AIWQVLQPSE GGERIPSGCS IGQIQESSDG SLGEADSKK DKAELISPTS PLSSCLPIHT MSSLGVDTHN STGQIHDVE NDIVEPRKRQ YVFPVSQKKG TIENERGKPL PSSPDLTRFP CTSSPEGNVT DFLISHMEE PRIEVLAIGE TKPPSSSSSS AKTLAFISGE RELEKAPKLL QDPCQKGTLG CAKKSREREK SLEARAGKSP GTLIAVTGSE EVKRKPEAPG SGKLAEGVKK KILSRVAALR LKLEEKENIR NOSAFLKKMP KLETSLSHTE EKQDPKKPSC KREGRAPVLL KHIQAEMFPE HSGNVKLSCO FAEIHEDSTI CHTKDSKSIA QVQRSAGDNS TVSFAIVQAS PKDQGLYYCC IKNSYGKVTA EFNLTAEVLK QLSSRQDTKG CEELEFSQLI FKEPFLHDSY PGGRLRGGIA TEELHFGEGY HRKAFRSTVM HGLMPVFKPG HACVLKVINA LAYGTRNNDE LIQRNYKLAA QECVYONTAR YYAKIYAAEA QPLEGRGEVP EIIPIFLIHR PENNIPYATV EEELIGEFVK YSIRDGKEIN FLRRESEAGQ KCCTFQHWYY QKTSGCLLVT DWGGYGKKLT DUGIATLARG YKGFKGNCSM TFIDQFKALR QCKKYCMLG LKSLQNNNOK	660 720 780 840 900 960 1020 1140 1200 1380 1380 1440 1500
13	OKOPSIGKSK VOTNSMTVKK AGPETPGEKK T	1531
20 25	Seq ID NO: 268 Protein Sequence Protein Accession #: NP_602293.1 1 11 21 31 41 51	60 120 180 193
23	RLLQCDPSSA SQF	.,,
30 35	Seq ID NO: 269 Protein Sequence Protein Accession #: NP_002140.2 1 11 21 31 41 51	60 120 180 193
33	Seq ID NO: 270 Protein Sequence Protein Accession #: NP 003937.1	
40	1 11 21 31 41 51 MCNAQERPSE TIDERKRLV ETLQADSGLL LDALLARGVL TGPEYEALDA LPDAERRVRR LLLLVQGKGE AAQQELLRCA QRTAGAPDPA WDWQHVGPGY RDRSYDPPCP GHWTPEAPGS GTTCPGLPRA SDPDEAGGPE GSEAVQSGTP EEPEPELEAE ASKEAEPEPE PEPELEPEAE AEPEPELEPE PDPEPEPEFE ERDESEDS	60 120 180 208
45	Seq ID NO: 271 Protein Sequence Protein Accession #: NP_004198.1	
50 55	1 11 21 31 41 51	60 120 180 240 300 360 420 465
60	Seq ID NO: 272 Protein Sequence Protein Accession #: NP_060705.1 1	
65 70	MAALTTLFKY IDENQDRYIK KLAKWVAIQS VSAWPEKRGE IRRMMEVAAA DVKQLGGSVE LVDIGKOKLP DOSEIPLPPI LLGRLGSDPO KKTVCIYGHL DVQPAALEGG WDSEPFILVE RDGKLYGRGS TDDKGPVAGW INALEAYOKT QQEIPVNVRF CLECMEESGS EGLDELIFAR KOTFFKDVDY VCISDNYMLG KKKPCITYGL RGICYFFIEV ECSNKOLHSG VYGGSVHEAM TDLILLMGSL VDKRGNILIP GINEAVAAVT EEEHKLYDDI DFDIEFFAXD VGAQILLHSH KKDILMHRWR YPSLSLHGIE GAFSGSGAKT VIPRKVVGKF SIRLVPNMTP EVVGEQVTSE LTKKRAELRS PNEFKVYMGH GGKPWVSDFS HPHYLAGRRA MKTVFGVEPD LTREGGSIPV TLTPQEATGK NVMLLPVGSA DDGAHSQNEK LNRYNYIEGT KMLAAYLYEV SQLKD	60 120 180 240 300 360 420 475
70	Seq ID NO: 273 Protein Sequence	
75 80	Protein Accession #: AP258592_1 1 11 21 31 41 51	180 240 300
	Seq ID NO: 274 Protein Sequence Protein Accession #: NP 060871.1	
	747	

	1	11	21	31	41	51 I	
	MGGNHSHKPP	VFDENEEVNF	DHFQILRAIG	KGSFGKVCIV	QKRDTKKMYA	MKYMNKQKCI	60
-	ERDEVRNVFR	ELOIMOGLEH	PPLVNLWYSP	QDEEDMFMVV	DLLLGGDLRY	HLQQNVHPTE	120
5	GTVKLYICEL	ALALEYLORY	HIHRDIKPD	NILLDEHGHV	HITDFNIATV	VKGAERASSM	180 240
	AGTKPYMAPE	WCKCWUALLR	KLUTKOPESE	LGITAYELLR VSSLHDIQSV	PYLADMNWDA	VPKKALMPGF	300
	VPNKGRLNCD	PTPELEEMIL	ESKPLHKKKK	RLAKNRSRDG	TROSCPLNGH	LOHCLETVRE	360
• •	EPIIFNREKL	RRQQGQGSQL	LDTDSRGGGQ	AQSKLQDGCN	NNLLTHTCTR	GCSS	414
10							
		275 Protei cession #: 1					
	1	11	21	31	41	51	
16	1	1	1	1	1		
15	MGGAVVDEGP	TGVKAPDGGW	GWAVLFGCFV	ITGPSYAPPK	AVSVFFKELI	QEFGIGYSDT 11QVYLTTGV	60 120
	ITGIGIAINF	OPSLIMLNRY	FSKRRPMANG	LAAAGSPVFL	CALSPLOOLL	QDRYGWRGGP	180
	LILGGLLLNC	CVCAALMRPL	VVTAQPGSGP	PRPSRRLLDL	SVFRDRGFVL	YAVAASVHVL	240
20	GLFVPPVFVV	SYAKDLGVPD	TKAAFLLTIL	GFIDIFARPA	AGPVAGLGKV	RPYSVYLFSP	300 360
20	SMFFNGLADL	AGSTAGDYGG	LVVFCIFFGI	SYGMVGALQF	EVLMAIVGTH	KPSSAIGLVL RKKPKEPQPE	420
	VAAAEEEKLH	KPPADSGVDL	REVEHFLKAE	PEKNGEVVHT	PETSV		465
25		276 Protei					
25	Protein Ac	cession #:	NP_006589.1 21	31	41	51	
	î	1	1	i	1	1	
	MPTNFTVVPV	EAHADGGGDE	TAERTEAPG7	PEGPEPERPS	PGDGNPRENS	PPLNNVEVEQ	60
30	ESFFEGINMA	LFEEEMDSNE	MVSSLLNKL	NYTNLSQGVV	CTCTMLTAI	REAKAPRMGT MSAIATNGVV	120 180
50	PAGGSYYMIS	RSLGPEFGG	VGLCFYLGT	FAGAMYILG	IEIFLTYIS	GAATPQAEAA	240
	GGEAAAMLHD	I MRVYGTCTL\	LMALVVFVG	V KYVNKLALVE	LACVVLSIL	IYAGVIKSAF	300
	DPPDIPVCLI	GNRTLSRRSI	DACVKAYGII	H NNSATSALWO	LECNGSQPS	ACDEYFIQNN	360 420
35	VTEIQGIPGA	A ASGVELENLY	STYAHAGAF	V EKKGVPSVPI C IPTGTILAII	V ABESKASILI V TTSPIYLSC	VLFGACIEGV	480
33	VI.RDXFGEAT	. OGNLVIGMLI	WPSPWVIVI	G SFFSTCGAG	L OTLTGAPRL	L QAIARDGIVP	540
	FLOVFGHGKA	A NGEPTWALLI	L TVLICETGI	L IASLDSVAP	I LSMFFLMCY	L FVNLACAVQT	600
	LLRTPNWRPI	R FKFYHWTLSI	P LGMSLCLAL	M FICSWYYAL	S AMLIAGCIY	K YIEYRGAEKE R LLSFTSQLKA	660 720
40	CKGLTIVGS	L NAARTALLK	V ENGPPHIKN V EAGRAFENI	R SLMSTEKTK	G FCOLVVSSS	L RDGMSHLIQS	780
	AGLGGLKHN	T VLMAWPASW	K QEDNPFSWK	N PVDTVRDTT	A AHQALLVAK	N VDSFPQNQER	840
	FGGGHIDVW	W IVHDGGMLM	L LPFLLRQHK	V WRKCRMRIF	T VAQVDDNSI	Q MKKDLQMFLY	900
	HLRISAEVE	V VEMVENDIS	A FTYERTLMM	E ORSOMLKOM	Q LSKNEQERE	A QLIHDRNTAS D QSNVRRMHTA	960 1020
45	NI AAAARIQ	K SUDBOTATI	N MPGPPKNRO	G DENYMEFLE	V LTEGLNRVL	L VRGGGREVIT	1080
	IYS						1083
		: 277 Prote ccession #:					
50	1	11	21	31	41	51	
	1	1	1	1	<u> </u>		
	MASPHQEPK	P GDLIEIFRL	G YEHWALYIC	D GYVIHLAPP	S EYPGAGSSS	Y FSVLSNSAEV S RNCEHFVAQL	60 120
	KKCKTEDAA	G GCCYRVNNS	A TAIGILAVA	G CSFAIRRYC	K KATA	3 RACELLI TAGE	164
55	KIGIDKCIQ	LIGHTLIGE					
		: 278 Prote					
		ccession #:	NP_004687	.1 31	41	51	
	1	i	Î	j.	ï	Ĩ	
60	MLKREGKVC	P YTKTLDGGV	IG WMIVIHPFI	LV NVFVNGMTI	CT FAIFFVVF	E EFEGTSEQIG	60
	WIGSIMSSI	R FCAGPLVAI	I CDILGEKT	S ILGAFVVTO	G YLISSWAT	SI PFLCVTMGLL	120 180
	PGLGSAFLY	O VAAVVIIKI	IF KKKLALSI	KD KGSSLSAH	OP EAHATETH	ID LYDWTGALIL TH ETEESTIKDS	
	TTOKAGLPS	K NLTVSQNQS	SE EFYNGPNR	NR LLLKSDEES	SD KVISWSCK	OL POISLERNEE	300
65	FYIPTWSFI	LL SQLAYFIP	F HLVARAKT	LG IDIMDASY	LV SVAGILET	VS QIISGWVADQ	360
						LI LPVLVDLCRN	
	RWKNSLT	LA SPEAGMAVI	DS GERTAGME	ID IIQIINGS	ri radicida	js vsfffvplæ	487
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70		0: 279 Prot					
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	1	11 !	1	î.	ï	ĩ	
	MALFVRLL	AL ALALALGP	AA TLAGPAKS	PY QLVLQHSR	LR GROHGPNV	CA VOKVIGTNRK	60
75	YFTNCKQW	YQ RKICGKST	VI SYECCPGY	EK VPGEKGCP	AA LPLSNLYE	TL GVVGSTTTQL	120
	YTDRTEKL	RP EMEGPGSF	TI FAPSNEAW	AS LPAEVLDS	LV SNVNIELL	NA LRYHMVGRRV VH LIDKVISTIT	180
	UTDELKHG	M. LISMYUNS IE DTPRTLPA	AV AASGLNTN	LE GNGOYTLL	AP TNEAFEKI	PS ETLNRILGDE	
	EALRDLLN	NH ILKSAMCA	EA IVAGLSVE	TL EGTTLEVG	CS GDMLTING	KA IISNKOILAT	360
80	NGVIHYID	EL LIPDSAKT	LF ELAAESDY	ST AIDLFRQA	GL GNHLSGSE	RL TLLAPLNSVE	420
	KDGTPPID	AH TRNLLRNH	II KDQLASKY	LY HGQTLETL	AG KKLRVFVY VA ATOSACUT	RN SLCIENSCIA ET LNREGVYTVE	480
	ANDKKGRY	AL PPRERSEL	LG DAKELANI	LK YHIGDEIL	VS GGIGALVE	LK SLOGDKLEVS	
						SA LEIFKQASAF	

	SRASQRSVRL A	APVYQKLLER I	чкн				683
•	Seq ID NO: 2 Protein Acce	ession #: N	P_663623				
5	1 : MEGSGGGAGE FLNGAPFCWE (RAPLIGARRA	AAAAAAAGAP	 AGRRAACGAV	 LLTELLERAA	51 FYGITSNLVL ALVILONIAE	60 120
10	PLLAAPATRA DQVKDRGPEA LCGQSVFITK MSHGGPFTEE	ALCGSARLLN TRRPFNWPYW PPDGSAFTDH	CTAPGPDAAA SINLGAILSL PKILTYSCCS	RCCSPATFAG GGIAYIQQNV QKRSGERQSN	LVLVGLGVAT SFVTGYAIPT GEGIGVFQQS	VKANITPFGA VCVGLAFVVF SKQSLFDSCK	180 240 300 360
15	PHTLPAAWLT ILESKRLNLV PKSMQSAIMG AIQGATLLLF	MFDAVLILLL KEKTINQTIG LFPPPSGVGS	IPLKDKLVDP NVVYHAADLS FVGSGLLALV	ILRRHGLLPS LWWQVPQYLL SIKAIGWMSS	SLKRIAVGMF IGISEIFASI	PVMCSAFAAG AGLEFAYSAA	420 480 540 577
	Seq ID NO:	281 Protein	Sequence				
20	Protein Acc	ession #: N 11	P_001241.1 21	31	41	51	
25	PCGESEPLDT LHRSCSPGFG	WNRETHCHQH VKQIATGVSD	EPPTACREKQ KYCDPNLGLR TICEPCPVGF IFGILFAILL	VQQKGTSETD PSNVSSAFEK	TICTCEEGWH CHPWTSCETK	CTSEACESCV DLVVQQAGTN	60 120 180 240
23			VTQEDGKESR			42.422	277
30	Protein Acc	282 Proteir		31	41	51	
30	1	11	 GPREARGARP	Ī	ı	1	60
	LAPQQRAAPQ	QKRSSPSEGL	CPPGHH1 SED	GRDCISCKYG	QDYSTHWNDL	LFCLRCTRCD TPWSDIECVH	120 180
35	KESGTKHSGE	APAVEETVTS	SPGTPASPCS	LSGIIIGVTV	AAVVLIVAVF	VCKSLLWKKV	240 300
	NMLSPGESEH	LLEPAEAERS	QRRRLLVPAN	EGDPTETLRQ	CFDDFADLVP	VQEPAEPTGV FDSWEPLMRK	360
40		AKAEAAGHRD LEGNADSAMS	TLYTML1KWV	NKTGRDASVH	TLLDALETLG	ERLAKQKIED	420 440
40	Seq ID NO:	283 Protei	n Sequence				
			NP_671716.1 21	31	41	51	
45	1		1	1	VVAAVI.I.I.VS	 AESALITQQD	60
73	LAPOQRAAPQ	QKRSSPSEGL	CPPGHHISED	GRDCISCKYG	QDYSTHWNDL	LFCLRCTRCD TPWSDIECVH	120 180
	KESGI I IGVT	VAAVVLIVAV	FVCKSLLWKK	VLPYLKGICS	GGGGDPERVE	RSSQRPGAED	240 300
50	NEGDPTETLR	QCPDDFADLV		KLGLMDNEIK	VAKAEAAGH	SQRRRLLVPA DTLYTMLIKW S	360 411
		284 Protei cession #:	NP_002002.2		0.5		
55	1	11 [21 	31 	41 	51 	
						QPVRLCCGRA QNLTLITGDS	60 120
60	LTSSNDDEDF TIRWLKDGOA	KSHRDLSNRF PHGENRIGGI	SYPQQAPYWT	HPQRMEKKLE MESVVPSDRO	AVPAGNTVK	RCPAAGNPTP GSIRYNYLLD	180 240
	VLERSPHRPI	LOAGLPANTI	AVVGSDVELL	CKVYSDAQPI	I IQWLKHIVII	N GSSFGADGFP V LPEEDPTWTA	300 360
	AAPEARYTDI	ILYASGSLAI	. AVLLLLAGLY	RGQALHGRH	RPPATVQKL	S RFPLARQFSL S KPLGEGCFGQ	420 480
65	VVRAEAFGMI	PARPDQAST	/ AVKMLKDNAS	DKDLADLVSI	MEVMKLIGR	H KNIINLLGVC	540 600
	QYLESRKCII	RDLAARNVL	/ TEDNVMKIA	FGLARGVHH:	DYYKKTSNG	V SCAYQVARGM R LPVKWMAPEA	660
70	LMRECWHAAI	SQRPTFKQL	EALDKVLLA			R PPHCPPELYG D ASSTCSSSDS	720 780
70	VFSHDPLPLC	3 SSSFPFGSG	V QT				802
			in Sequence NP_075252.	1			
75	1	11	2 <u>1</u>	31 	41 	S1 J	
. •	MRLLLALLG					G OPVRLCCGRA L ONLTLITGDS	
	LTSSNDDED	P KSHRDLSNR	H SYPQQAPYW	T HPQRMEKKL	H AVPAGNTVK	F RCPAAGNPTP	180
80	VLERSPHRP.	I LQAGLPANT	T AVVGSDVEL	L CKVYSDAQP	H IQWLKHIVI	V GSIRYNYLLD N GSSFGADGFP	300
						V LPGTGRIPHL V SLDLPLDPLW	420
	EFPRDRLVL	G KPLGEGCFG	Q VVRAEAFGM	D PARPDQAST	V AVKMLKDNA	S DKDLADLVSE P DLSPDGPRSS	480

	EGPLSFPVLV SCATUVARGA CIDESRACIA REGISTRACIA	500 560
	LIREGHRADR PPHCPPELYG LARECWHAAP SQRPTFKQLV EALDKVLLAV SEEYLDLRLT	720
_	FGPYSPSGGD ASSTCSSSDS VFSHDPLPLG SSSFPFGSGV QT	762
5	C ID NO. Das Backein Companse	
	Seq ID NO: 286 Protein Sequence Protein Accession 8: NP_002836.2	
	1 11 21 31 41 51	
10	MRGLGTCLAT LAGLLLTAAG ETFSGGCLFD EPYSTCGYSQ SEGDDFNMEQ VNTLTKPTSD	60
10	PWMPSGSLML VNASGRPEGQ RAHLLLPQLK ENDTHCIDFH YFVSSKSNSP PGLLNVYVKV	120
	MUCDICADID NISCODTRIW MRAELAISTE WPNFYOVIFE VITSCHOOTE ALUEVAVIGH	180
		240 300
15	PINSPRANT INCHESTIC HINICAGO CONTINUE TO THE PERSON OF THE	360
	CCTCSPCPAL RTRIKCADPM RGPRKLEVVE VKSRQITIRW EPPGYNVTRC HSYNLTVHYC	420
	YOUGGOFOUR FEVSWOTENS HPORTITULS PYTNVSVKLI LANPEGRKES QULIVQTDED	480 540
	Thewasters Costeffut Marketidir Carrenters	600
20	DNTVTVMLKP AHSRGAPVSV YOIVVEERP RRTKKTTEIL KCYPVPIHFQ NASLLNSQYY	660
	PAREFPARSI GAMOPETIGD NKTYNGYWNT PLLPYKSYRI YFQAASRANG ETKIDCVQVA	720 780
	INDMITTER PERCUIPAT ANIMOTINGS TOTAL	840
	VEDETHIMAS DISSILVOSHI YKKREPADVP YOTGOLHPAI RVADLLQHII QMKCAEGYGP	900
25	REEYESFFEG OSAPWDSAKK DENRMKNRYG NIIAYDHSRV RLQTIEGDIN SDYINGNYID	960 1020
	GYHRPNHYIA TQGPMQETIY DFWRMVWHEN TASIIMVTNL VEVGRVKCCK YWPDDTEIYK DIKVTLIETE LLAEYVIRTP AVEKRGVHEI REIRQFHFTG WPDHGVPYHA TGLLGFVRQV	1080
	WEWEDDEAGD LAVHCSAGAG RIGCPIVIDI MLDMAEREGV VDIYNCVREL RSRRVNMVQT	1140
30	EEQYVFIHDA ILEACLCGDT SVPASQVRSL YYDMNKLDPQ TNSSQIKEEF RTLNMVTPTL RVEDCSIALL PRNHEKNRCM DILPPDRCLP FLITIDGESS NYINAALMDS YKQPSAFIVT	1200 1260
30	QHPLPNTVKD FWRLVLDYHC TSVVMLNDVD PAQLCPQYWP ENGVHRHGPI QVEFVSADLB	1320
	EDIISRIFRI YNAARPODGY RMVQQFQFLG WPMYRDTPVS KRSFLKLIRQ VDKWQEEYNG	1380
	GEGPTVVHCL NGGGRSGTFC AISIVCEMLR HQRTVDVFHA VKTLRNNKPN MVDLLDQYKF	1440 1452
35	CYEVALEYLN SG	
	Seq ID NO: 287 Protein Sequence	
	Protein Accession #: NP_057635.1 1 11 21 31 41 51	
40	MCFLOLLVVA VLASEHRVAG AAEVFGNSSE GLIEFSVGKF RYFELNRPFP EEAILHDISS	60 120
	NVTFLIFQIH SQYQNTTVSF SPTLLSNSSE TGTASGLVFI LRPEQSTCTW YLGTSGIQPV QNMAILLSYS ERDPVPGGCN LEFDLDIDPN IYLEYNFFET TIKFAPANLG YARGVDPPPC	180
	DAGTDODSRW RLOYDVYQYF LPENDLTEEM LLKHLQRMVS VPQVKASALK VVTLTANDKT	240
AE	SVSFSSLPGO GVIYNVIVWD PFLNTSAAYI PAHTYACSFE AGEGSCASLG RVSSKVFFTL	300 360
45	FALLGFFICF FGHRFWKTEL PFIGPIIMGP PPYILITRLT PIKYDVNLIL TAVTGSVGGM PLVAVWWRFG ILSICMLCVG LVLGPLISSV TPPTPLGNLK 1FHDDGVFWV TFSCIAILIP	420
	VVFMGCLRIL NILTCGVIGS YSVVLAIDSY WSTSLSYITL NVLKRALNKD FHRAPTNVPF	480
	QTNDPIILAV WGMLAVSGIT LQIRRERGRP FFPPHPYKLW KQERERRVTN ILDPSYHIPP	540 570
50	LRERLYGRLT QIKGLFQKEQ PAGERTPLLL	370
50	Seq ID NO: 288 Protein Sequence	
	Protein Accession #: NP_003811.1	
	1 11 21 31 41 51	
55	MEPPGDWGPP PWRSTPRTDV LRLVLYLTFL GAPCYAPALP SCKEDEYPVG SECCPKCSPG	60
	YRVKEACGEL TGTVCEPCPP GTYIAHLNGL SKCLQCQMCD PAMGLRASRN CSRTENAVCG CSPGHFCIVQ DGDHCAACRA YATSSPGQRV QKGGTESQDT LCQNCPPGTP SPNGTLEECQ	120 180
	HOTKCSMLVT KAGAGTSSSH MYMWFLSGSL VIVIVCSTVG LIICVKRRKP RGDVVKVIVS	240
C 0	VQRKRQEAEG EATVIEALQA PPDVTTVAVE ETIPSFTGRS PNH	283
60	Seq ID NO: 289 Protein Sequence	
	Protein Accession #: NP_000943.1	
	1 11 21 31 41 51	
65	MEPHDSSHMD SEFRYTLFPI VYSIIFVLGV IANGYVLHVF ARLYPCKKFN EIKIFMVNLT	60
05	MADMLFLITL PLWIVYYQNQ GNWILPKFLC NVAGCLFFIN TYCSVAFLGV ITYNRFQAVT	120
	RPIKTAOANT RKRGISLSLV IWVAIVGAAS YFLILDSTNT VPDSAGSGNV TRCFEHYEKG	180 240
	SVPVLITHIF IVFSFFLVFL IILPCNLVII RTLLMQPVQQ QRNAEVKRRA LMMVCTVLAV FIICFVPHHV VQLPMTLAEL GFQDSKFHQA INDAHQVTLC LLSTNCVLDP VIYCFLTKKP	300
70	RKHLTEKFYS MRSSRKCSRA TIDIVTEVVV PFNQIPGNSL KN	342
	O ID NO. 200 Despois Company	
	Seq ID NO: 290 Protein Sequence Protein Accession #: NP_003262.1	
75	1 11 21 31 41 51	
75	GCLGAIKENK CLLLTFFLLL LLVFLLEATI AILFFAYTDK IDRYAQQDLK KGLHLYGTQG	60
	NVGLTNAWSI IQTDFRCCGV SNYTDWFEVY NATRVPDSCC LEFSESCGLH APGTWWKAPC	120
	YETVKVWLQE NLLAVGIFGL CTALVQILGL TFAMTHYCQV VKADTYCA	168
80	Seq ID NO: 291 Protein Sequence	
00	Protein Accession #: NP_005620.1	
	1 11 21 31 41 51	
	MAKKSAENGI YSVSGDEKKG PLIAPGPDGA PAKGDGPVGL GTPGGRLAVP PRETWTRQMD	60
	750	

	FIMSCVGFAV	GLGNVWRPPY I	LCYKNGGGVF	LIPYVLIALV	GGIPIFFLEI	SLGQFMKAGS	120
	INVWNICPLF	KGLGYASHVI '	VEYCNTYYIM '	VLAWGFYYLV :	KSFTTTLPWA	TCGHTWNTPD	180
	CVEIFRHEDC .	ANASLANLTC I	DOLADRRSPV	iefwenkvlr	LSGGLEVPGA	LNWEVTLCLL	240
_	ACWVLVYFCV I	WKGVKSTGKI '	VYPTATFPYV '	VLVVLLVRGV	LLPGALDGII	AATKADM2KT	300
5	GSPQVWIDAG	TOIFFSYAIG	LGALTALGSY	NRFNNNCYKO .	aiilalinsg	TSFFAGPVVF	360
	STLGEMAAED :	GVHISKVAES	GPGLAFIAYP	RAVTLMPVAP	LWAALFFFML	LLLGLDSQFV	420
	GVEGFITGLL	DLLPASYYFR	FQREISVALC	CALCEVIDLS	MVTDGGMYVF	QLFDYYSASG	480
	TTLLWQAFWE	CVVVAHVYGA	DRIMODIACM	IGYRPCPWMK	WCWSFFTPLV	CMGIFIFNVV	540 600
10	YYEPLVYNNT	YVYPWWGEAM	Gwafalssml	CALTHURCT	LRAKGIMAER	MONDIGRIMG	
10	LHHLBYRAQD	ADVRGLTTLT	PVSESSKVVV	VESVM			635
		292 Protein					
	1	ession #: N 11	21	31	41	51	
15	i	i.	ī	ī	1	Ī	
	MKHVLNLYLL	CVVLTLLSIF	VRVMESLEGL	LESPSPGTSW	TTRSQLANTE	PTKGLPDHPS	60
	RSM						63
20		293 Proteir					
20		ression #: }			41	51	
	1	11	21	31	1	ĭ	
	MAGASICARE	YRQIKRHPGI	I PHIGLICLG	MGSAALYLLR	LALRSPOVCW	DRKNNPEPWN	60
		LAVSTDYKKL					87
25							
	Seq ID NO:	294 Protein	n Sequence				
	Protein Ac	cession #: 1	NP_002195.1				
	1	11	21	31	41	51	
20			1		I	I POVOVALUD	60
30	MGPGPSRAPR	APRIMICALA	DDCVTNDTCA	UVICULTAUK	DOCEDMAIT	LFGYSVALHR KNDPGHHIIE	120
	DWIGUTUAS	OCDACDULAC	PUGITARION	GSEDORRMVG	KCYVRGNDLE	LDSSDDWQTY	180
	HNEMCNSNTD	YLETGMCOLG	TSGGFTONTV	YFGAPGAYNW	KGNSYMIQRK	EWDLSEYSYK	240
	DPEDOGNLYI	GYTMQVGSFI	LHPKNITIVT	GAPRHRHMGA	VFLLSQEAGG	DLRRRQVLEG	300
35	SOVCAYEGSA	TALADIANNOG	MODLLVGAPY	YFERKEEVGG	AIYVFMNQAG	TSFPAHPSLL	360
	LHGPSGSAFG	LSVASIGDIN	QDGFQDIAVG	APPEGLGKVY	IYHSSSKGLI	ROPOQVINGE	420
	KLGLPGLATF	' GYSLSGOMDV	DENFYPOLLV	GSLSDHIVLL	. RARPVINIVI	KTLVPRPAVL	480 540
	DPALCTATSC	VQVELCPAYN	QSAGNPNYRR	NITLAYTLEA	DKDKKPPKL	R FAGSESAVFH	600
40	GFFSMPEMRC	QKLELLLMDN	CKDKCKP111	SWITSTERM	PURPRIOURS	ADAYPILAQA	660
40	DECEDECEDA	PORECGPONS	DALLICUUM	PGACOANETI	FCELGNPFK	C LLLSINVTNT R NORMELLIAF	720
	FVICVTLHTE	DIAVOLALST	SSHODNLWPH	ILTLLVDYTI	OTSLSKVNIH	LOSFFGGTVM	780
	GESCHICTVEL	VGSPLKYEFO	VGPMGEGLVC	LGTLVLGLEY	PYEVSNGKW	L LYPTEITVHG	840
	NGSWPCRPPC	DLINPLNLTI	. SDPGDRPSSE	QRRRRQLDPC	GGQGPPPVT	L AAAKKAKSET	900
45	VI.TCATGRAP	CVWLECPIPE	APVVTNVTVI	ARVWNSTFI	: DYRDFDRVR	V NGWATLFLRT	960
	SIPTINMEN	C TTWFSVDIDS	ELVEELPAE	ELWLVLVAVO	AGLLLLGLI	I LLLWKCGFFK	1020
	RARTRALYE	A KROKAEMKSO) PSETERLTDI	Y			1051
		205					
50		: 295 Protei ccession #:		1			
50	1	11	21	31	41	51	
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	MGPGPSRAPI	R APRIMICAL	LMVAAGGCV	V SAFNLDTRF	L VVKEAGNPG	S LFGYSVALHR	60
	QTERQQRYL	L LAGAPRELA	V PDGYTNRTG	A VYLCPLTAH	K DDCERMNIT	V KNDPGHHIIE	120
55	DMWLGVTVA:	S QGPAGRVLV	C AHRYTQVLW	S GSEDQRRMV	G KCYVRGNDL	E LDSSDDWQTY	180 240
	HNEMCNSNT	D YLETGMCQL	3 TSGGFTQNT	V YPGAPGAYN	W KGNSIMIQK	K EWDLSEYSYK	300
	DPEDQGNLY	I GYIMQVGSF	C MUDITACYD.	v verbkerne	C ATVVEMNOA	G DLRRRQVLEG G TSFPAHPSLL	360
	LUCDECEAR	G ISVASIGNI	N ODGEODIAV	G APPEGLGKV	Y IYKSSSKGL	L RQPQQVIHGE	420
60	KLGLPGLAT	P GYSLSGOMD	V DENFYPDLL	V GSLSDHIVL	L RARPVINIV	H KTLVPRPAVL	480
• • •	DPALCTATS	C VQVELCFAY	N QSAGNPNYR	R NITLAYTLE	A DRDRRPPRI	R FAGSESAVFH	540
	GFFSMPEMR	C OKLELLUMD	N LRDKLRPII	I SMNYSLPLR	M PDRPRLGLE	S LDAYPILNQA	600
	QALENHTEV	Q FQKECGPDN	K CESNLQMRA	a pvseqqqkl	S RLQYSRDVF	K LLLSINVTNT	660
45	RTSERSGED	A HEALLTLVV	P PALLLSSVR	P PGACQANET	I FCELGNPF	CR NORMELLIAF	720 780
65	EVICVTLHT	R DLQVQLQLS	T SSHQDNLWP	M ILTLLVDYT	L OTSLSMAN	R LOSFFGGTVM	840
	GESGMKTVE	D VGSPLKYEF	C ACAMCECTA	C DOLLARGE	C CCCCPPPV	IL AAAKKAKSET	900
	VITCATCRA	H CVMLECPTE	D APVUTNUTU	K ARVWNSTFI	E DYRDFDRVI	NOWATLELET	960
	SIPTINMEN	K TTWFSVDIE	S ELVEELPAR	I ELWLVLVA	G AGLLLLGL	I I LLLWKCDFFK	1020
. 70		K YHAVRIREE					1066
		: 296 Prote		1			
		Accession #:			43	61	
75	1	11	21	31	41	51 I	
13	 	er Cekenness	.c vutevonia	l Lb CEURSII vi	MA BCIALMAN.	LP CYLLYLRHHO	60
	POVITION	C KIKWAICA PP GREENPONI	T MCACASOLI	Y SEHGIVHO	RA PAPUFFUT	PL VVGVTMLLAT	
	LLIOYED1/	OG VOSSGVLI	IF WELCVVCA	IV PERSKILL	AK AEGEISDP	PR FTTFYIHPAL	
	VLSALILA	CF REKPPFFS	AK NVDPNPYPI	ET SAGFLERL	FF WWFTKMAI	YG YRHPLEEKDI	
80	WSLKEEDR	SQ MVVQQLLE	AW RKQEKQTAI	RH KASAAPGK	NA SGEDEVLL	GA RPRPRKPSFI	. 300
	KALLATFG:	SS FLISACPK	LI QDLLSFIN	PQ LLSILIRF	IS NPMAPSWW	GF LVAGLMFLCS	360
	MMQSLILQI	HY YHYIFVTG	VK FRTGIMGV	IY RKALVITN	SV KRASTVGE	IV NUMSVDAQRI	420
						VA VKMRAFQVK	
	MKLKDSRI	KL MSEILNGI	KV LKLYAWED:	SF LKQVEGIR	QG ELQLLRTA	WTTTTTHLL YA	4 540

		600
		660 720
		780
5	VDSHVAKHIP DHVIGPEGVL AGKTRVLVTH GISFLPQTDF IIVLADGQVS EMGPYPALLQ	840
•	RNGSFANFLC NYAPDEDOGH LEDSWTALEG AEDKEALLIE DTLSNHTDLT DNDPVTYVVQ	900
	KOFWRQLSAL SSDGEGOGRP VPRRHLGPSE KVQVTEAKAD GALTQEEKAA IGTVELSVFW	960
	DYAKAVGLCT TLAICLLYVG QSAAAIGANV WLSAWTNDAM ADSRQNNTSL RLGVYAALGI	1020
10	LOGFLYMLAA MAMAAGGIQA ARVLHQALLH NKIRSPQSFF DTTPSGRILN CFSKDIYVVD	1080 1140
10	EVLAPVILML LNSFFNAIST LVVIMASTPL FTVVILPLAV LYTLVQRFYA ATSRQLKRLE SVSRSPIYSH FSETVTGASV IRAYNRSRDF EIISDTKVDA NQRSCYPYII SNRWLSIGVE	1200
	FVGNCVVLFA ALFAVIGRSS LNPGLVGLSV SYSLQVTFAL NWMIRMSDL ESNIVAVERV	1260
	KEYSKTETEA PWVVEGSRPP EGWPPRGEVE FRNYSVRYRP GLDLVLRDLS LHVHGGEKVG	1320
	IVGRTGAGKS SMTLCLFRIL EAAKGEIRID GLNVADIGLH DLRSQLTIIP QDPILFSGTL	1380
15	RMNLDPFGSY SEEDINWALE LSHLHTFVSS QPAGLDFQCS EGGENLSVGQ RQLVCLARAL	1440
	LRKSRILVLD EATAAIDLET DNLIQATIRT QFDTCTVLTI AHRLNTIMDY TRVLVLDKGV	1500 1527
	VAEFDSPANL IAARGIFYGM ARDAGLA	
	Seq ID NO: 297 Protein Sequence	
20	Protein Accession #: NP_002692.1	
	1 11 21 31 41 51	
	TOTAL PROPERTY OF THE PROPERTY	60
	MHFYRLFLGA TRRPLNPEWK GEIDNMCVYV LTSLLPFKIQ SQDIKALQKE LEQFAKLLKQ KRITLGYTQA DVGLTLGVLF GKVFSQTTIC RFEALQLSFK NMCKLRPLLQ KMVEEADNNE	120
25	NLQEICKAET LVQARKRKRT SIENRVRGNL ENLFLQCPKP TLQQISHIAQ QLGLEKDVVR	180
	VWFCNRROKG KRSSSDYAOR EDFEAAGSPF SGGPVSFPLA PGPHFGAPGY GSPHFTALYS	240
	SVPFPEGEAP PPVSVTTLGS PLHSN	265
30	Seq ID NO: 298 Protein Sequence	
50	Protein Accession #: NP_005449.1 1 11 21 31 41 51	
	MASPRRSGOP GRPPPPPPPP ARLLLLLLLP LLLPLAPGAW GWARGAPRPP PSSPPLSIMG	60
25	LMPLTKEVAK GSIGRGVLPA VELAIEQIRN ESLLRPYFLD LRLYDTECDN AKGLKAFYDA	120
35	IKYGPNHLMV FGGVCPSVTS IIAESLQGMN LVQLSFAATT PVLADKKKYP YFFRTVPSDN	180 240
	AVNPAILKLL KHYOWKRYGT LTQDVQRPSE VRNDLTGVLY GEDIEISDTE SFSNDPCTSV KKLKGNDVRI ILGQFDQNMA AKVFCCAYEE NMYGSKYQWI IPGWYEPSMW EQVHTEANSS	300
	RCLRKVLLAA MEGYIGVDFE PLSSKQIKTI SGKTPQQYER EYNNKRSGVG PSKFHGYAYD	360
	GIWVIAKTLQ RAMETLHASS RHORIODFNY TOHTLGRIIL NAMNETNFFG VTGQVVFRNG	420
40	ERMGTIKFTQ FQDSREVKVG EYNAVADTLE IINDTIRFQG SEPPKDKTII LEQLRKISLP	480
	LYSILSALTI LGMIMASAPL FFNIKNRNQK LIKMSSPYMN NLIILGGMLS YASIPLFGLD	540
	GSFVSEKTFE TLCTVRTWIL TVGYTTAFGA MPAKTWRVHA IFKNVKMKKK IIKDQKLLVI	600 660
	VGGMLLIDLC ILICMQAVDP LRRTVEKYSM EPDPAGRDIS IRPLLEHCEN THMTIMLGIV YAYKGLLMLF GCFLAWETRN VSIPALMDSK YIGMSVYNVG IMCIIGAAVS FLTRDQPNVQ	720
45	FCIVALVIIF CSTITLCLVF VPKLITLRTN PDAATQNRRF QFTQNQKKED SKTSTSVTSV	780
	NQASTSRLEG LQSENHRLRM KITELDKDLE EVTMQLQDTP EKTTYIKQNH YQELNDILNL	840
	CNFTESTDGG KAILKNHLDQ NPQLQWNTTE PSRTCKDPIE DINSPEHIQR RLSLQLPILH	900
	HAYLPSIGGV DASCVSPCVS PTASPRHRHV PPSFRVMVSG L	941
50	C TD NO. 200 Dunkala Comuna	
50	Seq ID NO: 299 Protein Sequence Protein Accession #: NP 055632	
	1 11 21 31 41 51	
55	MEAARALRLL LVVCGCLALP PLAEPVCPER CDCQHPQHLL CTNRGLRVVP KTSSLPSPHD	60
55	VLTYSLOGHF ITNITAFDFH RLOQURRLDL QYNQIRSLHP KTFEKLSRLE ELYLCHNLLQ	120 180
	ALAPGTLAPL RKLRILYANG NEISRLSRGS FEGLESLVKL RLDGNALGAL PDAVFAPLGN LLYLHLESNR IRFLGKNAFA QLGKLRFLNL SANELQPSLR HAATFAPLRS LSSLILSANS	240
	LOHLGPRIFO HUPRIGLISL RENOLTHLAP EAFWGLEALR ELRLEGNRLS QUPTALLEPL	300
	HSLEALDLSG NELSALHPAT FGHLGRLREL SLRNNALSAL SGDIFAASPA LYRLDLDGNG	360
60	WTCDCRLRGL KRWMGDWHSQ GRLLTVFVQC RHPPALRGKY LDYLDDQQLQ NGSCADPSPS	420
	ASLTADRRRQ PLPTAAGEEM TPPAGLAEEL PPQPQLQQQG RFLAGVAWDG AARELVGNRS	480
	ALRISRRGPG LOOPSPSVAA AAGPAPQSLD LHKKPQRGRP TRADPALAEP TPTASPGSAP	540 600
	SPAGDPWQRA TKHRLGTEHQ ERAAQSDGGA GLPPLVSDPC DFNKFILCNL TVEAVGADSA SVRWAVREHR SPRPLGGARF RLLFDRFGQQ PKFHRFVYLP ESSDSATLRE LRGDTPYLVC	660
65	VEGVLGGRVC PVAPRDHCAG LVTLPEAGSR GGVDYQLLTL ALLTVNALLV LLALAAWASR	720
•••	WLRRKLRARR KGGAPVHVRH MYSTRRPLRS MGTGVSADFS GFQSHRPRTT VCALSEADLI	780
	EFPCDRFMDS AGGGAGGSLR REDRLLQRFA D	811
70	Seq ID NO: 300 Protein Sequence Protein Accession #: NP 001783.2	
70	1 11 21 31 41 51	
	MCRIAGALRT LLPLLAALLQ ASVEASGEIA LCKTGFPEDV YSAVLSKDVH EGQPLLNVKF	60
75	SNCNGKRKVQ YESSEPADPK VDEDGHVYAV RSPPLSSEHA KPLIYAQDKE TQEKWQVAVK	120
75	LSLKPTLTEE SVKESAEVEE IVFPROFSKH SCHLOROKED WVIPPINLPE NSRGPFPOEL	180 240
	VRIRSDRDKN LSLRYSVTGP GADQPPTGIF IINPISGQLS VTKPLDREQI ARFHLRAHAV DINGNOVENP IDIVINVIDM NDNRPEFLHQ VWNGTVPEGS KPGTYVMTVT AIDADDPNAL	
	NGMLRYRIVS QAPSTPSPHM FTINNETGDI ITVAAGLDRE KVQQYTLIIQ ATDMEGNPTY	360
	GLSNTATAVI TVTDVNDNPP EFTAMTFYGE VPENRVDIIV ANLTVTDKDQ PHTPAWNAVY	420
80	RISGGDPTGR FAIQTDPNSN DGLVTVVKPI DFETNRMFVL TVAAENQVPL AKGIQHPPQS	480
	TATVSVTVID VNENPYFAPN PKIIRQEEGL HAGTMLTTFT AQDPDRYMQQ NIRYTKLSDP	
	ANWLKIDPVN GQITTIAVLD RESPNYKNNI YNATPLASDN GIPPMSGTGT LQIYLLDIND	
	NAPOVLPQEA ETCETPOPNS INITALDYDI DPNAGPFAFD LPLSPVTIKR NWTITRLNGD	660 720
	FAQLNLKIKF LEAGIYEVPI IITDSGNPPK SNISILRVKV CQCDSNGDCT DVDRIVGAGL	

	GTGAIIAILL (EDQDYDLSQL (780 840
5	KAADNDPTAP YGGGDD	PYDSLLVFDY	EGSGSTAGSL	SSLNSSSSGG	EODADAFINDM	GPRPKKLADM	900 906
	Seq ID NO: Protein Acc	ession #: N	P_058637.1	31	41	51	
10	 MVSPRMSGLL	i	Ī	1	1	1	60
	RVCLKPGLSE SPIIETWREE	EAAESPCALG . LGDQIGGPAW	AALSARGPVY SLLARVAGRR	TEOPGAPAPD RLAAGGPWAR	LPLPDGLLQV DIQRAGAWEL	PFRDAWPGTF RFSYRARCEP	120 180 240
15		PVSTSSCLSP VSGVTCADGP	RGPSSATTGC	LVPGPGPCDG	NPCANGGSCS	ETPRSFECTC	300 360
	PCRNGGLCLD FGGRDCRERA	LGHALRCRCR DPCAARPCAH	AGPAGPRCEH GGRCYAHFSG	DLDDCAGRAC LVCACAPGYM	ANGGTCVEGG GARCEFPVHP	GAHRCSCALG DGASALPAAP	420 480
20	PGLRPGDPQR PDALNNLRTQ GQRQHLLFPY	YLLPPALGLL EGSGDGPSSS PSSILSVK	VAAGVAGAAL VDWNRPEDVD	PQGIYVISAP	SIYAREVATP	LFPPLHTGRA	540 600 618
		302 Protein		ction			
25	1	11 	21 	31 	41	51	
	KRLERKYPSL HVEGMVNISK	TLWLLKNARC LNGEIEAQIC ASSGQM	KTSSLELPSC	DLVTADGSTE	VTISENLPAV	GPHICQQQDS	60 120 136
30		303 Proteir cession #: N					
	1	11 	21 	31 	41	51 	
35	PSNGVPRSTA	IEPRYYESWT PGGIPNPEKK QQMDRSRRIT	TNCETQCPNP			LHSGMLEDGL KRDAKRMPAK	60 120 145
		304 Protein cession #: 3					
40	1	11	21 	31 	41 	51 	
	QPVVFNHVYN	INVPLDNLCS	SGLEASAEQE	VSAEDETLAE	YMGQTSDHES	IANYNTSSKE QVTFTHRINP	60 120
45						YIPHCSGHGN SELRCPTDCS	180 240
	SRGLCVDGEC	VCEEPYTGED	CRELRCPGDC	SGKGRCANGT	CLCEEGYVGE	DCGQRQCLNA AVTEYVISYQ	300 360
	PTALGGLQLQ	QRVPGDWSGV	TITELEPGLT	YNISVYAVIS	NILSLPITAK	VATHLSTPQG	420
50						QTGLKPGEEY VDFILLKYGL	480 540
	VGGEGGRTTF	RLQPPLSQYS	VQALRPGSRY	EVSVSAVRGT	NESDSATTQF	TTEIDAPKNL	600
						ATLTDLVPGT GPIDHYRITF	660 720
55	TPSSGIASEV	TVPKDRTSYT	LTDLEPGAEY	IISVTAERGR	QQSLESTVDA	FTGFRPISHL	780
55						LMGLQPATEY FDYYRVSYRP	840 900
	TQVGRLDSSV	VPNTVTEFTI	TRLNPATEYE	ISLNSVRGRE	ESERICTLY	TAMONPVOLI	960
						LLPSTHYTAT VVLTYKSTDG	1020 1080
60	SRKELIVDAE	DTWIRLEGLE	ENTDYTVLLQ	AAQDTTWSSI	TSTAFTTGG	VFPHPQDCAQ	1140
	HLMNGDTLSG	CIDVIDLE	SQKLQVYCD	TTDGGGWIVE	QRRQNGQTDI	FRKWADYRVG NLYKLRIGSY	1200 1260
						KYGESRHSQG	1320
65	INWYHWKGHE	FSIPFVEMKM	RPYNHRLMAG	RKRQSLQF			1358
	Seq ID NO:	305 Protei	n Sequence				
	Protein Ac	cession #:	NP_005874.1	31	41	51 .	
70	1	1	1	1	1	1	
70						L KHLQGKLEQE V HGSGPSKDSF	60 120
	GELSRATIRI	L LEELDRERCE	LLNEIEKEE	K EKLWYYSQLA	GLSKRLDEL	P HVETQFSHQM	180
	DLIRQQLEF	E AQHIRSLMEI	REGTSDEMV	RAQIRASRL	E QIDKELLEA	Q DRVQQTEPQA D TARTLLAMSS	240
75						A LHNIVFSQPD	300 360
	QGLARKEMR ¹	V LHVLEQIRA	CETCWDWLQ	A RDGGPEGGG	A GSAPIPIEP	Q ICQATCAVMK	420
						L TNLTFGDVAN E AGSVTALVQC	480 540
00	VLRATKEST	L KSVLSALWNI	L SAHSTENKA	A ICQVDGALG	F LVSTLTYKO	Q SNSLATIESG	600
80						W NLSARSARDQ S PGSCVPSLYV	660
						D YASDSGCFDD	
	DDAPSSLAA	A AATGEPASP	A ALSLFLGSP	P LQGQALART	P PTRRGGKEA	E KDTSGEAAVA	840
	akakaklal	A VARIDQLVE	D ISALHTSSD	D SFSLSSGDP	g qeapregra	Q SCSPCRGPEG	900

		960
		1020 1080
		1140
5	DATPSSSSEN YVQETPLVLS RCSSVSSLGS PESPSIASSI PSEPCSGQGS GTISPSELPD	1200
,	SPECOTMPPSR SKTPPLAPAP OGPPEATOPS LOWESYVKRP LDIADCRERC RLPSELDAGS	1260
	VRFTVEKPDE NFSCASSLSA LALHEHYVQQ DVELRLLPSA CPERGGGAGG AGLHFAGHRR	1320
	REEGPAPTGS RPRGAADOEL ELLRECLGAA VPARLRKVAS ALVPGRRALP VPVYMLVPAP	1380
10	APAGEDDSCT DSAEGTPVNF SSAASLSDET LQGPPRDQPG GPAGRQRPTG RPTSARQAMG	1440 1500
10	HRHKAGGAGR SAEDSRGAGK NRAGLELPLG RPPSAPADED GSKPGRTRGD GALQSLCLTT	1560
	PTEEAVYCFY GNDSDEEPPA AAPTPTHRRT SAIPRAPTRE RPQGRKEAPA PSKAAPAAPP PARTQPSLIA DETPPCYSLS SSASSLSEPE PSEPPAVHPR GREPAVTKDP GPGGGRDSSP	1620
	SPRAAGELLO RCISSALPRE RPPVSGLERE KPRATELDER PAGGSREEGE EAAGSDRASD	1680
	LDSVEWRAIO EGANSIVTWL HOAAAATREA SSESDSILSF VSGLSVGSTL QPPKHRKGRQ	1740
15	AEGEMGSARR PEKRGAASVK TSGSPRSPAG PEKPRGTQKT TPGVPAVLRG RTVIYVPSPA	1800
	PRAOPKGTPG PRATPRKVAP PCLAQPAAPA KVPSPGQQRS RSLHRPAKTS ELATLSQPPR	1860
	SATPPARLAK TPSSSSSQTS PASQPLPRKR PPVTQAAGAL PGPGASPVPK TPARTLLAKQ	1920
	HKTORSPURI PFMORPARRG PPPLARAVPE PGPRGRAGTE AGPGARGGRL GLURVASALS	1980 2040
20	SGSESSDRSG FRRQLTPIKE SPGLRRRRSE LSSAESAASA PQGASPRRGR PALPAVFLCS SRCEELRAAP RQGPAPARQR PPAARPSPGE RPARRTTSES PSRLPVRAPA ARPETVKRYA	2100
20	SLPHISVARR PDGAVPAAPA SADAARRSSD GEPRPLPRVA APGITWRRIR DEDVPHILRS	2160
	TLPATALPLE GSTPEDAPAG PPPEKTSDAV VQTEEVAAPK TNSSTSPSLE TREPPGAPAG	2220
	GOLSLIGSDY DGPSLAKAPI SAPFVHEGLG VAVGGFPASR HGSPSRSARV PPFNYVPSPM	2280
	VVAATTDSAA EKAPATASAT LLE	2303
25		
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	1 11 21 31 41 51	
30	MPLTEDLITF NLRNFLLFQL WESSFSPGAG GPCTTLPPSF LRVDDRATSS TTDSSRAPSS	60
30	PRPPGSTSHC GISTRCTERC LCVLPLRTSQ VPDVMAPQHD QEKFHDLAYS CLGKSPSMSN	120
	QDLYGYSTSS LALGLAWLSW ETKKKNVLHL VGLDSL	156
25	Seq ID NO: 307 Protein Sequence	
35	Protein Accession #: AAH32726.1	
	1 11 21 31 41 51	
	MASTRSIELE HFEERDKRPR PGSRRGAPSS SGGSSSSGPK GNGLIPSPAH SAHCSFYRTR	60
	TLQALSSEKK AKKARFYRNG DRYFKGLVFA ISSDRFRSFD ALLIELTRSL SDNVNLPQGV	120
40	RTIYTIDGSR KVTSLDELLE GESYVCASNE PFRKVDYTKN INPNWSVNIK GGTSRALAAA	180
	SSVKSEVKES KDFIKPKLVT VIRSGVKPRK AVRILLNKKT AHSFEQVLTD ITEAIKLDSG	240
	VVKRLCTLDG KQVTCLQDFF GDDDVFIACG PEKFRYAQDD FVLDHSECRV LKSSYSRSSA	300
	VKYSGSKSPG PSRRSKSPAS VNGTPSSQLS TPKSTKSSSS SPTSPGSFRG LKISAHGRSS	360
45	SNVNGGPELD RCISPEGVNG NRCSESSTLL EKYKIGKVIG DGNFAVVKEC IDRSTGKEFA	420 480
43	LKIIDKAKCC GKEHLIENEV SILRRVKHPN IIMLVEEMET ATELFLUMEL VKGGDLFDAI TSSTKYTERD GSAMVYNLAN ALRYLHGLSI VHRDIKPENL LVCEYPDGTK SLKLGDFGLA	540
	TYVEGPLYTY CGTPTYVAPE IIAETGYGLK VDIWAAGVIT YILLCGFPPP RSENNLQEDL	600
	FDQILAGKLE FPAPYWDNIT DSAKELISQM LQVNVEARCT AGQILSHPWV SDDASQENNM	660
	QAEVTGKLKQ HFNNALPKQN STTTGVSVIM FDLTV	695
50		
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	Protein Accession #: NP_055978.2	
	1 11 21 31 41 51	
55	MEEMEEELKC PVCGSFYREP IILPCSHNLC QACARNILVQ TPESESPQSH RAAGSGVSDY	60
33	DYLDLDKMSL YSEADSGYGS YGGFASAPTT PCQKSPNGVR VFPPAMPPPA THLSPALAPV	120
	PRNSCITCPO CHRSLILDDR GLRGFPKNRV LEGVIDRYQQ SKAAALKCQL CEKAPKEATV	180
	MCEOCDVFYC DPCRLRCHPP RGPLAKHRLV PPAQGRVSRR LSPRKVSTCT DHELENHSMY	240
-	CVQCKMPVCY QCLEEGKHSS HEVKALGAMW KLHKSQLSQA LNGLSDRAKE AKEFLVQLRN	300
60	MVQQIQENSV EFEACLVAQC DALIDALNRR KAQLLARVNK EHEHKLKVVR DQISHCTVKL	360
	ROTTGLMEYC LEVIKENDPS GFLQISDALI RRVHLTEDOW GKGTLTPRMT TDFDLSLDNS	420 480
	PLIQSIHOLD FVQVKASSPV PATPILQLEE CCTHNNSATL SWKQPPLSTV PADGYILELD DGNGGQFREV YVGKETMCTV DGLHFNSTYN ARVKAFNKTG VSPYSKTLVL QTSEVAWFAF	540
	DPGSAHSDII LSNDNLTVTC SSYDDRVVLG KTGPSKGIHY WELTVDRYDN HPDPAFGVAR	600
65	MDVMKDVMLG KDDKAWAMYV DNNRSWFMIN NSHTNRTEGG ITKGATIGVL LDLNRKNLTF	660
	FINDEQQCPI AFDNVEGLPF PAVSLNRNVQ VTLHTGLPVP DFYSSRASIA	710
	Seq ID NO: 309 Protein Sequence	
70	Protein Accession #: NP_116025.1	
70		
	MEDLEEDVRF IVDETLDFGG LSPSDSREEE DITVLVTPEK PLRRGLSHRS DPNAVAPAPO	60
	GVRLSLGPLS PEKLEEILDE ANRLAAQLEQ CALQDRESAG EGLGPRRVKP SPRRETFVLK	120
	DSPVRDLLPT VNSLTRSTPS PSSLTPRLRS NDRKGSVRAL RATSGKRPSN MKRESPTCNL	180
75	FPASKSPASS PLTRSTPPVR GRAGPSGRAA ASPPTPIRSV LAPQPSTSNS QRLPRPQGAA	240
	AKSSSQLPIP SAIPRPASRM PLTSRSVPPG RGALPPDSLS TRKGLPRPST AGHRVRESGH	300
	KVPVSQRLNL PVMGATRSNL QPPRKVAVPG PTR	333
	Con ID NO. 210 Protein Comence	
80	Seq ID NO: 310 Protein Sequence Protein Accession #: ref[XP_166946.2	
00	1 11 21 31 41 51	
	MGSDSRLPEM EEKGSGDKAG WSGALLAEVK NQGLKLCEWM LVLKAELVEW YTSVIVGQQG	60
	HRLKMOLLKE RHHRKYLQKP IKRCSGLMGL NWSLRPAISS SPLARSQEKH HGAKGNEGVK	120
	•	

	ALSFRKLRKL KRPPTPPSQA KSWRGRTGSA ADSPGAAAMA VQAALLSTHP PVPFGFGGSP	180
	DGLGGAFGAL DKGCCFEDDE TGAPAGALLS GAEGGDVREA TRDLLSFIDS ASSNIKLALD	240
	KPGKSKRKVN HRNAPTVAAP AHGKAAPRRE ASQAAAAASL QSRSLAALFD SLRHVPGGAE	300
5	PAGGEVAAPA AGLGGAGTGG AGGDVAGPAG ATAIPGARKV PLRARNLPPS FFTEPSRAGG	360
3	GGCGPSGPDV SLGDLEKGAE AVEFFELLGP DYGAGTEAAV LLAAEPLDVF PAGASVLRGP PELEPGLFEP PPAVVGNLLY PEPWSVPGCS PTKKSPLTAP RGGLTLNEPL SPLYPAAADS	420 480
	PGGEDGRGHL ASFAPPFPDC ALPPPPPPHQ VSYDYSAGYS RTAYSSLWRS DGVWEGAPGE	540
	EGAHRD	546
• •		
10	Seq ID NO: 311 Protein Sequence	
	Protein Accession #: NP_071406.1 1 11 21 31 41 51	
1.5	MAPTKPSFQQ DPSRRERLQA LRKEKSRDAA RSRRGKENFE FYELAKLLPL PAAITSQLDK	60
15	ASTIRLTISY LKHRDPANOG DPPWHLRHEG PPPHTSVKGA QRRRSPSALA IEVFEAHLGS	120 180
	HILQSLDGFV FALNQEGKFL YISETVSIYL GLSQVELTGS SVFDYVHPGD HVEMAEQLGM KLPPGRGLLS QGTAEDGASS ASSSSQSETP EPVESTSPSL LITDNTLERS PFIRMKSTLT	240
	KROVHIKSSG YKVIHITGRL RLRVSLSHGR TVPSQIMGLV VVAHALPPPT INEVRIDCHM	300
	FVTRVNMDLN IIYCENRISD YMDLTPVDIV GKRCYHFIHA EDVEGIRHSH LDLLNKGQCV	360
20	TKYYRHMOKN GGYIWIQSSA TIAINAKNAN EKNIIWVNYL LSNPEYKDTP MDIAQLPHLP	420
	EKTSESSETS DSESDSKOTS GITEDNENSK SDEKGNOSEN SEDPEPDRKK SGNACDNOWN	480 540
	CNDDGHSSSN PDSRDSDDSF EHSDFENPKA GEDGFGALGA MQIKVERYVE SESDLRLQNC ESLTSDSAKD SDSAGEAGAQ ASSKHQKRKK RRKRQKGGSA SRRRLSSASS PGGLDAGLVE	600
	PPRILISPNS ASVLKIKTEI SEPINFONDS SIWNYPPNRE ISRNESPYSM TKPPSSEHFP	660
25	SPOGGGGGG GGGLHVAIP DSVLTPPGAD GAAARKTQPG ASATAALAPV ASDPLSPPLS	720
	ASPRDKHPGN GGGGGGGG AGGGGPSASN SLLYTGDLEA LQRLQAGNVV LPLVHRVTGT	780
	LAATSTAAQR VYTTGTIRYA PAEVTLANQS NLLPNAHAVN PVDVNSPGFG LDPKTPMEML YHHVHRLNMS GPFGGAVSAA SLTQMPAGNV PTTAEGLPST LPFPVYSNGI HAAQTLERKE	840 900
	D D D D D D D D D D D D D D D D D D D	901
30		
	Seq ID NO: 312 Protein Sequence	
	Protein Accession #: NP_005797.1 1 11 21 31 41 51	
	1 11 21 31 41 51	
35	MDSDASLVSS RPSSPEPDDL PLPARSKGSS GSAFTGGTVS SSTPSDCPPE LSAELRGAMG	60
	SAGAHPGDKL GGSGFKSSSS STSSSTSSAA ASSTKKDKKQ MTEPELQQLR LKINSRERKR	120
	MHDLNIAMDG LREVMPYAHG PSVRKLSKIA TLLLARNYIL MLTNSLEEMK RLVSEIYGGH	180
	HAGFHPSACG GLAHSAPLPA ATAHPAAAAH AAHHPAVHHP ILPPAAAAAA AAAAAAAVSS ASLPGSGLPS VGSIRPPHGL LKSPSAAAAA PLGGGGGGSG ASGGFQHWGG MPCPCSMCQV	240 300
40	PPPHHHVSAM GAGSLPRUTS DAK	323
	Seq ID NO: 313 Protein Sequence	
	Protein Accession #: XP_045127.3 1 11 21 31 41 51	
45	1 11 21 31 41 51	
	MTVLEESSIS LMSSVVADFS EFEEDPQVFN TLPPSRPIVP LSSRSMEISE TSVGISAEVD	60
	MSSVTTTQVP PAHGRLSVPA SLDPTAGSLS VAETQVTPSS VTTAFFSVIT SILLDSSFSV	120
	IANKNTPSLA VRDPSVFTPY SLVPSVESSL FSDQERSSFS EHKPRGALDF ASSFFSTPPL	180 240
50	ELSGSISSPS EAPASLSLMP SDLSPPTSQS PSPLVETPTL FDSSDLQSSQ LSLPSSTNLE FSQLQPSSEL PLNTIMLLPS RSEVSPWSSF PSDSLEFVEA STVSLTDSEA HFTSAFIETT	300
50	SYLESSLISH ESAVTALVPP GSESFDILTA GIQATSPLTT VHTTPILTES SLFSTLTPPD	360
	DOISALDGHV SVLASFSKAI PTGTVLITDA YLPSGSSFVS EATPFPLPTE LTVVGPSLTP	420
	TEVPLNTSTE VSTTSTGAAT GGPLDSTLMG DAASQSPPES SAAPPLPSLR PVTAFTLEAT	480
55	VDTPTLATAK PPYVCDITVP DAYLITTVLA RRAVQEYIIT AIKEVLRIHF NRAVELKVYE LPTDFTFLVT SGPFVYTAIS VINVLINSKL VRDQTPLILS VKPSFLVPES RFQVQTVLQF	540 600
33	VPPSVDTGFC NFTQRIEKGL MTALFEVRKH HQGTYNLTVQ ILMITISSSR VTPRRGPVNI	660
	IFAVKSTOGF LNGSEVSELL RNLSVVEFSF YLGYPVLQIA EPFQYPQLNL SQLLKSSWVR	720
	TVLLGVMEKQ LQNEVFQAEM ERKLAQLLSE VSTRRRMWRR ATVAAGNSVV QVVNVSRLEG	780
60	DDNPVQLIYF VEDQDGERLS AVKSSDLINK MDLQRAAIIL GYRIQGVIAQ PVDRVKRPSP ESQSNNLWVI VGVVIPVLVV MVIVVILYWK LCRTDKLDFQ PDTVANIQQR QKLQIPSVKG	840 900
00	FDFAKQHLGQ HNKDDILIIH EPAPLPGPLK DHTTPSENGD VPSPKSKIPS KNVRHRGRVS	960
	PSDADSTVSE ESSERDAGDK TPGAVNDGRS HRAPQSGPPL PSSGNEQHSS ASIFEHVDRI	1020
	SRPPEASRRV PSKIQLIAMQ PIPAPPVQRP SPADRVAESN KINKEIQTAL RHKSEIEHHR	1080
65	NKIRLRAKRR GHYEFPVVDD LSSGDTKERH RVYRRAQMQI DKILDPTASV PSVFIEPRKS	1140 1200
05	SRIKRSPKPR RKHQVNGCPA DAEKDRLITT DSDGTYRRPP GVHNSAYIGC PSDPDLPADV QTPSSVELGR YPALPPPASQ YIPPQPSIEE ARQTMHSLLD DAFALVAPSS QPASTAGVGP	1260
	GVPPGLPANS TPSQEERRAT QWGSFYSPAQ TANNPCSRYE DYGMTPPTGP LPRPGFGPGL	1320
	LOSTELVPPD POOPOASAEA PFAARGIYSE EMPSVARPRP VGGTTGSQIQ HLTQVGIASR	1380
70	IGAQPVEIPP SRGSQYGGPG WPSYGEDEAG RREAVPRTSG REPSAPSGNL PHRGLQGPGL	1440
70	GYPTSSTEDL QPGHSSASLI KAIREELLRL SQKQSTVQNP HS	1482
	Seq ID NO: 314 Protein Sequence	
	Protein Accession #: BAC04820.1	
75	1 11 21 31 41 51	
13		60
	DPEDEEDEEP ALEELEGREV LVLGLDGAGK STFLRVLSGK PPLEGHIPTW GFNSVRLPTK	
	DFEVDLLEIG GSONLRFYWK EFVSEVDVLV FVVDSADRLR LPWARQELHK LLDKDPDLPV	180
00	VVVANKQDLS EAMSMGELQR ELGLQAIDNQ REVFLLAASI APAGPTPEEP GTVHIWKLLL	
80	ELLS	244
	Seq ID NO: 315 Protein Sequence	
	Protein Accession #: NP_066563.1	
	1 11 21 31 41 51	

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	MARRAGGARM LEPSSPSHWG X	i FGSLLLFALL QLPTPPLRDQ	AAGVAPLSMD RLQLSHDLLG	i Lpeprsrask Illikkalgv	I IRVHSRGNLW SLSRPAPQIQ	ATGHFMGKKS YRRLLVQILQ	60 120 121
5		316 Protein					
	Protein Acc	:ession #: N 11 !		31	41	51 i	
10	GFKETRASER RELRLRLDQL	AEMMELNDRP TANSARLEVE	MVGGLAPGRR ASYIEKVRFL RDNLAQDLAT	EQQNKALAAE VRQKLQDETN	lnqlrakept Lrleaennla	KLADVYQAEL AYRQEADEAT	60 120 180
15	QYEAMASSNM GTNESLEROM	Heaeewyrsk Reqeerhvre Egeenritip	RKIHEEEVRE FADLTDAAAR AASYQEALAR VQTPSNLQIR	NAELLRQAKH LEEEGQSLKD	EANDYRROLQ EMARHLQEYQ	SLTCDLESLR DLLNVKLALD	240 300 360 420 432
20		317 Protein	AAA19191.1		41	£1	
	 mpt.t.eet.ede	11 	21 PPIWKSYLYQ	 	41 	51 PKYYGREFHG	60
25	IISREQADEL IHDLVTDGLI THEEHTAVEK VRCSDCGLNV ARGLKSEGLY	LGGVEGAYIL TLYIETKAAE ISSLVRRAAL HKQCSKHVPN RVSGFTEHIE	RESQRQPGCY YISKMTTNPI THNDNHFNYE DCQPDLKRIK DVKMAFDRDG	TLALRFGNOT YEHIGYATLL KTHNPKVHTP KVYCCDLTTL EKADISANVY	LNYRLFHDGK REKVSRRLSR RGPHWCEYCA VKAHNTQRPM PDINIITGAL	HFVGEKRFES SKNEPRKTNV NFMWGLIAQG VVDICIREIE KLYFRDLPIP	120 180 240 300 360
30	VITYDTYSKP	IDAAKISNAD	ERLEAVHEVL TLTTLHDMRY	MLLPPAHYET	LRYLMIHLKK	VTMNEKDNFM	420 466
		318 Protei	n Sequence XP_113553.1				
35	1	11	21 	31	41	51 	
	RRDR INNSLS DYRSLGFREC	ELRRLVPSAF LAEVARYLSI	VEKESADENG EKOGSAKLEK IEGLDASDPL HGNAGTTASP	AEILQMTVDH RVRLVSHLNN	LKMLHTAGGK YASQREAASG	GYFDAHALAM AHAGLGHIPW	60 120 180 240
40	LPVVTSASKI IGAP	SPPLLSSVAS	LSAFPFSFGS	FHLLSPNALS	PSAPTQAANL	GKPYRPWGTE	300 304
		319 Protei	in Sequence NP_001927.2				
45	1 	11	2 <u>1</u> 	31 	41 	51 	
	NSLSQKKKVT	VEDLESEDE	E LVGSNPPQRN K IHDPEAKWIS	DTEFIYREQK	GTVRLWNVET	NTSTVLIEGK	60 120 180
50	QYAGWGPKG(QLIFIFENN	L FSYNVEPIYO I YYCAHVGKQA	IRVVSTGKE	VIYNGLSDWI		240 300
	GPTHDLEMMI	PODPRMREY	Y ITMVKWATS1	KVAVTWLNR	QNVSILTLC	ATTGVCTKKH S SNDNIQSITS	360 420
55	GDWDVTKIL	A YDEKGNKIYI	F LSTEDLPRRE	QLYSANTVGN	FNRQCLSCDI	VENCTYFSAS KVEYRDIEID	480 540
	DYNLPMQIL	K PATFTDTTH	Y PLLLVVDGT	GSQSVAEKF	VSWETVMVS	HGAVVVKCDG YGGYLSTYIL	600 660
	PAKGENQGQ QPLIIHPTA	T FTCGSALSP D EKIHPQHTA	I TOFKLYASAI E LITQLIRGK	F SERYLGLHGI	DNRAYEMTK	V AHRVSALEEQ K QHLYRSIINF	720 780
60		K LPTVTAKED					803
	Protein A		in Sequence XP_087461.: 21		41	51	
65	1	1	1	Ĩ.	Ī	 C WPRRPPGPPS	60
	ARARRRRRR	R RRLCNISVQ	R QMLSSLLVR	W GRPRGFQCD	L LLFSTNAHG	R AFFAAAFHRV A GAPTALPAYP	120
70	AAEPPGPLW	L QGEPLHFCC	L DESLEELQG	E PGWRLNRKP	I ESTLVACEM	T LVIVVWSVAA A AVTSGVATK	
			in Sequence NP_036393.				
75	1 MDLOGRGVE	11 S IDRLRVLLA	21 CL PHTMAQIMA	31 E OEVENLSGL	41 S THPEKDIFV	51 V RENGTTCLMA	60
	EFAAKFIVE FVKESHNMS	Y DVWASNYVI K GPEATWRLS	L ITEQADIAL	T RGAEVKGRO	G HSQSELQVE G KHTANSHHL	W VDRAYALKML S ALVTPAGKSY	120 180
80			T MILSAVHIQ H KMTANQVQI			R EQLEETLPLI	240 280
	Seq ID NO): 322 Prote					
	1	11	21	31	41	51	

	QSAGINYRKS CASSAACLIA SAGYQSFCSP GKLNSVCISC CNTPLCNGPR PKKRGSSASA	60 120 141
5	LRPGLRTTIL PLKLALFSAH C Seq ID NO: 323 Protein Sequence Protein Accession #: NP_004685	
10	1 11 21 31 41 51	60 120 180 240 300
15	GLFATLGFFA PSLYIIPLGI SLGIDODRAA FLLSTMAIAE VFGRIGAGFV LANGEIRKIY IELICVILLT VSLFAFTFAT EFNGLMSCSI FFGPMVGTIG GLTFHCLLKM MSNALQKMSS AAGVYIFIQS IAGLAGPPLA GLLVDGSKIY SRAFYSCAAG MALAAVCLAL VRPCKMGLCQ RHHSGETKVV SHRGKTLQDI PEDFLENDLA KNEHRVHVQM EPV	360 420 480 523
20	Seq ID NO: 324 Protein Sequence Protein Accession #: NP_004824.1 1 11 21 31 41 51 1	
25	MESKYKEILL LTGLDNITDE ELDRPKPFLS DEFNIATGKL HTANRIQVAT LMIQNAGAVS AVMKTIRIFQ KLMYMLLAKR LQEEKEKVDK QYKSYTKPKP LSQAEMSPAA SAAIRNDVAK QRADRVUSPH VKPEQKQMVA QQESIREGFQ KRCLPVMVLK AKKPFTFETQ EGKQEMFHAT VATEKEFFFV KVFNTLLKOK FIPKRIIIIA RYYRHSGFLE VNSASRVLDA ESDQKVNVPL NIIRKAGETP KINTLQTQPL GTIVMGLPVV QKVTEKKKNI LFDLSDNTGK MEVLGVRNED	60 120 180 240 300
30	TMKCKEGDKV RLTPPTLSKN GEKLQLTSGV HSTIKVIKAK KKT Seq ID NO: 325 Protein Sequence Protein Accession #: NP_005400.1	343
35	1 11 21 31 41 51 	60 94
40	Seq ID NO: 326 Protein Sequence Protein Accession #: NP_002553.1 1 11 21 31 41 51 MPACCSCSDV FQYETNKUTR IQSMNYGTIK WFFHVIIFSY VCFALVSDKL YQRKEPVISS WHTKVKGIAE VKEETVENGV KKLVHSVPDT ADYTFPLQGN SFFVMTNPLK TEGQEGRLCP	60 120
45	EYPTRITLCS SDRGCKKGWM DPOSKGIQTG RCVVHEGNQK TCEVSAMCPI EAVEEAPRPA LLISAENFTV LIKNNIDPPG HNYTTRILLP GINITCTFHK TONPOCPIFR LGDIFRETGD NFSDVAIQGG IMGIEIYWDC NLDRWPHHCH PKYSFRRLDD KTTNVSLYPG YNRYAKYYK ENNVEKRTLI KYPGIRPDIL VPGTGGKFDI IQLVVYIGST LSYFGLAAVF IDFLIDTYSS	180 240 300 360
50	NCCRSHIYPM CKCCOPCVVN EYYYRKKCES IVEPKPTLKY VSFVDESHIR WVNQQLLGRS LQDVKQGEVP RPAMDFTDLS RLPLALHDTP PIPGQPEEIQ LLRKEATPRS RDSPVMCQCG SCLPSQLPES HRCLEELCCR KKPGACITTS ELFRKLVLSR HVLQFLLLYQ EPLLALDVDS INSRLRHCAY RCYATWRFGS QDMADFAILP SCCRWRIRKE PPKSEQQYSG FKSPY	420 480 540 595
55	Seq ID NO: 327 Protein Sequence	60
60	QEPALFSTON DDFTVENGET VQERSLKER NPLKLFPSKR ILERHKROMV VAPISVEENG KOPPFQRLNQ LKSNKORDTK IPYSITGPGA DSPPECVFAV EKETGWLLLN KPLDREEIAK YELFGHAVSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT DEDDAIYTYN GTVAYSIHSQ EPKDPHDLMP TIRRSTGTIS VISSGLDREK VPEYTLTIQA TUMDGDGSTT TAVAVVEILD ANDNAPMFDP QKYEAHVPEN AVGHEVQRLT VTDLDAPNSP AWRATYLING GDDGDMFTIT THPESNQGIL TTRKGLDFFA KNOHTLYVEV TNEAFFVLKL	120 180 240 300 360 420
65	PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR DPAGHLAMDP DSGQYTAVGT LDREDEGPVR NNIYEVMVLA MDNGSPFTTG TGTLLLTLID VNDHGPVPEP RQITICNQSP VRQVLNITDK DLSPHTSPFQ AQLTDDSDIY WTAEVNEEGD TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDC HGHVETCPGP MKGGFILEVL GAVLALLFLL LVLLLLVRKK RKIKEPLLLP EDDTRDNVFY YGEEGGGEED QDYDITQLHR	480 540 600 660 720
70	GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIIE NLKAANTDPT APPYDTLLVF DYEGGGSDAA SLSSLTSSAS DQDQDYDYLN EMGSRFKKLA DMYGGGEDD Seq ID NO: 328 Protein Sequence	780 829
75	Protein Accession #: NP_002562.1 1	60 120 162
80	Seq ID NO: 329 Protein Sequence LEK6 Protein Accession #: NP_001318.1 1 11 21 31 41 51	
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	60

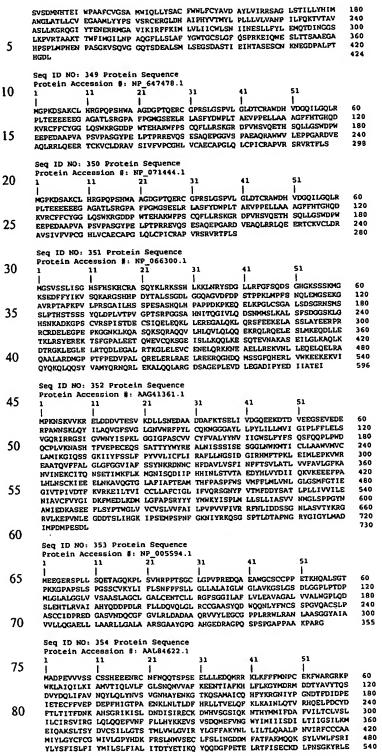
	PROPROGRAS GENGCERCON ROPESREDER TENTETT ENGENERAL VIII	120 180
5	Seq ID No: 330 Protein Sequence LEK6 Protein Accession 8: NP_066274 1	60
10	MQAEGOGTOG STCDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPRGGA PRGPHGGAAS AQDGRCPCGA RRPDSRLLQF RLTAADHRQL QLSISSCLQQ LSLLMWITQC PLPVFLAQAP SGQRR	120 135
	Seq ID NO: 331 Protein Sequence Protein Accession #: NP_008859.1 1 11 21 31 41 51	
15		60 120 180 240
20	ALQLHDPSGY LAEADLSYTM DFGDSSGTLI SRALVYTHTY LEFGPVTAQV VLQAAIPLTS CGSSFVPGTT DGRRPTAEAP NTTAGQVPTT EVVGTTPGQA PTAEPSGTTS VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM TPAEVSIVVL SGTTAAQVTT TEWVETTARE LPTPEPEGPD ASSIMSTESI TGSLGPLLDG TATLRLVKRQ VPLDCVLYRY	300 360 420 480
25	GSFSVTLDIV QGIESAEILQ AVPSGEIDAF ELTVSCOGGL PKEACHEISS PGCQPPAQRL COPVLPSPAC QLVLHQILKG GSGTYCLNVS LADTNSLAVV STQLIHPGQE AGLGQVPLIV GILLVLHAVV LASLIYRRRL HKQDFSVPQL PHSSSHMLRL PRIFCSCPIG ENSPLLSGOQ V	540 600 660 661
30	Seq ID NO: 332 Protein Sequence Protein Accession #: NP_001913.2 1	
35	MSPLWMGFLL SCLGCKILPG AGGGFPRVCM TVDSLVNKEC CPRLGAESAN VCGSQGGRQQ CTEVRADTRP WSGPYILRNQ DDRELWPRKP FHRTCKCTGN FAGYNOGDCK FGWTGBNCER KKPPVIRQNI HSLSPGEREG FLGALDLAKK RVHPDYVITT OHMLGLLGPN GTOPOFANCS VYDFFVNLHY YSVRDTLLGP GRPYRADIDS HQGPAFVTWH RYHLLCLERD LQRLIGNESF ALPYWNFATG RNECDVCTDQ LFGAARPDDP TLISRNSRFS SWETVCOSLD DYWHLVTLCN GTYEGLIRNN OMGRNSKKLP TLKDIRDCLS LQKFDNPPFF QNSTPSFRNA LEGFDKADGT	60 120 180 240 300 360
40	LDSQVMSLIM LVHSPLNGTN ALPHSAANDP IFVVLHSFTD AIPDEMMKRF NPPADAMPQE LAPIGHNRMY NMVPPPPPVT NEELPLTSDO LGYSYAIDLP VSVEETPGMP TTLLVVMGTL VALVGLFVLL APLQYRRLRK GYTPLMETHL SSKRYTEEA	420 480 519
45	Seq ID NO: 333 Protein Sequence	60
50	VICHIQUEAD GRIRQULAWV MRYGVNGVOK ILKKINKRIV SKKNKNIVTV ANAVFYKNAS EIEVPFVTRN KDVFQCEVRN VNPEDPASAC DSINAWVKNE TRDMIDNILS PDLIDGVLTR LVLVNAVYFK GLMKSRFQDE NTKKRTFVAA DGKSYQVPML AQLSVERGS TSAPNDLMYN FIELPYHGES ISMLIALPTE SSTPLSAIIP HISTKTIDSW MSIMVPKRYQ VUJPKFTAVA QTDLKEPLKV LGITDMPDSS KAMFAKITRS ENLAVSHILQ KAKIEVSEDG TKASAATTAI LIARSSPPWF IVDRPPLFFI RHNPTGAVLP MGQINKP	120 180 240 300 360 397
55	Seq ID NO: 334 Protein Sequence Protein Accession #: XP_040512.2 1 11 21 31 41 51	
60	PROHDTRIGR IVLISGRRSF CSIFSVLPYR DSTQVGDLKL DGGRQSTGAV SLKEIIGLEG VELGADGKTV SYTOPLLPTN AFGARRNTID STSSFSQFRN LSHRSLSIGR ASGTQGSLDT GSDLGDFMDY DPHLLDDPOM PCGKHKRVLI FPSYMTTVID YVKPSDLKKD MNETFKEKFP HIKLILSKIR SLKREMRKLA QEDGGLEEPT VAMAPVYFEK LALKGKLNKQ NRKLCAGACV LLAAKIGSDL KKHEVKHLID KLEEKFRLNR RELIAFEFPV LVALEFALHL PEHEVMPHYR	60 120 180 240 300 306
65	RLVQSS Seq ID NO: 335 Protein Sequence Protein Accession #: AAN08826	300
70	1 11 21 31 41 51	60 120 180 240
75	HYPDIYTREE LAQRAKLTEA RVQVWFSNRR ARWRKQAGAN QLMAFNHLIP GGFPPTAMPT LPTYQLSETS YQPTSIPQAV SDPSSTVHRP QPLPPSTVHQ STIPSNPDSS SAYCLPSTRH GPSSYTDSFV PPSGPSNPMN PTIGNGLSPQ NSIRHNLSLH SKPIRVQNEG TGKSKWMLN PEGGKSGKSP RRRASMDNN SKPAKSRSRA AKKKASLQSG QEGAGDSFGS QFSKWPASFG SHSNDDFDNM STFRPRTSSN ASTISGRUSP IMTEQDDLGE GDVMSMVYPP SAAKMASTLP	300 360 420 480 540
80	SLSEISNPEN MENLLDNINL LSSPTSLTVS TOSSPOTMMO OTPCYSFAPP NTSLNSPSPN YQKYTYGQSS MSPLPOMPIQ TLQDMXSSYG CMSQYNCAPG LLKELLTSDS PPHNDINTFY DPVAQPNSR VLGQNVMMGP NSVMSTYGSQ ASHNYOMNPS SHTHPGHAQQ TSAVNGRPLP HTVSTMPHTS GMRLTQVKT PYQVPLPHPM QMSALGGYSS VSSCMYGRM GLLHQEKLPS DLDGMFIERL DCDMESIIRN DLMDGDTLOP NFDNYLPNQS FPHSVKTTTH SWYSG	600 660 720

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	Seq ID NO: 3	36 Protein	Sequence				
	Protein Acce	ession #: N	P_005752.1	31	41	51	
_	1		Ī	ì	1	1	
5	MEVSRRKAPP I	RPPRPAAPLP	LLAYLLALAA I	PGRGADEPVW	RSEQAIGAIA	ASQEDGVFVA	60
	SGSCLDQLDY S	SLEHSLSRLY PCACEVERIC	RDQAGNCTEP '	VSLAPPARPR TEVVSCHPOG	PGSSFSKLLL STAGVVYRAG	RNNRWYLAVA	120 180
	ATYVLPEPET A	ASRONPAASD	HDTAIALKDT	EGRSLATQEL	GRLKLCEGAG	SLHFVDAFLW	240
10	NGSIYPPYYP	YNYTSGAATG	WPSMARIAQS	TEVLFQGQAS	LDCGHGHPDG	RRLLLSSSLV	300 360
10	EALDVWAGVF :	SAAAGEGQER	RSPTTTALCL GTVVMNRTVL	PRMSEIQAKA FLGTGDGOLL	KRVSWUFKTA	NCPEVIYEIK	420
	EETPVPYKLV :	PDPVKNIYIY	LTAGKEVRRI	rvanonkhks	CSECLTATOP	HCGWCHSLQR	480
	CTFQGDCVHS	ENLENWLDIS	SGAKKCPKIQ	IIRSSKEKTT	VTMVGSFSPR	HSKCHVRIVD	540 600
15	CVETCCAWCK	SARRCIHPET	PTRATYKOVS ACDPSDYERN	OEOCPVAVEK	TSGGGRPKEN	KGNRTNQALQ	660
	VFYIKSIEPQ :	KVSTLGKSNV	IVTGANFTRA	SNITHILKGT	STODKOVIQV	SHVLNDTHMK	720
	FSLPSSRKEM	KDVCIQFDGG	NCSSVGSLSY CVATYCGFLA	IALPHCSLIF	PATTWISGGQ	NITHINGRAFD	780 840
	REDPRETGYR	VESEVDTELE	VKIQKENDNP	NISKKDIEIT	LFHGENGQLN	CSFENITRNO	900
20	DLTTILCKIK	GIKTASTIAN	SSKKVRVKLG	NLELYVEGES	VPSTWYFLIV	LPVLLVIVIF	960
	AAVGVTRHKS	KELSRKQSQQ	LELLESELRK MENRDANDKN	EIRDGPAELQ	CNKSFLVTVI	HTLEKOKNES	1020 1080
	VKDRCLFASF	LTIALQTKLV	YLTSILEVLT	RDIMEQCSNM	QPKLMLRRTE	SAAEKTTIAM	1140
25	MSVCLSGFLR	ETVGEPFYLL	VTTLNQKINK	GPVDVITCKA	LYTLNEDWLL	WQVPEPSTVA	1200
25	LNVVFEKIPE OMCTPOKELL	NESADVCRNI DIDSSSVILE	SVNVLDCDTI DGITKLNTIG	GOAKEKIFOA HYRISNGSTI	KVFKKIANPT	SDVEYSDDHC	1260 1320
	HLILPDSEAF	QDVQGKRHRG	KHKFKVKEMY	LTKLLSTKVA	IHSVLEKLPR	SIWSLPNSRA	1380
	PFAIKYFFDF	LDAQAENKKI	TDPDVVHIWK	INSLPLREWV	NILKNPOFVF	DIKKTPHIDG	1440 1500
30	CLSVIAQAFM EEPLTOESKK	HENEFNEEVA	GKEAPTNKLL LTEIYKYIVK	YPDEILNKLE	RERGLEEAOK	QLLHVKVLFD	1560
	EKKKCKWM						1568
	Sec ID NO:	337 Protei	n Sequence				
26			XP_063670.1				
35	1	11	21	31	41	51	
	MORILEEPAD	DCTWSTRILL	TLSEFIMSLQ	RTVYPHSEKW	RALSVPSSSY	FOELVGTSQE	60
	LALTFWHLLS	MFGFFIVSYG	FLTAFGRTLF	HLDLLQPNLT	PSRFDKYTGL	FIYEIEGDGL	120
40	DPCFQSHVQG	ILEVLWMSKV	ESAYHTNDGD LCLPLVVMII	TAGEGVENGT	SQTRGGGGAR SAIPTSTWEE	RSRCREMEEP	180 235
40	IFBEVIVOVD	RODITACTVI	DCDI DVVIII			4	
		338 Protei		distant			
	Protein Acc	cession #:	FGENESH pre 21	31	41	51	
45	Ī		1	1	1	1	
	MEPSHSOPTM	DMKHMQERPA	ASPLKCQDGR	GSAQSPLSAA	GPGSPAPLG	LTPAEPGLGS LSKASAIATG	60 120
	TPPCEDSTIA	RFYLPPPLTI	HPELVGTSQE	LALTFWHLLS	MFGFFIVSY	FLTAFGRTLF	180
50	HLDLLQPNLT	PSRFDKYTGO	LLELPVHSKY	VLTIHWSQGI	. CIWSSHPCE/	GVENGTSQTR	240 300
20	GGGGAARSRC TSTWEEQHLD		VYVDVDKGLT	LACPVFLCLE	LVVMIIRCA	VIMDPYSAIP	311
			in Sequence FGENESH pre	dicted			
55	1	11	21	31	41	51	
	1	4	1	1	<u> </u>	1	
	MGKDFMSKTP	KAMATQAKII	NKWAKDMNR	CTAKETTIK	V NKOPTEWEK N RHMKKCSSS	I FAIYSSDEGL L AIREMQIKTT	60 120
	TRCHLTPVRM	ALIKKSGNN	R TAEEQPKLR	CEAVGSIEIF	R FADGLDITL	M ILGILASLVN	180
60	GACLPLMPLV	LGEMSDNLI	S GCLVQTNTT	YONCTOSOE	K LNEDMTLLT	L YYVGIGVAAL	240 300
	GDKIALLFON	MSTFSIGLA	V GLVKGWKLTI	. VTLSTSPLI	M ASAAACSRM	T DDIDKISDGI V ISLTSKELSA	360
	VSKAGAVAER	VLSSIRTVI.	A FRACEKELOS	YTONLKDAK	D FGIKRTIAS	K VSLGAVYFFM	420
65	NGTYGLAFWY	GTSLILNGE	P GYTIGTVLAV	/ FFSVIHSSY	C IGAAVPHFE P PSIKILKGL	T FAIARGAAFH N LRIKSGETVA	480 540
03	LVGLNGSGKS	TVVQLLQRL	Y DPDDGFIMVI	ENDIRALINV	R HYRDHIGY	S QEPVLFGTTI	600
	SNN I KYGRDI	VTDEEMERA	A REANAYDFI	4 EPPNKFNTL			660 698
	LVRNPKILII	L DEATSALDS	E SKSAVQAALI	E KOTPRISE		•	0,0
70			in Sequence				
			XP_166496.		41	51	
	1	11	1	31 	ï	ĵ.	
26	MVDENDIRA	L NVRHYRDHI	G VVSQEPVLF	G TTISNNIKY	G RDDVTDEE	E RAAREANAYD	60
75			M SGGQKQRIA	I ARALVRNPK	I LILDEATS	L DSESKSAVQA	120 131
	ALEKOTPRY						
			in Sequence				
80	Protein A	ccession #: 11	XP_166305. 21	1 31	41	51	
	Ĭ	1		-1	- 1	1	
	MEKFRAVLD	L HVKHHSALC	SY GLVTLLTAG	G ERIFSAVA	CPCSAAWNI	.P YGLVFLLVPA \P LTWVAVALLG	60 120
	GAFYECAAT	G SAAFAQRLO	L GRNRSCAAE	T brancesta	CA SDVQDLLKI	DL KAQSQVLGWI	180
				-			

	Liavviiill Fegshpkeyn Lgfvdssgin	TPSMKEWQQI	PVSFLQLKFW SSLYTFNPKG	ÖAAZWTHKAA Kiapeõeõõi	LKSKATEHAT NRKEKTHSIR	ELAKENIKCF STEGDTVIPV	240 300 315
5	Seq ID NO: Protein Acc			31	41	51	
10	KNSFWIHOVT	CRQLGFEAAL ICHPRRHRGY CDQGWTMINS CLGTEPHMAN	TWAHSAKYGQ LSETVSNALG RVVCGMLGPP CQVQVAPARG	GEGPIWLDNV PQGRRLEEVR SEVPVDSHYY KLRPACPGGM	QCVGTESSLD LKPILASAKQ RKVWDLKMRD HAVVSCVAGP	HSPVTEGAVE PKSRLKSLTN HFRPPKTKPQ	60 120 180 240 300
15	LFGARLGQGL VRLAGGRIPE WSGTPRAQEV LVOETAYLED	GPIHLSEVRC EGLLEVQVEV VMSGVRCSGT RPLSOLYCAH	EGRVEVLMNR RGYERTLSDC NGVPRWGSVC ELALQQCQRH EENCLSKSAD	PALEGSQNGC SENWGLTEAM GPVHCSHGGG HMDWPYGYRR	QHENAAAVRC VACRQLGLGP RFLAGVSCHD LLRFSTQIYN	NVPNMGFQNQ AIHAYKETWF SAPDLVMNAQ LGRTDFRPKT	360 420 480 540 600 660
20	FGEQGVTVGC	WDTYRHDIDC	QWVDITDVGP AELSLEQEQR	GNYIFQVIVN	PHYEVAESDP	GLQRRYACAN SNIMLQCRCK	720 756
25	Protein Acc	11	NP_001789.2 21 	31 ALKKIRLDTE	41 TEGVPSTAIR	51 EISLLKELNH	60
30	PNIVKLLDVI HRVLHRDLKP STAVDIWSLG	HTENKLYLVF QNLLINTEGA CIFAEMVTRR	EFLHODLKKF IKLADFGLAR	MDASALTGIP AFGVPVRTYT QLFRIFRTLG	LPLIKSYLFQ HEVVTLWYRA TPDEVVWPGV	LLQGLAFCHS PEILLGCKYY TSMPDYKPSF	120 180 240 298
35	Protein Ac 1 MENFOKVEKI	11 GEGTYGVVYK	NP_439892.1 21 ARNKLTGEVV	31 ALKKIRLDTE	41 TEGVPSTAIF	S1 EISLLKELNH	60
40	PNIVKLLDVI HRVLHRDLKP IFRTLGTPDE	HTENKLYLVE QNLLINTEGA	P EFLHODLKKI IKLADFGLAF DYKPSFPKW	MDASALTGII AFGVPVRTY	P LPLIKSYLF(F HEVTRRALF)	LLQGLAFCHS GDSEIDQLFR QMLHYDPYKR	120 180 240 264
45			in Sequence NP_116127.1 21 :	1 31 1	41	51 	
50	QVKAYTFSEE PPGPNREFSI EPQAGSPMTI EAATEDNQVV	FHLIVSYDWI TVVQKADSGI SCOTKLPLQI KQSPQLEIR	L ILQGPAKPVI H YHCSGIFQSI R SAARLLFSF	P EGDLLVLRC P GPGIPETAS Y KDGRIVQSR P TLNPAPQKS	Q AWQDWPLTQ V VAITVQELF G LSSEFQIPT A APGTAPEEA	DITDAREAGE TEYROGSALG PAPILRAVESA SEDHSGSYWC GPLPPPPTPS K PGTTKATAE	60 120 180 240 300 359
55			in Sequence NP_002337. 21	1 31	41	51	
60	 MKI FLPVLL VTFGHSLSK SLLPALLRF	T CSPACPIPE	s imcfsclho g vnvgvashg	K SNLYCLKPT I SCCQSFLCN	 CSDQDNYCV F SAADGGLRA	T VSASAGIGNL S VTLLGAGLLL	60 120 131
65	Protein A	ccession #:	in Sequence XP_113526. 21 	2 31 	41 	51 	
70	KSHLIQVER EEKMQEQLE KRLESEKQE	E KMQMELSHK R NRQCQQNLD L QEQLDLQHK	OR ARVELERAA DA ASKRLREKE UK CQEANQKIO	LS TSARNYERE ED SLAQAGETI DE LQASQEAR	TV DRNQELLTF IN ALKGRISEI AD HEQQIKDLE	IQ LEERAEQIRS II RQLQEREAGA Q WSVMDQEMRV IQ KLSLQEQDAA LL GRQEKMQETL	180 240
	VGLELENER GLEKARQQL ELTPAEYSP KSQSSSAEQ	L LAKLQSWER Q EELRQVSGQ Q LTRRMREAL S FLPSREEAL	L DOTMGLSIF L LEERKKRET D MVQKVHSHS T LRLKVEELF	kt pedlsrfv Th Ealarrloi Ba emeaolsoi BG ersrleeei	/E LQQRELALI CR VLLLTKERI AL EELGGQKQI KR MLEAQLERI	O KNSAVTSSAR X3 MRAILGSYDS XA DMLEMELKML XA LQGDYDQSRT	360 420 480 540
75	VAELKKQVE DCL1FKATS	S AELKNORLI P SGSKMOLLI	KE VFQTKIQEI ET EFSHTVGEI	FR KACYTLTG	'Q IDITTENQ'	EA AAASLPSSKE YR LTSLYAEHPG LE LFSRQTVA	600 660 718
80			ein Sequence : NP_000264 21 		41 	51 	
	MTQAGRRGI	G TPEPRPRT	OP MASPRIGT	FC CPTRDAAT	QL VLSFQPRA LL GCLGMVIR	FH ALCLGSGGLR ST VWLGFPNFVD 760	60 120





PEGETYAPTA LOGSENGIS GODAMEGARE HIRERECTE TYRDRECTVY CHLOITUNS SINSTARKTO REEGKYEVE DOOSAGALDL HIPRIMIPSS LALAPSTOPS CLEGGAP SEQ ID NO: 356 Protein Sequence Protein Accession 8: NP_00347.2 1 11 21 21 31 41 51 MGCGCSSHP DIMMENIEUVE DOCKEPLEIU II. SEVENDRAY YESSINPPASP LQDNIVIALH SYEPSINDOL GPEKGEPLEI LEQGISHMIA GILTOGEF IPPHFVAKAN SLEPEPHFR MILSHDAREN LLARCHTIGS FILESSETA GSSTSLYRED DONGSTVINE YKIRHLINGS PTISPHITPE CHECKIPHTY HASOGLETIL SERGOTROK RYMEDEVE V VKIRHLINGS PTISPHITPE CHECKIPHTY HASOLUTER SERGOTROK RYMEDEVE V VKIRHLINGS PTISPHITPE CHECKIPHTY HASOLUTER SERVICITY REPORTED AND AND AND AND AND AND AND AND AND AN		DDPPVSLFCC	CKK					553
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PEGTYAPTA LOGSENGING OBDANESARE HHRSRRCTC TYRDRECVTY CHLOITUNS SINSTREKTO REEGKIVEVE DOGSKOALDL HHPKLMFOSG LALAPSTCPR CLFOEGAP SEQ ID NO: 356 Protein Sequence Protein Accession 8: NP_003147.2 15	5				31	41	51	
Protein Accession 8: NP_005347.2 1 11 21 31 41 51	10	PGEGTVAPTA PEQTVPYGLS	LQGPSPGSPG NYRGSPRGKR	QEQAAEGAPE SAGPLPGNLQ	HHRSRRCTCP LSHRPHLRCA	TYKDKECVYY CVGRYDKACL	CHLDIIWINT HFCTQTLDVS	60 120 180 238
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HIGGOSSHER DOMNENDOV ÉNCHYPIVEL DEKATILIEM SEVERPLYT YESSNPASP LQONLYLALH SYPERHOOL GERGERIAL LEGSCHWAR GALTTOGEF PERFYNARA 20 PRETIKUMER KISRKOAERO LLAPONTHOS PLIRESESTA GSFSLSVADP DONOGEVVEN YKIRALDSKO PYISRITTPE GIAGOPGEVE MGYYKGHTEV AVKSLKOGSM SPDAFLARAN LKKOLGHORL YRLYAVYTOS PIVITITEME MISCHDENT MASCHKTISK LÜDAMAJAGE GMAPTERNY HIROLADANI LUSDTISCKI ADPGLARLIE DNEYTARECA KPPIKNTAPE ATMYGTFTIK SOWESCILL TELVHGRIP YPCHYNIEVI (MILERGYRMV RPDMCPEELY QUARLCWKER PEDRYFDYL RSVLEDFFTA TEGOYOPOP 25 Seq ID NO: 157 Protein Sequence Protein Accession 6: NP_005146.1 1 11 21 31 41 51 1 MAIAYLOSSC PSOPPSIALA SLSPTPSDEP GESGIETAM FSPDVALAVATA TETOPTVAT LOPGTPREE LESERTLEP ATSPLLVYTEV PEEPSQRATT VSTTMATATA TSTGDPTVAT VPATVATATP STPAAPPFTA TAVIRTTOKY RRILDELTIT VATAAATTPE APSPPTTAAV LDTEATPFOL VSTATSRERA LEPRATTORE DIEBRSTLUP GITTAGTEVA APSPPTTAAV LDTEATPFOL VSTATSRERA LEPRATTORE DIEBRSTLUP GITTAGTEVA APPRENTATA TIEDEPEVP VSGGPSGOFE LPEESTTOPD TAMEVUNVOG AAAKASSPRC TLPKGARCAP 35 GLIDANISOS SAAGLOPKS LIERKEVIJA VIVGGVVGAL FAAFLVTLLI YRHKKNDEGS YTLEEPKQAS VTYOKPDKOE BYA 40 1 11 21 31 41 51 1 11 21 31 41 51 1 MTGHYSHEM FPAGYGGSGF HTGSTSMSPS AALSTGKPHO SHPSYTOTEV SAPRILSAVG TPLHALGSFY RVITSAMPPS GALLAPPCI HLVAPPSSQL NVWNSVSSSE DIKPLFCLEG CINRONYPSTS POSILVEHICA TGGDRSSGKH YGVYSCDGKC GFPKRTIRKO LIYTCRONKO LERGANNEL LASSKRSV VOGURLAVGREAVO EERGSRERA SEEACATSG HEDWYBVEIL LERGANNEL TASSKRSV VOGULALATO HAADROLFTL VEHARRIPHP SULTLEDGVI LLRAGNINEL TASSKRSVS VOGULALATO HAADROLFTL VEHARRIPHP SULTLEDGVI LLRAGNINEL TASSKRSVS VOGULALATO HAADROLFTL VEHARRIPHP SULTLEDGVI LLRAGNINEL TASSKRSVS VOGULALATO HAADROLFTL VEHARRIPHP SULTLEDGVI LLRAGNINEL TASSKRSVS VOGULALATO HAADROLFTL VEHARRIPHP SULTLEDGVI LLRAGNINEL TASSKRSVS VOGULALATO HAADROLFTL VEHARRIPHP SULTLEDGVI LLRAGNINEL TASSKRSVS VOGULALATO HAADROLFTL VEHARRIPHP SULTLEDGVI LLRAGNINEL TASSKRSVS VOGULALATO HAADROLFT VEHARRIPHP SULTLEDGVI LLRAGNINEL TASSKRSVS VOGULALATO HAADROLFT VEHARRIPHP FORDSSTRAS PERSCHATS HAADROLFT VEHARRIPH SULTLEDGVI 1 11 11 11 11 11 11 11 11 11 11 11 11 1	15	1	11	21	31	41	51	
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Seq ID NO: 357 Protein Sequence Protein Accession #: NP_055469.1 1 11 21 31 41 51 MAIAYLOSSC PSQPPSSIAL SLSPTPSDFE QESGIETAMR FSPDVALAVS TTPAVLPTIN IOPVCTPFEE LESERPTLEP ATSPLVVTEV PEEPSQRATT VSTTMATTAA TSTGDFTVAT VPATVATATP STRAAPPFTA TTAVIRTTOR RRILDELPLT VATARATTPE APSPETTAAV LDTEAPTPEL VSTATSAPPA LPRATTORE DIERSTLPL, GTTACOPTEV AUGTTEFTEL 35 GLIDNAIDGS SAAQLONGS ILEREVALVA VIVGGVVGAL FAAFLVTLLI YRKKKDEGS YTLEEPKQAS VTYOKPDKQE EFVA Seq ID NO: 359 Protein Sequence Protein Accession #: NP_008848.1 1 11 21 31 41 51 MYGNYSHFMK PFAGYGGSPG HTGSTSMSPS AALSTGKPMD SHPSYTDTPV SAPRTLSAVG TPLNALGSPY RVITSAWGIPP SGALMAPPGI HLVAPPSSGL MYVNSVSSSE DIRELEGLEG GENERYSTR COLORSSGKH YGVSCECK GPFKRIRKD LIVTCOBNKD MOMENSENCE LANGUNGHIC LORDSSGKH YGVSCECK GPFKRIRKD LIVTCOBNKD MOMENSENCE LANGUNHUCH ACCESSION # SHAADKOLFTL VEHAKRIPHP SULTLEDQUI LIRAGMWELL IASFSHRSVS VOOGILLATG LHVIRSSARS AGVOSIFDRV LTELVSKNKD MOMENSELGC LANGUNHUNG ANGUNSPES TETRERVYAT LEAVKRIPHP EQPGRFAKLL LALPALRSIG LKCLEHLFFF KLIGDTPIDT FLAMMLETPL QIT Seq ID NO: 359 Protein Sequence Protein Accession #: NP_002176.1 1 11 21 31 41 51 Seq ID NO: 359 Protein Sequence Protein Accession # NP_002176.1 Seq ID NO: 359 Protein Sequence Protein Accession # NP_002176.1 Seq ID NO: 359 Protein Sequence Protein MCCESSION # NF NP NP NP NP NP NP NP NP NP NP NP NP NP	20	VRLYAVVTQE IHRDLRAANI SDVWSFGILL	PIYIITEYME LVSDTLSCKI TEIVTHGRIP	NGSLVDFLKT ADFGLARLIE YPGHTNPEVI	PSGIKLTINK DNEYTAREGA	LLDMAAQIAE KPPIKWTAPE	GMAPIEERNY AINYGTPTIK	300 360 420 480 509
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1 11 21 31 41 51 MSELEKANVA LIDVPHQYSG REGDKHKLKK SELKELINNE LSHFLEEIKE QEVVDKVMET LDNDGDGECD FQEFMAFVAM VTTACHEFFE HE Seq ID NO: 361 Protein Sequence Protein Accession #: NP_006148.1 75 1 11 21 31 41 51 MPMDLILVVM FCVCTARTVV GFGMDPDLQM DIVTELDLVN TTLGVAQVSG MMNASKAFLF QDIERINAA PHYSEKLIQL FQNKSEFTIL ATVQKVESTS GVILSIRELE HSYFELESSG LERDETRYHYI HNGKPRTEAL PYRMADGOMH KVALSVSASH LLLMVDVDRI YERVIDPPDT NLPPGINLML GQRNQKHGLP KGIIQDGKII FMPNGYITQC PNLNHTCPTC SDFLSVQGI MDLQELLAKM TAKLMYAETR LSQLENCHGE KTCQVSGLLY RDQDSWVDGH HCRNTCKSG AVECRMSCOP PLINCSPOSLEV HILAGQCKV CRPKCIYGGK VLAEGGRILT KSCRECRGGV LVKITEMCPP LNCSEKDHIL PENQCCRVCR GHNFCAEGPK CGENSECKNW NTKATCECKS GYISVQGDSA YCEDIDECAA KMHYCHANTV CVNLPGLYRC DCVPGYIRVD DFSCTEIDEC	60	ESPLDCQIHE FGRDSSLTCI LQSGILTLNI	VDDIQARDEN AGNVSACDAI VAQGQPILT:	EGFLQDTFP(FILSSSRSLDG LGSNQEEAY	QLEESEKQRI RESGKNGPH	GGDVQSPNCI	SEDVVVTPES	360 420 459
70 MSELEKANVA LIDVPHQYSG REGDKHKLKK SELKELINNE LSHFLEEIKE QEVVDKVMET LDNDGDGCD FQEFMAFVAM VTTACHEFFE HE Seq ID NO: 361 Protein Sequence Protein Accession #: NP_006148.1 75 1 11 21 31 41 51 MPMDLILVVM FCVCTARTVV GFGMDPDLQM DIVTELDLVN TTLGVAQVSG MMNASKAFLF QDIEREIRAA PHVSEKLIQL FQNKSEFTIL ATVQQKPSTS GVILSTRELE HSYFELESSG NEBELTNYTH INGKPRTEAL PYRMADGOMH KVALSVASH LLLHVVORHT YERVIDPPDT NLPPGINLML GQRNQKHGLP KGI1QDGKII FMPNGYITQC PNLNHTCPTC SDFLSVQGI MDLQELLAKM TAKLMYAETR LSQLENCHGE KTCQVSGLLY RQDSWVDGD HCRNCTCKSG AVECRMSCOP PLINCSPOSLEV WHIAGQCKIV CPRKCIYGGK VLAEGGRILT KSCRECRGGV LVKITEMCPP LNCSEKDHIL PENQCCRVCR GHNFCAEGPK CGENSECKNW NTKATCECKS GYISVQGDSA YCEDIDECAA KMHYCHANTV CVNLPGLYRC DCVPGYIRVD DFSCTEIDEC	65	Protein Ad	cession #:	NP_006263.				
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762	80	nlppginlw MDLQELLAK AVECRRMSC LVKITEMCP	L GORNOKHGL M TAKLNYAET P PLNCSPDSL P LNCSEKDHI	P KGIIQDGKI R LSQLENCHC P VHIAGQCCK L PENQCCRVC	I FMPNGYITQ E KTCQVSGLL V CRPKCIYGG R GHNFCAEGP	C PNLMHTCPT Y RDQDSWVDG K VLAEGQRIL K CGENSECKN C DCVPGYIRV	C SDFLSLVQGI D HCRNCTCKSG T KSCRECRGGV W NTKATCECKS D DFSCTEHDEC	240 300 360

5	GSGQHNCDEN A FTGSHCEKDI I ALRTHTCWND S DGKIFCRRTA C GEVDCWPLTC I WTMAGSPCTT C	DECSEGIIEC I BACINLAGGP I DCQNPSADL I PNLSCEYTAI I	ENHSRCVNLP OCLCPSGPSC FCCPECDTRV LEGECCPRCV	GWYHCECRSG SGDCPHEGGL TSQCLDQNGH	FHDDGTYSLS (KHNGQVWTLK KLYRSGDNWT	GESCIDIDEC EDRCSVCSCK HSCQQCRCLE	540 600 660 720 780 810
10	MGSNSGOAGR I	ession #: N 11 	P_057264.1 21 	31 PTSRLINHSM	 AMFGREFCYA	51 VEAAYVTPVL	60
15	LSVGLPSSLY LNGATVVAAL HYHALFTGFG PLTEVAKGIP MTLKSLLRAL LIYERGVEVG	Sivwplspil Ianprrklvw Galgyllgai PQQTPQDPPL VNMPPHYRYL	GFLLQPVVGS AISVTMIGVV DWAHLELGRL SSDGMYEYGS CISHLIGWTA	ASDHCRSRWG LFDFAADFID LGTEFQVMFF IEKVKNGYVN FLSNMLFFTD	RRRPYILTLG GPIKAYLFDV PSALVLTLCP PELAMQGAKN PMGQIVYRGD	VMMLVGMALY CSHQDKEKGL TVHLCSISEA KNHAEQTRRA. PYSAHNSTEF	120 180 240 300 360 420
20	VYSTLVLCSL CMVQLAQILV	PGVMSSTLYT	VPFNLITEYH	REEEKERQQA	PGGDPDNSVR	GKGMDCATLT	480 530
	Seq ID NO: Protein Acc			31	41	51	
25	 MELALLOGLY	ADHIRLÓGCE AMYCAI bióg I	TAKDAAKANE GITMTNKWAK 	 QVTGKMPILS	AMBAGCHCGT CEMCEGÓTCY CEMCEGÓTCY	GGRGQPKDAT CDKEVAFCLK	60 120 145
30		364 Protein					
	1	11	21 	31 DOCUMENT	41 EGTLRLGGLW	CITAL BOTTO	60
35	FVGTLLLPLC PPGAQEKEQD GGDFDPHAFA FOETKTGELN	LATPLTVSLR QVNNKVLMWR SAIFFMCLFS SRLSSDTTLM	ALVAGASRAP LLKLSRPDLP FGSSLSAGCR SNWLPLNANV	PARVASAPWS LLVAAFFFLV GGCFTYTMSR LLRSLVKVVG	WLLVGYGAAG LAVLGETLIP INLRIREQLF LYGPMLSISP	LSWSLWAVLS HYSGRVIDIL SSLLRQDLGF RLTLLSLLKM	120 180 240 300
40	QCRQLYWRRD SYVQTLVYIY PDRPVLKGLT YLHSQVVSVG	LERALYLLIR GDMLSNVGAA FTLRPGEVTA QEPVLFSGSV	RVLHLGVQMI EKVFSYMDRQ LVGPNGSGKS RNNIAYGLQS	MLSCGLQQMQ PNLPSPGTLA TVAALLQNLY CEDDKVMAAA	DGELTQGSLL PTTLQGVVKF QPTGGQVLLD	EVCRYKEALE SFMIYQESVG QDVSFAYPNR EKPISQYEHC EMEHGIYTDV	360 420 480 540 600
45		QKQRLAIARA 365 Protei		•			630
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50	 MKKSGVLFLL IEIIATLKNG QKKTT	 GIILLVLIGV VQTCLNPDS#	QGTPVVRKGI QCTPVVRKGI	CSCISTNOGT	K NGKKHÖKKK L IHTÖSTKOTA	QFAPSPSCEK LKVRKSQRSR	60 120
55		366 Protestession #:		1 31	41	51	
60	i Marslyclgv Fltihrggvv Vktokwdfyc	YVPSKLKGR	P GVRGGPMPK G RLFWGGSVQ	L ADRKLCADO G DYYGDLAAR	E ČSHPISMAVI L GYFPSSIVRI	A LQDYMAPDCR E DQTLKPGKVD	60 120 131

It is understood that the examples described above in no way serve to limit the true

scope of this invention, but rather are presented for illustrative purposes. All publications,
sequences of accession numbers, and patent applications cited in this specification are herein
incorporated by reference as if each individual publication or patent application were
specifically and individually indicated to be incorporated by reference.





WHAT IS CLAIMED IS:

1	1.	A method for determining the presence or absence of a pathological cell in a
2	patient, said n	nethod comprising detecting a nucleic acid comprising a sequence at least 80%
3	identical to a	sequence as described in Tables 2A-68 in a biological sample from said patient,
4	thereby deten	mining the presence or absence of said pathological cell.
1	2.	The method of Claim 1, wherein:
2		d pathology is described in Table 1, including a cancer; and/or
3	•	d biological sample comprises isolated nucleic acids.
,	U) Sai	d biological sample comprises isolated nucleic acids.
1	3.	The method of Claim 1, wherein said biological sample is tissue from an organ
2	which is affect	cted by said pathology of Table 1, including a cancer.
1	4.	The method of Claim 2, wherein said nucleic acids are mRNA
1	5.	The method of Claim 2:
2		ther comprising a step of amplifying nucleic acids before said step of detecting
3		id nucleic acid; or
4		here said detecting is of a protein encoded by said nucleic acid.
7	0) WI	nere said detecting is or a protein encoded by said indiciere acid.
1	6.	The method of Claim 1, wherein said nucleic acid comprises a sequence as
2	described in	Tables 2A-68.
1	7.	The method of Claim 2, wherein:
2	a) sa	id detecting step is carried out by:
3	i)	using a labeled nucleic acid probe;
4	ii	utilizing a biochip comprising a sequence at least 80% identical to a sequence
5		as described in Tables 2A-68, Sr
6	ii	i) detecting a polypeptide encoded by said nucleic acid; or
7	b) sa	id patient is:
8	i)	undergoing a therapeutic regimen to treat said pathology of Table 1; or
9	ii) is suspected of having said pathology or cancer.
1	8.	An isolated nucleic acid molecule comprising a sequence as described in
2	Tables 2A-6	8.



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9. 1 The nucleic acid molecule of Claim 8, which is labeled. 1 10. An expression vector comprising the nucleic acid of Claim 8. 1 11. A host cell comprising the expression vector of Claim 10. 1 12. An isolated polypeptide which is encoded by a nucleic acid molecule 2 comprising a sequence as described in Tables 2A-68. 13. An antibody that specifically binds a polypeptide of Claim 12. 1 14. The antibody of Claim 13: 1 2 a) conjugated to an effector component; 3 b) conjugated to a detectable label, including a fluorescent label, a radioisotope, or a 4 cytotoxic chemical; 5 c) which is an antibody fragment; or 6 d) which is a humanized antibody. 1 15. A method for specifically targeting a compound to a pathological cell in a 2 patient, said method comprising administering to said patient an antibody of Claim 13, 3 thereby providing said targetting. 1 16. A method for determining the presence or absence of a pathological cell in a 2 patient, said method comprising contacting a biological sample with an antibody of Claim 13. 1 17. The method of Claim 16, wherein: 2 a) said antibody is conjugated to: 3 i) an effector component; or ii) a fluorescent label; or 5 b) said biological sample is a blood, serum, urine, or stool sample. 1 18. A method for identifying a compound that modulates a pathology-associated

polypeptide, said method comprising the steps of:





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3	a) contacting said compound with a pathology-associated polypeptide, said
4	polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence
5	at least 80% identical to a sequence as described in Tables 2A-68; and
6	b) determining the functional effect of said compound upon said polypeptide.
1	19. A drug screening assay comprising the steps of:
2	a) administering a test compound to a mammal having a pathology of Table 1 or a
3	cell isolated therefrom; and
4	b) comparing the level of gene expression of a polynucleotide that selectively
5	hybridizes to a sequence at least 80% identical to a sequence as described in
6	Tables 2A-68 in a treated cell or mammal with the level of gene expression of said
7	polynucleotide in a control cell or mammal, wherein a test compound that
8	modulates said level of expression of the polynucleotide is a candidate for the
9	treatment of said pathology.
10	

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Declaration under Rule 4.17:

of inventorship (Rule 4.17(iv)) for US only

Published:

- with international search report
- before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments
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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

25138 A3

(54) Title: METHODS OF DIAGNOSIS OF CANCER COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers. Related methods and compositions that can be used for diagnosis and treatment of those cancers are disclosed. Also described herein are methods that can be used to identify modulators of selected cancers.





INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/29560 CLASSIFICATION OF SUBJECT MATTER IPC(7) : C12Q 1/68 US CL 435/6 According to International Patent Classification (IPC) or to both national classification and IPC FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) U.S.: 435/6, 7.1, 287.2; 436/63, 64 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the International search (name of data base and, where practicable, search terms used) Please See Continuation Sheet DOCUMENTS CONSIDERED TO BE RELEVANT Relevant to claim No. Category * Citation of document, with indication, where appropriate, of the relevant passages US 6,426,186 B1 (JONES et al.) 30 July 2002 (30.07.2002), see especially Detailed 1-6 X,P Description of the Invention and Sequence 62. Y,P US 6,194,158 B1 (KROES et al.) 27 Pebruary 2001 (27.02.2001), see especially 2-5 X Background of the Invention and Detailed Description of the Invention. 1.6.7 Y US 6,440,676 B1 (KROES et al.) 27 August 2002 (27.08.2002), see especially Background 2-5 X,P of the Invention and Detailed Description of the Invention. Y,P 1, 6, 7 US 6,500,938 B1 (AU-YOUNG et al.) 31 December 2002 (31.12.2002), see especially 1-7 Y,P Summary of the Invention and Description of the Invention. 1-7 SMYTH TEMPLETON et al. Cloning and Characterization of Human Tumor Cell Insterstitial Collagenase. September 1990, Volume 50, Number 17, pages 5431-5437, especially Figure 2. Further documents are listed in the continuation of Box C. See patent family annex. later document published after the international filing date or priority date and not in conflict with the application but clied to understand the principle or theory underlying the invention Special categories of cited documents: document defining the general state of the art which is not considered to be of particular relevance document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone earlier application or patent published on or after the international filing date document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as document of particular relevance; the chalmed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art specified) document referring to an oral disclosure, use, exhibition or other means document published prior to the international filing date but later than the priority date claimed ·&" document member of the same patent family Date of mailing of the international search report Date of the actual completion of the international search 03 March 2003 (03.03.2003) Authorized officer Ardin Marsh Name and mailing address of the ISA/US

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Washington, D.C. 20731



INTERNATIONAL SEARCH REPORT

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Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)
This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
Claim Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
Claim Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)
This International Searching Authority found multiple inventions in this international application, as follows: Please See Continuation Sheet x
As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite
payment of any additional fee. 3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; It is covered by claims Nos.: 1-7 for Specie A(hemangiomas) and B (SEQ ID NO: 1)
Remark on Protest The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet(1)) (July 1998)



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This application contains the following inventions or groups of inventions, which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional examination fees must be paid.

Groups 1-104,648, claim(s) 1-7, drawn to a method for determining the presence or absence of a pathological (Specie A) cell in a patient via detection of polynucleotides that are at least 80% identical to listed sequences (Specie B). If electing from this Group Set, Applicants are asked to elect one species from A and B. Species A has 254 possibilities (see Table 1). Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions in this Group Set including all possible combinations of Species A and B is 104,648.

Groups 104,649-105,060, claim(s) 8-12, drawn to an isolated nucleic acid molecules from Tables 2A-68, expression vectors, host cells, and polypeptides encoded by nucleic acid molecules with listed sequences from Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 105,061-105,472, claim(s) 13-14, drawn to an antibody that binds to a polypeptide encoded by a polynucleotide with sequences from Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 105,473-105,884, claim(s) 15, drawn to a method for targeting a compound to a pathological cell in a patient via administering an antibody that binds to a polypeptide encoded by a polynucleotide from Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 105,885-106,296, claim(s) 16-17, drawn to a method for determining the presence or absence of a pathological cell in a patient via contacting the sample with an antibody that binds to a polypeptide encoded by a polynucleotide from Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 106,297-106,708, claim(s) 18, drawn to a method for identifying a compound that modulates a pathology-associated polypeptide encoded by a polynucleotide that hybridizes to a sequence in Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 106,709-211,356, claim(s) 19, drawn to drug screening assay by administering a compound to a mammal or cell having a pathology (of Table 1) and comparing the level of gene expression of a polynucleotide that hybridizes to a sequence that is 80% identical to sequences as described in Tables 2A-68 (Species B) to gene expression in control cells or mammals. If electing from this Group Set, Applicants are asked to elect one species from A and B. Species A has 254 possibilities (see Table 1). Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions in this Group Set including all possible combinations of Species A and B is 104,648.

This International Searching Authority considers that the international application does not comply with the requirements of unity of invention (Rules 13.1, 13.2, and 13.3) for the reasons indicated below:

The inventions listed as all Group Sets (Groups 1-211,356) do not relate to a single general inventive concept under PCT Rule 13.1, because under PCT Rule 13.2 they lack the same or corresponding special technical features for the following reasons:

Groups 1-104,648 and Groups 105,472-211,356 are directed to methods or assays which vary in one or more of the following: reactants, steps, and/or goals which are not coextensive and which do not share the same technical feature. Groups 104,649-105,472 have two separate special technical features, a nucleic acid and an antibody, respectively. These are directed to different chemical entity types regarding the critical limitations featuring different structures and functions. The antibodies undergo recognition and binding reactions

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wherein what is bound is different from what is bound by the compositions including the nucleic acids. Thus, in summary, each Group is directed to a different special technical feature and thus supports this lack of unity.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single general inventive concept under PCT Rule 13.1.

In order for more than one species to be examined, the appropriate additional examination fees must be paid. The species are as follows:

The claims in the Groups 1-104,648 and 106,709-211,356 include a series of species A directed to different pathologies which are listed in Table 1. Each of these types of pathologies are separate entities which affect patients differently, meaning each has its own special technical feature.

The claims in all Groups (1-211,356) include a series of species B directed to nucleic acid sequence listed (412 possibilities) which are considered separate as each defines its own special technical feature.

The first listed pathology (Specie A) and SBQ ID NO: 1 (Species B) will be automatically searched. For each additional Group with a specie combination elected, the fee is an additional \$210.00.

Continuation of B. FIELDS SEARCHED Item 3:

WEST, PUBMED, BIOSIS, CAPLUS, MEDLINE, SCISEARCH, EMBASE searching terms: diagnosis, cancer, screen, modulator, pathological cell, patient, nucleic acid, tissue, mRNA, detect, probe, blochip, array, therapeutic

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